



Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCGGACGCCCCCTCTCCA 20  
1 GAGCGGACGCCCCCTCTCCA 20

Db

RESULT 2  
LOCUS AX286668 57 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 9 from Patent WO0181554.  
ACCESSION AX286668  
VERSION AX286668.1 GI:17048736  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Conzelmann,K.K.  
TITLE Pneumovirus ns proteins antagonising the interferon (ifn) response  
JOURNAL Patent: WO 0181554-A 9 01-NOV-2001;  
Conzelmann, Karl-Klaus, Prof. Dr. (DE)  
Location/Qualifiers

FEATURES  
source 1..57  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer hns1-Nor15"

ORIGIN

Query Match  
Best Local Similarity 77.0%; Score 15.4; DB 6; Length 57;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGCGGACGCCCCCTCTC 18  
6 AGCGGACGCCCCCTCTC 22

Db

RESULT 3  
LOCUS A00424/c 60 bp DNA linear PAT 28-JAN-1993  
DEFINITION Nucleotide sequence 11 from patent number WO8903877.  
ACCESSION A00424  
VERSION A00424.1 GI:14496  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 60)  
AUTHORS Nigon,V.M.  
TITLE INTEGRATION AND EXPRESSION VIRAL VECTORS  
JOURNAL Patent: WO 8903877-A 11 05-MAY-1989;  
Institut de la Recherche Agronomique  
Location/Qualifiers

FEATURES  
source 1..60  
/organism="unclassified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match  
Best Local Similarity 74.0%; Score 14.8; DB 6; Length 60;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCGGACGCCCCCTCTCC 19  
22 AGCGGACGCCCCCTCTAC 5

Db

RESULT 4  
LOCUS CQ818714 70 bp DNA linear PAT 07-JUN-2004

DEFINITION Sequence 144 from Patent WO2004039825.  
ACCESSION CQ818714  
VERSION CQ818714.1 GI:48427320  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS fresky Rd,P.O., Franch,T., Gouliayev,A.H., Lundorf,M.D., Felding,J.,  
Olsen,E.K., Holcman,A., Jakobsen,S.R., Sans,C., Glad,S.S.,  
Jensen,K.B. and Pedersen,H.  
TITLE Enzymatic encoding  
JOURNAL Patent: WO 2004039825-A 144 13-MAY-2004;  
Nuevolucion A/S (DK)  
Location/Qualifiers

FEATURES  
source 1..70  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Artificially produced"  
46..50  
/note="n represents inosine (I)"

ORIGIN misc\_feature

Query Match  
Best Local Similarity 74.0%; Score 14.8; DB 6; Length 70;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGGACGCCCCCTCTC 18  
17 GAGCGGACGCCCCCTCTC 34

Db

RESULT 5  
LOCUS CHKER5LD/c 80 bp DNA linear VRT 28-APR-1993  
DEFINITION Chicken RAV-O endogenous retrovirus, 5' leader region.  
ACCESSION M13372  
VERSION M13372.1 GI:211747  
KEYWORDS mutational analysis.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 80)  
AUTHORS Katz,R.A., Terry,R.W. and Skalka,A.M.  
TITLE A conserved cis-acting sequence in the 5' leader of avian sarcoma  
virus RNA is required for packaging  
JOURNAL J. Virol. 59 (1), 163-167 (1986)  
PUBMED 3012114  
COMMENT Original source text: Chicken DNA, clone pUD62.  
Draft entry and clean copy of sequence for [1] kindly provided by  
R.A.Katz, 10-Oct-1986.  
The 5' leader of the RAV-O endogenous retrovirus was inserted into  
Rous sarcoma virus (SR-B). Deletions (positions 17-47) in the 5'  
leader region of the insert resulted in loss of infectivity of  
SR-B, although the envelope gene was expressed normally. The  
amount of mutant viral RNA encapsidated into virions was severely  
reduced, despite the presence of helper-virus. The deleted DNA is  
probably an essential cis-acting packaging signal in SR-B.  
Location/Qualifiers

FEATURES  
source 1..80  
/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9031"  
<1..>80  
/product="env mRNA"

ORIGIN mRNA

Query Match  
Best Local Similarity 74.0%; Score 14.8; DB 5; Length 80;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



QY 2 AGCGGACGCCCTCTCC 19  
DB 23 AGCGGACGCCCTCTAC 6

RESULT 6  
LOCUS AX523638/c 81 bp DNA linear PAT 24-OCT-2002  
DEFINITION Sequence 18 from Patent WO02064760.  
ACCESSION AX523638  
VERSION AX523638.1 GI:24412440  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Mueller,R., Thalhofer,J.P., Geipel,F., Glaser,S., Hoelke,W.,  
Schoen,H. and Kirschaum,T.  
TITLE Expression of recombinant proteinase k from tritirachium album in  
yeast  
JOURNAL Patent: WO 02064760-A 18 22-AUG-2002;  
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)  
FEATURES  
source 1..81  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 81;  
Best Local Similarity 88.9%; Pred. No. 7.5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTCCA 20  
DB 75 GCGGACGACCCGCTCCA 58

RESULT 7  
LOCUS AX538742/c 81 bp DNA linear PAT 23-NOV-2002  
DEFINITION Sequence 18 from Patent WO02072634.  
ACCESSION AX538742  
VERSION AX538742.1 GI:25271389  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Mueller,R., Thalhofer,J.P., Rexer,B., Schmuck,R., Geipel,F.,  
Glaser,S., Schoen,H., Meier,T., Rudolph,R., Lalle,H. and Schott,B.  
TITLE Recombinant proteinase k  
JOURNAL Patent: WO 02072634-A 18 19-SEP-2002;  
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)  
FEATURES  
source 1..81  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 81;  
Best Local Similarity 88.9%; Pred. No. 7.5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTCCA 20  
DB 75 GCGGACGACCCGCTCCA 58

RESULT 8  
LOCUS CQ008211 50 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 6851 from Patent WO0147944.  
ACCESSION CQ008211  
VERSION CQ008211.1 GI:41014903  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shinkels,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0147944-A 6851 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES  
source 1..50  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
25..26  
/note="Nucleotide deleted between bases 25 and 26  
Accession number cg43950268"

misc\_Feature  
ORIGIN  
Query Match 72.0%; Score 14.4; DB 6; Length 50;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGAGCCCTCTCCA 20  
DB 17 GCGAGCCCACTCCA 32

RESULT 9  
LOCUS AX073623 55 bp DNA linear PAT 06-FEB-2001  
DEFINITION Sequence 14 from Patent WO0104335.  
ACCESSION AX073623  
VERSION AX073623.1 GI:12710046  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Buchholz,U., Collins,P.L., Murphy,B.R., Whitehead,S.S. and  
Kremp,C.D.  
TITLE Human-bovine chimeric respiratory syncytial virus vaccines  
JOURNAL Patent: WO 0104335-A 14 18-JAN-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)  
FEATURES  
source 1..55  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="Synthetic respiratory syncytial virus"

ORIGIN  
Query Match 72.0%; Score 14.4; DB 6; Length 55;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTC 18  
DB 22 GCGGCCGCCCTCTC 37

RESULT 10  
LOCUS AX359862 55 bp DNA linear PAT 13-FEB-2002

```

DEFINITION Sequence 13 from Patent WO0200693.
ACCESSION AX359862
VERSION AX359862.1 GI:18675538
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Krempel,C.D., Collins,P.L., Murphy,B.R., Buchholz,U. and
TITLE Whitehead,S.S.
JOURNAL Respiratory syncytial virus vaccines expressing protective antigens
from promotor-proximal genes
Patent: WO 0200693-A 13 03-JAN-2002;
FEATURES
location/Qualifiers
source 1..55
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial Respiratory Syncytial Virus"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 55;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGCGAGCCCTCTC 18
| | | | | | | | | | | | | | | |
Db 22 GCGGCGAGCCCTCTC 37

RESULT 11
LOCUS AX286671 60 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 12 from Patent WO0181554.
ACCESSION AX286671
VERSION AX286671.1 GI:17048739
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Conzelmann,K.K.
TITLE Pneumovirus ns proteins antagonising the interferon (ifn) response
JOURNAL Patent: WO 0181554-A 12 01-NOV-2001;
FEATURES
location/Qualifiers
source 1..60
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer mNS1-NC1BCORV5"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 60;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGCGAGCCCTCTC 18
| | | | | | | | | | | | | | | |
Db 10 GCGGCGAGCCCTCTC 25

RESULT 12
LOCUS CQ818711 71 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 141 from Patent WO2004039825.
ACCESSION CQ818711
VERSION CQ818711.1 GI:48427317
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
FEATURES
location/Qualifiers
source 1..71
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
| | | | | | | | | | | | | | | |
Db 17 GAGCGGAGCCCTCTC 32

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REFERENCE
1
AUTHORS freskg Rd,P.O., Franch,T., Goulliaev,A.H., Lundorf,M.D., Felding,J.,
Olsen,E.K., Holtmann,A., Jakobsen,S.R., Sams,C., Glad,S.S.,
Jensen,K.B. and Pedersen,H.
TITLE Enzymatic encoding
JOURNAL Patent: WO 2004039825-A 141 13-MAY-2004;
FEATURES
location/Qualifiers
source 1..71
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
misc_feature 47..51
/note="n represents inosine (I)"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
| | | | | | | | | | | | | | | |
Db 17 GAGCGGAGCCCTCTC 32

RESULT 13
LOCUS CQ818717 71 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 147 from Patent WO2004039825.
ACCESSION CQ818717
VERSION CQ818717.1 GI:48427323
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS freskg Rd,P.O., Franch,T., Goulliaev,A.H., Lundorf,M.D., Felding,J.,
Olsen,E.K., Holtmann,A., Jakobsen,S.R., Sams,C., Glad,S.S.,
Jensen,K.B. and Pedersen,H.
TITLE Enzymatic encoding
JOURNAL Patent: WO 2004039825-A 147 13-MAY-2004;
FEATURES
location/Qualifiers
source 1..71
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
| | | | | | | | | | | | | | | |
Db 17 GAGCGGAGCCCTCTC 32

RESULT 14
LOCUS CQ818720 71 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 150 from Patent WO2004039825.
ACCESSION CQ818720
VERSION CQ818720.1 GI:48427326
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS freskg Rd,P.O., Franch,T., Goulliaev,A.H., Lundorf,M.D., Felding,J.,
Olsen,E.K., Holtmann,A., Jakobsen,S.R., Sams,C., Glad,S.S.,

```

TITLE Jensen, K.B. and Pedersen, H.  
Enzymatic encoding  
JOURNAL Patent: WO 2004039825-A 150 13-MAY-2004;  
Nucleotide A/S (DK)

FEATURES  
source 1..71  
Location/Qualifiers

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Artificially produced"

## ORIGIN

Query Match 72.0%; Score 14.4; DB 6; Length 71;  
Best Local Similarity 93.8%; Pred. No. 1.1e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTC 16  
Db 17 GAGCGGAGCCCCCC 32

## RESULT 15

AX204378 51 bp DNA linear PAT 30-AUG-2001  
LOCUS AX204378/c  
DEFINITION Sequence 484 from Patent WO0148245.  
ACCESSION AX204378  
VERSION AX204378.1 GI:15393911  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0148245-A 484 05-JUL-2001;  
Curagen Corporation (US)

FEATURES  
source 1..51  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## variation

26  
/note="single nucleotide polymorphism"  
Accession number CG40310734"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 51;  
Best Local Similarity 84.2%; Pred. No. 1.5e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTC 19  
Db 19 GAGCGGAGGACCACTCC 1

Search completed: December 24, 2005, 14:06:00  
Job time : 585 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 seconds  
(without alignments)  
777.677 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20  
Sequence: 1 gagcgagcagccccctcctcca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneeqn1990s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001s:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002as:\*  
7: geneeqn2002bs:\*  
8: geneeqn2003as:\*  
9: geneeqn2003bs:\*  
10: geneeqn2003cs:\*  
11: geneeqn2003ds:\*  
12: geneeqn2004as:\*  
13: geneeqn2004bs:\*  
14: geneeqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3 AA231431	AA231431 Human neu
2	20	100.0	20	3 ADA74683	ADA74683 GTR1601 a
3	20	100.0	35	8 ACC80168	ACC80168 Human neu
4	15.2	76.0	28	10 ADK71246	ADK71246 Drug-tole
5	15.2	76.0	45	14 ABA31362	ABA31362 Human DNA
6	14.8	74.0	21	12 ADP75955	ADP75955 Human leu
7	14.8	74.0	81	6 ABO81759	ABO81759 Triticach
8	14.8	74.0	81	6 ABV73412	ABV73412 Triticach
9	14.4	72.0	50	4 AAL33643	AAL33643 Human SNP
10	14.4	72.0	55	5 AAF25148	AAF25148 Nucleotid
11	14.4	72.0	55	6 AAK13065	AAK13065 Recombina
12	14.4	72.0	71	12 ADO04209	ADO04209 Identifie
13	14.4	72.0	71	12 ADO04205	ADO04205 Identifie
14	14.2	71.0	30	2 AAO97261	AAO97261 Not-dc ol
15	14.2	71.0	51	4 AAH79869	AAH79869 Human DNA
16	14.2	71.0	71	10 ADE93755	ADE93755 Human tra
17	13.8	69.0	65	6 ABA52872	ABA52872 Mouse spl
18	13.8	69.0	90	2 AAO49420	AAO49420 Cytochrom
19	13.6	68.0	30	13 ADU86387	ADU86387 U6 promot

20	13.6	68.0	50	6 AB200178	AB200178 Human leu
21	13.6	68.0	55	6 ABA91984	ABA91984 Single nu
22	13.6	68.0	57	2 ABA96211	ABA96211 Extracell
23	13.6	68.0	65	6 ABA57612	ABA57612 Mouse spl
24	13.6	68.0	70	14 AD227568	AD227568 Chemosen
25	13.6	68.0	84	2 AAX87463	AAX87463 Plasmid p
26	13.6	68.0	92	3 AAC07582	AAC07582 Human sec
27	13.4	67.0	31	11 ADL35330	ADL35330 Ant1-PCga
28	13.4	67.0	37	5 AAH43131	AAH43131 Primer: F
29	13.4	67.0	42	5 AAH43133	AAH43133 Primer: F
30	13.4	67.0	50	4 AAH78099	AAH78099 Human gll
31	13.4	67.0	51	4 AAH73503	AAH73503 Human gll
32	13.4	67.0	51	4 AAH78098	AAH78098 Human gll
33	13.4	67.0	51	4 AAH73502	AAH73502 Human gll
34	13.4	67.0	93	10 ADG38769	ADG38769 Frog fibr
35	13.4	67.0	100	10 ADE94000	ADE94000 Multiclon
36	13.4	67.0	100	10 ADE94001	ADE94001 Multiclon
37	13.2	66.0	20	4 AAH48586	AAH48586 Human Fas
38	13.2	66.0	20	8 AB275980	AB275980 Human GAV
39	13.2	66.0	24	12 ADL67243	ADL67243 Human 4-1
40	13.2	66.0	24	14 AEB93504	AEB93504 Human SIP
41	13.2	66.0	25	9 ACT121922	ACT121922 Human mtc
42	13.2	66.0	27	2 AAV21278	AAV21278 Tissue pl
43	13.2	66.0	29	12 ADO22496	ADO22496 Human EDG
44	13.2	66.0	29	12 ADO22495	ADO22495 Human EDG
45	13.2	66.0	30	2 AAT09304	AAT09304 Murine an

## ALIGNMENTS

RESULT 1  
ID AA231431 standard; DNA; 20 BP.  
XX  
XX AA231431;  
AC  
XX  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Human neuropilin mRNA specific antisense oligo GTR1601.  
XX  
XX Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;  
KW papilloma; diabetic retinopathy; antisense; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO955855-A2.  
XX  
XX PD 04-NOV-1999.  
XX  
XX PF 23-APR-1999; 99WO-CA000324.  
XX  
XX FR 23-APR-1998; 98US-0082791P.  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
XX Wright JA, Young AH, Lee YS;  
XX WPI; 2000-023357/02.  
XX  
PT Antisense oligonucleotides that inhibit neuropilin expression, useful for  
PT treating cancer.  
XX  
XX  
XX  
XX  
PS Claim 4; Page 16; 57pp; English.  
XX  
CC Sequences AA231431-460 represent antisense oligonucleotides which inhibit  
CC human neuropilin expression. The antisense oligonucleotides can be used  
CC to inhibit the growth or metastasis of a mammalian tumor and inhibit  
CC neovascularisation. The oligonucleotides may be used to treat various  
CC forms of cancers or tumors, such as sarcomas, melanomas, adenomas,  
CC carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of  
CC the mouth, throat, larynx and lung, genitourinary cancers such as

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
CC cancer, head and neck cancers, and nervous system cancers, as well as  
CC benign lesions such as papillomas. The methods may be used to treat  
CC neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration  
CC  
SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 1 GAGCGGAGCCCCCTCTCCA 20  
RESULT 2  
ADA74683  
ID ADA74683 standard; DNA; 20 BP.  
XX  
AC ADA74683;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE GT13601 antisense oligonucleotide targeted to human neuropilin mRNA.  
XX  
KW neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
KM cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;  
KW GT13601; antisense; human; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003083274-A1.  
XX  
PD 01-MAY-2003.  
XX  
PF 22-APR-1999; 99US-00296264.  
XX  
PR 23-APR-1998; 98US-0082791P.  
XX  
PA (WRIG/) WRIGHT J A.  
PA (YOUNG/) YOUNG A H.  
PA (LEEV/) LEE Y S.  
XX  
PI Wright JA, Young AH, Lee YS;  
XX  
DR WPI; 2003-576622/54.  
XX  
PT New antisense oligonucleotide that inhibits neuropilin expression, useful  
PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
PT mammalian tumor.  
XX  
PS Claim 1; Page 5; 27pp; English.  
XX  
CC The invention relates to a novel antisense oligonucleotide that inhibits  
CC the expression of neuropilin, also known as VEGF165R (vascular  
CC endothelial growth factor receptor). The oligonucleotide of the invention  
CC demonstrates cytostatic activity and may be useful for inhibiting the  
CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in  
CC mammals. Furthermore, the oligonucleotide may be utilised during gene  
CC therapy. The current sequence is that of the GT13601 antisense  
CC oligonucleotide of the invention which is targeted to human neuropilin  
CC mRNA.  
XX  
SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGCGGAGCCCCCTCTCCA 20

Db 1 GAGCGGAGCCCCCTCTCCA 20  
RESULT 3  
ACC80168/c  
ID ACC80168 standard; DNA; 35 BP.  
XX  
AC ACC80168;  
XX  
DT 04-AUG-2003 (first entry)  
XX  
DE Human neuropilin-1 gene PCR primer #1.  
XX  
KW Cytostatic; Neuropilin-1 receptor; NP-1 receptor; angiogenesis; cancer;  
KW Vascular Endothelial Growth Factor Receptor-2; VEGFR-2; PlGF; VEGF;  
KW Placental Growth Factor; Vascular Endothelial Growth Factor;  
KW anti-angiogenic; human; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003029275-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 02-OCT-2002; 2002WO-US031386.  
XX  
PR 03-OCT-2001; 2001US-0326712P.  
XX  
PA (REGG-) REGENERON PHARM INC.  
PA (PROC) PROCTER & GAMBLE CO.  
XX  
PI Rosenbaum JS, Jones DR, Whitaker GB;  
XX  
DR WPI; 2003-371982/35.  
XX  
PT New anti-angiogenic peptides that are capable of binding to NP-1 or  
PT vascular endothelial growth factor receptor (VEGFR)-2/NP-1 complex,  
PT useful for treating diseases characterized by abnormal angiogenesis, such  
PT as cancer.  
XX  
PS Disclosure; Page 21; 115pp; English.  
XX  
CC The present invention relates to peptides that are capable of binding to  
CC Neuropilin-1 (NP-1) receptor or the Vascular Endothelial Growth Factor  
CC Receptor (VEGFR)-2/NP-1 complex. The peptides are derived from a  
CC combination of peptides from Exon 6 of Placental Growth Factor (PlGF),  
CC coupled at the carboxyl terminus to either Exon 8 of Vascular Endothelial  
CC Growth Factor (VEGF) Isoform 165 (VEGF165, also referred to as P6V8) or  
CC Exon 7 of PlGF (referred to as P6P7). The peptides and compositions are  
CC useful for treating diseases characterised by abnormal angiogenesis, such  
CC as cancer. The present peptide is a PCR primer, which was used to  
CC illustrate the invention  
XX  
SQ Sequence 35 BP; 7 A; 8 C; 11 G; 9 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 31 GAGCGGAGCCCCCTCTCCA 12  
RESULT 4  
ADK71246  
ID ADK71246 standard; DNA; 28 BP.  
XX  
AC ADK71246;  
XX  
DT 06-MAY-2004 (first entry)  
XX

DE Drug-tolerant gene related PCR primer.  
XX  
XX detection; drug-tolerant gene; gene chip; probe; PCR; amplification;  
KM hybridisation; primer; ss.  
XX  
OS Synthetic.  
XX  
PN CN1396271-A.  
XX  
PD 12-FEB-2003.  
XX  
XX  
PF 13-JUL-2001; 2001CN-00120441.  
XX  
PR 13-JUL-2001; 2001CN-00120441.  
XX  
PA (SANX-) SANXIONG HI TECH DEV CO LTD BEIJING.  
XX  
PI Liu Y, Wang H, Li L;  
XX  
XX WPI; 2003-442250/42.  
DR  
XX  
XX  
PT Detection to drug tolerant gene by gene chip technique.  
XX  
PS Claim 4; Page 15; 32pp; Chinese.  
XX  
CC The present invention describes a process for detecting a drug-tolerant  
CC gene with a gene chip technique. The method comprises fixing the DNA  
CC sequence of an oligonucleotide probe to a carrier of a gene chip, the DNA  
CC sequence of an elongation primer for the PCR linear amplification of a  
CC target drug-tolerant gene, PCR amplification, and hybridisation of the  
CC PCR resultant with a probe on the chip. The present sequence represents a  
CC PCR primer which is used in the exemplification of the present invention.  
XX  
SQ Sequence 28 BP; 6 A; 10 C; 6 G; 6 T; 0 U; 0 Other;  
Query Match 76.0%; Score 15.2; DB 10; Length 28;  
Best Local Similarity 85.0%; Pred. No. 7.3e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 GAGCGGAGCCCCCTCTCCA 20  
DB 6 GAGCGGAGCACTATCTCCA 25  
RESULT 5  
AEA31362/C  
ID AEA31362 standard; DNA; 45 BP.  
XX  
AC AEA31362;  
XX  
DT 11-AUG-2005 (first entry)  
XX  
XX  
DE Human DNA oligonucleotide #4.  
XX  
KM Transposon; retrotransposon; genetic disorder; hemophilia;  
KM Parkinsons disease; Fabry disease; hypercholesterolemia;  
KM Gauchers disease; cystic fibrosis; adrenoleukodystrophy;  
KM adenosine deaminase deficiency; alpha-1 antitrypsin deficiency;  
KM Duchenne dystrophy; phenylketonuria; sickle cell anemia;  
KM Tay Sachs disease; thalassemia; lysosomal storage disease;  
KM metabolic disorder; antiparkinsonian; hemostatic; metabolic;  
KM CNS-Gen.; respiratory-gen.; antianemic; cerebroprotective; muscular-gen.;  
KM dermatological; nootropic; antisticking; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO2005049789-A2.  
XX  
PD 02-JUN-2005.  
XX  
XX 18-MAY-2004; 2004WO-US015810.  
PF  
XX 28-MAY-2003; 2003US-0473658P.  
PR

XX  
PA (UYUO ) UNIV JOHNS HOPKINS.  
XX  
XX Boeke JD, Han US;  
PI  
XX  
XX WPI; 2005-396089/40.  
DR  
XX  
XX  
PT New synthetic mammalian (retro)transposon open reading frame 2 (ORF2) or  
PT ORF1 gene exhibiting a higher level of expression relative to a natural  
PT L1 (retro)transposon ORF2 or ORF1 gene, useful for treating e.g.,  
PT metabolic diseases.  
XX  
XX  
PS Disclosure; SEQ ID NO 213; 66pp; English.  
XX  
XX  
CC The invention relates to a synthetic mammalian (retro)transposon ORF2 or  
CC ORF1 gene exhibiting a higher level of expression relative to a natural  
CC L1 (retro)transposon ORF2 or ORF1 gene. The invention also relates to a  
CC (retro)transposon comprising the synthetic gene, a mammalian L1  
CC retrotransposon comprising the synthetic gene, a recombinant vector  
CC construct comprising the synthetic gene, a eukaryotic cell transfected,  
CC transformed or infected with the recombinant vector construct, a method  
CC of delivering a desired gene, or its biologically active fragment, to the  
CC cells of a mammal, a composition comprising a cassette comprising the  
CC gene, a desired gene and a pharmaceutical carrier, and a method of  
CC identifying an uncharacterized gene, or its biologically active fragment,  
CC in cells. The composition is useful for treating a genetic disorder in a  
CC mammal such as hemophilia, Parkinsons disease, Fabry disease,  
CC hypercholesterolemia, Gauchers disease, cystic fibrosis,  
CC adrenoleukodystrophy, disorders associated with mutations in the  
CC dystrophin gene, adenosine deaminase deficiency, alpha-antitrypsin  
CC deficiency, Duchenne muscular dystrophy, phenylketonuria, sickle cell  
CC anemia, Tay Sachs disease, thalassemia, lysosomal storage diseases and  
CC metabolic disorders. The synthetic gene is useful for treating the  
CC diseases. This sequence represents a human DNA oligonucleotide used in  
CC the scope of the invention.  
XX  
SQ Sequence 45 BP; 0 A; 12 C; 23 G; 10 T; 0 U; 0 Other;  
Query Match 76.0%; Score 15.2; DB 14; Length 45;  
Best Local Similarity 85.0%; Pred. No. 7.2e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 GAGCGGAGCCCCCTCTCCA 20  
DB 44 GAGCGGAGCCCCCCCCCA 25  
RESULT 6  
ADP75955  
ID ADP75955 standard; DNA; 21 BP.  
XX  
AC ADP75955;  
XX  
XX  
DT 09-SEP-2004 (first entry)  
XX  
XX  
DE Human leukaemia inhibiting factor PCR primer SeqIDS.  
XX  
XX matrix binding region; cell surface; extracellular matrix;  
XX leukaemia inhibitory factor region; cell differentiation;  
XX embryonic stem cell; PCR; primer; ss; human.  
XX  
OS Homo sapiens.  
XX  
PN JP2004166641-A.  
XX  
XX 17-JUN-2004.  
PD  
XX 21-NOV-2002; 2002JP-00338373.  
PF  
XX 21-NOV-2002; 2002JP-00338373.  
PR  
XX (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.  
PA (AIZU/) AIZU Y.

```
XX DR WPI; 2004-445579/42.
XX PT Novel protein which has matrix binding region which assembles to cell
XX PT surface, or to extracellular matrix surrounding cell and leukemia
XX PT inhibitory factor region that suppresses cell differentiation of
XX PT embryonic stem cell.
XX PS Example 1; SEQ ID NO 5; 49pp; Japanese.
XX CC This invention relates to a novel protein (and the gene which encodes it)
XX CC which has a matrix binding region which assembles to a cell surface, or
XX CC extracellular matrix surrounding the cell, and a leukemia inhibitory
XX CC factor region which suppresses cell differentiation of embryonic stem
XX CC cells. The invention is useful for suppressing cell differentiation. The
XX CC differentiation can be used for the efficient inhibition of embryonic stem cell
XX CC proliferation. The invention thus enables efficient and continuous
XX CC proliferation of embryonic stem cells. Therefore, embryonic stem cells
XX CC can be prepared in large quantities and utilized for fundamental research
XX CC and applications. The present sequence is that of a PCR primer which was
XX CC used for amplification of a region of the human leukaemia inhibitory
XX CC factor CDNA in the exemplification of the invention.
SQ Sequence 21 BP; 2 A; 13 C; 4 G; 2 T; 0 U; 0 Other;
Query Match          74.0%; Score 14.8; DB 12; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GCGGCGAGCCCTCTCCA 20
   |||||
Db 2 GCGGCGAGCCCTCTCCA 19

RESULT 7
AB081759/c
ID AB081759 standard; DNA; 81 BP.
XX AC AB081759;
XX DT 29-AUG-2003 (revised)
XX DT 29-NOV-2002 (first entry)
XX DE Trifirachium album limber proteinase K PCR primer SEQ ID NO 18.
XX DE Trifirachium album limber; proteinase K; enzyme; PCR; primer; ss.
XX KW Trifirachium album; limber.
XX OS Trifirachium album; limber.
XX PN DE10105912-A1.
XX PD 14-AUG-2002.
XX PF 09-FEB-2001; 2001DE-01005912.
XX PR 09-FEB-2001; 2001DE-01005912.
XX PA (HOF) ROCHE DIAGNOSTICS GMBH.
XX PI Mueller R, Schoen H, Schmuck R, Geipel F, Meier T, Glaser S;
XX PI Rexer B, Thalhofer J, Scholt B, Rudolph R, Lill H;
XX DR WPI; 2002-667991/72.
XX PT Renaturing denatured zymogenic proteinase K, useful e.g. for analysis, by
XX PT incubation in folding buffer, especially applied to material solubilized
XX PT from inclusion bodies.
XX PS Example 1; Page 18; 36pp; German.
XX CC The invention relates to renaturing (M1) denatured, zymogenic proteinase
XX CC K (I), at 0-3pHsuc, by transfer to a folding buffer (A) that has pH 7.5
XX CC -10.5 and includes: (i) low molecular weight folding auxiliaries; (ii) a
```

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CC redox shuffling system; and (iii) a complexing agent at less than the
CC stoichiometric amount relative to calcium ions present. (I) is useful in
CC analysis and diagnosis (no details given). M1 allows the high expression
CC potential and quick, simple growth of Escherichia coli to be exploited;
CC permits genetic modification of the recombinant DNA used; reduces the
CC extent of purification required after renaturation, and avoids
CC contamination with eukaryotic materials. (I) is produced in homogeneous
CC form. The present sequence is that of a PCR primer used to generate
CC vectors expressing the Trifirachium album limber proteinase K protein
CC gene sequence, used in examples of the invention. However, the disclosed
CC gene sequence (AB081743) does not encode the disclosed proteinase K
CC standard (AB083956) of the invention. (Updated on 29-AUG-2003 to
XX CC standard OS field)
SQ Sequence 81 BP; 18 A; 19 C; 33 G; 11 T; 0 U; 0 Other;
Query Match          74.0%; Score 14.8; DB 6; Length 81;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GCGGCGAGCCCTCTCCA 20
   |||||
Db 75 GCGGCGAGCAGCCGCTCCA 58

RESULT 8
ABV73412/c
ID ABV73412 standard; DNA; 81 BP.
XX AC ABV73412;
XX DT 29-AUG-2003 (revised)
XX DT 05-DEC-2002 (first entry)
XX DE Trifirachium album limber proteinase K PCR primer SEQ ID NO 18.
XX DE Trifirachium album limber; proteinase K; enzyme; PCR; primer; ss.
XX KW Trifirachium album; limber.
XX OS Trifirachium album; limber.
XX PN DE10105911-A1.
XX PD 14-AUG-2002.
XX PF 09-FEB-2001; 2001DE-01005911.
XX PR 09-FEB-2001; 2001DE-01005911.
XX PA (HOF) ROCHE DIAGNOSTICS GMBH.
XX PI Mueller R, Thalhofer J, Geipel F, Glaser S, Hoelke W, Schoen H;
XX PI Kirchbaum T;
XX DR WPI; 2002-667990/72.
XX PT Preparing recombinant proteinase K in yeast, useful for analysis and
XX PT diagnosis, using a signal peptide for secretion of a precursor which is
XX PT activated autocatalytically.
XX PS Example 1; Page 13; 18pp; German.
XX CC The invention relates to preparing recombinant proteinase K (I) by: (a)
XX CC transforming a yeast cell with a vector containing DNA (II) that encodes
XX CC a zymogenic precursor of (I), fused, upstream and in frame, with a
XX CC sequence encoding a signal peptide (SP); (b) expressing the precursor;
XX CC and (c) secretion of (I) in soluble form, followed by autocatalytic
XX CC activation. (I) is useful in analysis and diagnosis (no details given).
XX CC The method provides economical amounts of (I) in soluble, homogeneous and
XX CC active form. Secretion avoids the toxic effects of cytosolic (I); ensures
XX CC correct formation of disulfide bonds and unexpectedly, (I) has no effect
XX CC on the surface proteins of the host cell. Yeast have a higher growth rate
XX CC and are easier to handle than Trifirachium album, the native source of
XX CC (I). The present sequence is that of a PCR primer for amplification of
```



CC the Triticichium album limber proteinase K encoding DNA sequence of the  
CC invention. (Updated on 29-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 81 BP; 18 A; 19 C; 33 G; 11 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 6; Length 81;  
Best Local Similarity 88.9%; Pred. No. 1e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GCGGACGCCCTCTCCA 20  
DB 75 GCGGACGACCCGCTCCA 58  
GGGACGACCCCTCTCCA 20  
GGGACGACCCGCTCCA 58  
RESULT 9  
AAL33643  
ID AAL33643 standard; DNA; 50 BP.  
XX  
AC AAL33643;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #6851.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PP 28-DEC-2000; 2000WO-US035498.  
XX  
PR 28-DEC-1999; 99US-0173419P.  
PR 27-DEC-2000; 2000US-00173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkels RA, Leach M;  
XX  
DR WPI; 2001-465210/50.  
XX  
FT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
FT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
FT autoimmune diseases and infections.  
XX  
PS Claim 1; Page 3341; 4133pp; English.  
XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms

SQ Sequence 50 BP; 10 A; 16 C; 18 G; 6 T; 0 U; 0 Other;  
Query Match 72.0%; Score 14.4; DB 4; Length 50;  
Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 GCGAGCCCTCTCCA 20  
DB 17 GCGAGCCCTCTCCA 32  
GGGAGCCCTCTCCA 20  
GGGAGCCCTCTCCA 32  
RESULT 10  
AAF25148  
ID AAF25148 standard; DNA; 55 BP.  
XX  
AC AAF25148;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of a recombinant Respiratory syncytial virus.  
XX  
KW Respiratory syncytial virus; RSV; attenuated vaccine; RSV A; RSV B; BRSV;  
KW HSRV; ss.  
XX  
OS Respiratory syncytial virus.  
XX  
FN WO200104335-A2.  
XX  
PD 18-JAN-2001.  
XX  
PP 23-JUN-2000; 2000WO-US017755.  
XX  
PR 09-JUL-1999; 99US-0143132P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Buchholz U, Collins PL, Murphy BR, Whitehead SS, Krempf CD;  
XX  
DR WPI; 2001-103088/11.  
XX  
FT Isolated chimeric human-bovine respiratory syncytial virus (RSV), useful  
FT in an attenuated vaccine to elicits an immune response against either or  
FT both human RSV A or RSV B.  
XX  
PS Disclosure; Page 145; 148pp; English.  
XX  
CC The specification describes a chimeric human-bovine respiratory syncytial  
CC virus (RSV) that is infectious and attenuated in humans. The virus  
CC comprises a major nucleocapsid protein, a nucleocapsid phosphoprotein, a  
CC large polymerase protein, a RNA polymerase elongation factor, and a  
CC partial or complete RSV background genome, or antigenome of a human RSV  
CC or bovine RSV, combined with one or more heterologous genes or genome  
CC segment of a different RSV to form a human-bovine chimeric RSV genome or  
CC antigenome. The chimeric RSV is useful in an attenuated vaccine to  
CC elicits an immune response against either or both human RSV A or RSV B.  
XX  
PS The present sequence represents a fragment of a recombinant RSV  
XX  
SQ Sequence 55 BP; 14 A; 16 C; 11 G; 14 T; 0 U; 0 Other;  
Query Match 72.0%; Score 14.4; DB 5; Length 55;  
Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GCGGACGCCCTCTC 18  
DB 22 GCGGACGCCCTCTC 37  
GGGACGCCCTCTC 18  
GGGACGCCCTCTC 37  
RESULT 11  
ABK13065  
ID ABK13065 standard; DNA; 55 BP.  
XX  
AC ABK13065;

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XX 23-APR-2002 (first entry)
XX Recombinant BRSV genome construct rBRSV/A2-G1F2 leader sequence.
DE Respiratory syncytial virus; RSV; vaccine; immunostimulatory; antiviral;
XX gene therapy; rBRSV/A2-G1F2; ds.
XX Bovine respiratory syncytial virus.
OS Synthetic.
XX WO200200693-A2.
XX 03-JAN-2002.
XX 22-JUN-2001; 2001WO-US020107.
XX 23-JUN-2000; 2000US-0213708P.
XX (USGO ) US GOVERNMENT.
XX Krempf CD, Collins PL, Murphy BR, Buchholz U, Whitehead SS;
XX WPI; 2002-090518/12.
XX An isolated infectious recombinant respiratory syncytial virus (RSV)
XX having one or more shifted RSV gene(s) or genome segment(s) within the
XX recombinant genome or antigenome, useful as an attenuated vaccine against
XX RSV strains.
XX Example 3; Fig 6; 168bp; English.
XX The invention relates to an isolated infectious recombinant respiratory
XX syncytial virus (RSV) having one or more shifted RSV gene(s) or genome
XX segment(s) within the recombinant genome or antigenome that is/are
XX positionally shifted to a more promoter-proximal or promoter-distal
XX position relative to a position of the RSV gene(s) or genome segment(s)
XX within a wild type RSV genome or antigenome. Also described is (1) a
XX method for stimulating the immune system of an individual to induce
XX protection against RSV which comprises administering to the individual an
XX immunologically sufficient amount of the recombinant RSV combined with a
XX physiologically acceptable carrier; and (2) an isolated infectious
XX chimeric RSV comprising a major nucleocapsid protein, a RNA polymerase elongation
XX phosphoprotein, a large polymerase protein, a RNA polymerase elongation
XX factor, and a partial or complete bovine RSV background genome or
XX antigenome combined with heterologous gene(s) and/or genome segment(s) of
XX a human RSV selected from heterologous gene(s) and/or genome segment(s)
XX of RSV NS1, NS2, M, SH, G, and/or F, to form a human-bovine chimeric RSV
XX genome or antigenome. The recombinant RSV is useful in an attenuated
XX vaccine to elicit an immune response against either human RSV A or RSV B
XX or both human RSV A and RSV B. The present sequence represents
XX recombinant BRSV genome construct rBRSV/A2-G1F2 leader sequence as
XX described in the method of the invention
XX
XX Sequence 55 BP; 14 A; 16 C; 11 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 72.0%; Score 14.4; DB 6; Length 55;
XX Best Local Similarity 93.8%; Pred. No. 1.5e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GCGGCGAGCCCTCTC 18
DB 22 GCGGCGAGCCCTCTC 37

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DE Identifier oligonucleotide E58.
XX Bifunctional complex; ss.
XX Synthetic.
XX WO2004039825-A2.
XX 13-MAY-2004.
XX 30-OCT-2003; 2003WO-DK000739.
XX 30-OCT-2002; 2002DK-00001652.
XX 30-OCT-2002; 2002US-0422167P.
XX 19-DEC-2002; 2002DK-00001955.
XX 19-DEC-2002; 2002US-0434425P.
XX 11-JUL-2003; 2003DK-00001064.
XX 11-JUL-2003; 2003US-0486199P.
XX (NUEV-) NUCLEOLATION AS.
XX
XX Freshgard P, Franch T, Goulaev AH, Lundorf MD, Felding J;
XX Olsen EK, Holtmann A, Jakobsen SN, Sams C, Glad SS, Jensen KB;
XX Pedersen H;
XX WPI; 2004-376154/35.
XX
XX Obtaining bifunctional complex with display molecule and coding part,
XX where bifunctional complex with priming site for adding tag is reacted at
XX reaction site with reactants and provided with tag identifying reactant
XX at priming site.
XX Example 13; Page 175; 220bp; English.
XX
XX The present invention relates to a method (M1) for obtaining a
XX bifunctional complex. (M1) comprises a display molecule part and a coding
XX part, where a nascent bifunctional complex comprising a chemical reaction
XX site and a priming site for enzymatic addition of a tag is reacted at the
XX chemical reaction site with reactant(s), and provided with respective
XX tag(s) identifying the reactant(s) at the priming site using one or more
XX enzymes. The present sequence was used to illustrate the invention.
XX
XX Sequence 71 BP; 14 A; 32 C; 14 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 72.0%; Score 14.4; DB 12; Length 71;
XX Best Local Similarity 93.8%; Pred. No. 1.5e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGCGGAGCCCTCTC 16
DB 17 GAGCGGAGCCCTCTC 32

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RESULT 12
AD004209
ID AD004209 standard; DNA; 71 BP.
AC AD004209;
XX 29-JUL-2004 (first entry)
DT
XX

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RESULT 13
AD004205
ID AD004205 standard; DNA; 71 BP.
AC AD004205;
XX 29-JUL-2004 (first entry)
DT
XX
XX Identifier oligonucleotide E57.
XX Bifunctional complex; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 47..51
XX FT /*tag= a
XX FT /mod_base= i
XX
XX WO2004039825-A2.

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XX PD 13-MAY-2004.
XX PF 30-OCT-2003; 2003WO-DK000739.
XX PR 30-OCT-2002; 2002DK-00001652.
XX PR 30-OCT-2002; 2002US-0422167P.
XX PR 19-DEC-2002; 2002DK-00001955.
XX PR 19-DEC-2002; 2002US-0434425P.
XX PR 11-JUL-2003; 2003DK-00001064.
XX PR 11-JUL-2003; 2003US-0486199P.
XX PA (NREV-) NREVOLUTION AS.
XX PI Freekard P, Franch T, Goulinev AH, Lundorf MD, Felding J;
PI Olesen EK, Holtmann A, Jakobsen SN, Sams C, Glad SS, Jensen KB,
PI Pedersen H;
XX DR WPI; 2004-376154/35.
XX PT Obtaining bifunctional complex with display molecule and coding part,
XX PT where bifunctional complex with priming site for adding tag is reacted at
XX PT reaction site with reactants and provided with tag identifying reactant
XX PT at priming site.
XX PS Example 13; Page 174; 220pp; English.
XX CC The present invention relates to a method (M1) for obtaining a
XX CC bifunctional complex. (M1) comprises a display molecule part and a coding
XX CC part, where a nascent bifunctional complex comprising a chemical reaction
XX CC site and a priming site for enzymatic addition of a tag is reacted at the
XX CC chemical reaction site with reactant(s), and provided with respective
XX CC tag(s) identifying the reactant(s) at the priming site using one or more
XX CC enzymes. The present sequence was used to illustrate the invention.
XX SQ Sequence 71 BP; 14 A; 27 C; 14 G; 11 T; 0 U; 5 Other;

Query Match 72.0%; Score 14.4; DB 12; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTTC 16
   |||||
Db 17 GAGCGGAGCCCCCCC 32

RESULT 14
AAQ97261
ID AAQ97261 standard; cDNA; 30 BP.
XX AC AAQ97261;
XX DT 28-DEC-1995 (first entry)
XX DE Noc-dc oligo primer.
XX KM Astrocyte-type 1, AT1; neuron; ss.
XX OS Synthetic.
XX PN MO9517203-A1.
XX PD 29-JUN-1995.
XX PF 22-DEC-1994; 94WO-US014771.
XX PR 22-DEC-1993; 93US-00172327.
XX PR 18-JUL-1994; 94US-00275709.
XX PR 20-DEC-1994; 94US-00359480.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Schaar DG, Dreyfuss CF, Black IB;

```

```

XX DR WPI; 1995-240472/31.
XX PT New astrocyte-derived neurotrophic factor proteins - related nucleic
XX PT acid, vectors and transformed cells, useful for stimulating neuronal cell
XX PT survival and growth.
XX PS Example 2; Page 43; 107pp; English.
XX CC cDNA was synthesized from astrocyte total RNA using reverse transcriptase
XX CC primed by a Not-dt oligo (given in AAQ97260). Products were used for non-
XX CC sequence specific cDNA amplification, using Noc-dt (AAQ97260) and Not-dc,
XX CC asymmetric PCR and subtractive hybridization to isolate novel astrocyte
XX CC type 1 cDNA clones (AAQ97243-46)
XX SQ Sequence 30 BP; 1 A; 21 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 2; Length 30;
Best Local Similarity 84.2%; Pred. No. 1.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTTCC 19
   |||||
Db 8 GAGCGGAGCCCCCCCC 26

RESULT 15
AAH79869/c
ID AAH79869 standard; DNA; 51 BP.
XX AC AAH79869;
XX DT 19-SEP-2001 (first entry)
XX DE Human DNA containing single nucleotide polymorphism SEQ ID NO. 484.
XX KM Human; single nucleotide polymorphism; SNP; angiotensin;
XX KM 4-hydroxybutyrate; dehydrogenase; protein therapy;
XX KM adenosine triphosphate-dependent RNA helicase;
XX KM major histocompatibility complex Class I histocompatibility antigen; MHC;
XX KM phosphoglycerate kinase; immunosuppressive; immunostimulatory;
XX KM antipneumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
XX KM antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; de.
XX OS Homo sapiens.
XX PN WO200148245-A2.
XX PD 05-JUL-2001.
XX PF 27-DEC-2000; 2000WO-US035346.
XX PR 27-DEC-1999; 99US-00472688.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2001-418297/44.
XX PT Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
XX PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
XX PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
XX PT diseases and infections.
XX PS Claim 1; Page 195; 484pp; English.
XX CC The invention relates to nucleic acids (AAH79386-AAH80036) encoding
XX CC polymorphic variants of proteins (AAH96010-AAH98238) related to
XX CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
XX CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
XX CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
XX CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded

```

CC proteins have potential immunosuppressive, immunostimulatory,  
 CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,  
 CC antileukemic, neuroprotective and antimicrobial activity and may be  
 CC useful in gene/protein therapy, vaccines, modulation of the expression  
 CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,  
 CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major  
 CC histocompatibility complex (MHC) Class I histocompatibility antigen  
 CC and/or phosphoglycerate kinase. Disorders that may be prevented,  
 CC diagnosed and/or treated by the above methods include multifactorial  
 CC diseases with a genetic component, such as autoimmune diseases (e.g.  
 CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus  
 CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers  
 CC of the bladder, brain, breast, colon and kidney, leukemia), diseases of  
 CC the nervous system, an infection of pathogenic organisms. They may also  
 CC be used to alter phenotypic traits such as longevity, appearance,  
 CC strength, speed and endurance

XX Sequence 51 BP; 3 A; 15 C; 20 G; 13 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 51;

Best Local Similarity 84.2%; Pred. No. 1.9e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAGCGGACGCCCCCTCTCC 19

Db 19 GAGCAGCAGCACCCACTCC 1

Search completed: December 24, 2005, 12:28:50  
 Job time : 174.4 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 : Search time 1572 Seconds  
(without alignments)  
595.256 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20  
Sequence: 1 gagcgagcagcccccctccca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_ests1:\*  
2: gb\_ests2:\*  
3: gb\_ests3:\*  
4: gb\_hnc:\*  
5: gb\_ests4:\*  
6: gb\_ests5:\*  
7: gb\_ests6:\*  
8: gb\_ests7:\*  
9: gb\_ests1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.2	76.0	98	2	BE425297 WHE0311_D
C 2	14.8	74.0	65	1	AI1270452 qu88C06.x
C 3	14.8	74.0	76	9	BZ286339 KG09603.D
C 4	14.8	74.0	91	5	BU861576 S003H06.P
C 5	14.4	72.0	82	6	CD672055 FG09F02.Y
C 6	14.2	71.0	50	1	AU107434 AU107434
C 7	14.2	71.0	58	1	AI123506 qao1909.x
C 8	14.2	71.0	59	9	BH855612 SALK 0848
C 9	14.2	71.0	62	8	CH001505 iv41D08.G
C 10	14.2	71.0	85	5	BO808288 1030003A0
C 11	14.2	71.0	87	11	TA2H03P
C 12	14.2	71.0	93	8	DR731394 MG6.4.1.
C 13	14.2	71.0	95	4	AK217328 Mus muscu
C 14	14.2	71.0	97	5	BU862683 S018G02.P
C 15	13.8	69.0	60	10	CG716533 1119045G0
C 16	13.8	69.0	60	10	CG716535 1119045G0
C 17	13.8	69.0	74	2	BG315169 POL 0.136
C 18	13.8	69.0	82	8	DN428053 LIB4216-1
C 19	13.8	69.0	84	3	BM090905 1g17d06.x
C 20	13.8	69.0	86	1	AW593901 h928h03.x
C 21	13.8	69.0	95	1	AI051259 oy49f02.x
C 22	13.8	69.0	96	1	AA835222 ak65b02.s

C 23	13.8	69.0	97	9	AZ356019
C 24	13.8	69.0	100	1	AM605663
C 25	13.6	68.0	57	9	AZ962155
C 26	13.6	68.0	61	6	CB213009
C 27	13.6	68.0	66	11	TA391A11P
C 28	13.6	68.0	67	3	BI908580
C 29	13.6	68.0	77	6	CD285974
C 30	13.6	68.0	81	7	CR446349
C 31	13.6	68.0	82	1	AA870618
C 32	13.6	68.0	83	7	CR291222
C 33	13.6	68.0	89	1	AA579142
C 34	13.6	68.0	89	9	CC941103
C 35	13.4	67.0	53	10	BX979943
C 36	13.4	67.0	75	9	AZ339132
C 37	13.4	67.0	93	11	TA358C080
C 38	13.4	67.0	96	1	AU713458
C 39	13.2	66.0	43	9	BH855596
C 40	13.2	66.0	50	1	AU103490
C 41	13.2	66.0	53	11	CR185627
C 42	13.2	66.0	58	10	CG712685
C 43	13.2	66.0	61	7	CA482613
C 44	13.2	66.0	61	9	AZ791343
C 45	13.2	66.0	76	8	DN444762

#### ALIGNMENTS

RESULT 1  
LOCUS BE425297/c 98 bp mRNA linear EST 24-JUN-2000  
DEFINITION WHE0311\_D02\_D0225 wheat unstressed seedling shoot cDNA library  
Triticum aestivum cDNA clone WHE0311\_D02\_D02, mRNA sequence.

ACCESSION BE425297  
VERSION BE425297.1 GI:9423056  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

REFERENCE  
AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Izzo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., and Tong, D.C.  
The structure and function of the expressed portion of the wheat 1 (bases 1 to 98)  
Pooideae; Triticaceae; Triticum.

TITLE  
The structure and function of the expressed portion of the wheat 1 (bases 1 to 98)

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: oanderson@w.usda.gov  
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20  
Seq primer: StrataGene SK primer.  
Location/Qualifiers  
1..98  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultiar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="WHE0311\_D02\_D02"  
/issue\_type="Etiolated shoot"  
/dev stage="Five day old seedling"  
/lab\_host="E. coli SOLR"  
/clone\_id="Wheat unstressed seedling shoot cDNA library"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water.

mystatin and cefotaxime in covered crystallization dishes. Shoots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give phagescript phagemids in the 17 close lab (Choi, Close, Fenton) at the University of California, Riverside, Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

## ORIGIN

Query Match 76.0%; Score 15.2; DB 2; Length 98;  
Best Local Similarity 85.0%; Pred. No. 5.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTCCA 20  
|||||  
Db 94 GAGCGGAGCCCTCTCCA 75

RESULT 2  
LOCUS AI270452 65 bp mRNA linear EST 17-NOV-1998  
DEFINITION q88c06.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA IMAGE:1979146 3',  
mRNA sequence.  
ACCESSION AI270452  
VERSION AI270452.1 GI:3889619  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 65)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL  
AUTHORS  
TITLE  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: c9ab8-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbp/image/image.html](http://www.bio.llnl.gov/dbp/image/image.html)  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

## FEATURES

source

1. 65  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1979146"  
/issue\_type="poorly differentiated adenocarcinoma with  
signet ring cell features"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP Gas4"  
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo #1.  
Average insert size 1.69 kb. Life Technologies catalog #:  
11549-011"

## ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 65;  
Best Local Similarity 88.9%; Pred. No. 8.1e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCTCTCC 19  
|||||  
Db 1 AGCGGAGCCCTCTCC 18

RESULT 3  
LOCUS BZ286339/c 76 bp DNA linear GSS 15-OCT-2002  
DEFINITION KG09603 Drosophila melanogaster P(SUPor-P) P element insertion  
lines Drosophila melanogaster genomic Sequence recovered from Both  
5' and 3' ends of P element, genomic survey sequence.

ACCESSION BZ286339  
VERSION BZ286339.1 GI:24018111  
KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 76)  
Levis, R., Hoskins, R., Liao, G., Mozer, N., Tsang, G., He, Y.,  
Karpén, G., Belien, H., Rubin, G., and Spradling, A.,  
The Berkeley Drosophila Genome Project Gene Disruption Project  
Unpublished (2001)  
JOURNAL  
AUTHORS  
TITLE  
COMMENT  
Contact: Gerald Rubin  
Berkeley Drosophila Genome Project  
University of California, Berkeley  
LSA Building, Berkeley, CA 94720-3200, USA  
Fax: 5106433947  
Email: [germy@fruitfly.berkeley.edu](mailto:germy@fruitfly.berkeley.edu)  
Sequence recovery method was inverse PCR.  
Sequence orientation is forward strand relative to 5' end of P  
element

The P element insertion position is base 52 in the 76 bases. This  
insertion position refers to the first base of the 8 base target  
recognition sequence.  
Class: transposon-tagged.

## FEATURES

source

1. 76  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="Drosophila melanogaster P(SUPor-P) P element  
insertion lines"  
/note="Inverse PCR was performed on Drosophila  
melanogaster strains each of which contains one or more  
P(SUPor-P) P-element transposon insertion. The resultant  
fragment for each strain was directly sequenced to  
determine the genomic sequence at the site of insertion.  
Details of the protocols used can be found at  
<http://www.fruitfly.org/about/methods/inverse.pcr.html>."

## ORIGIN

Query Match 74.0%; Score 14.8; DB 9; Length 76;  
Best Local Similarity 88.9%; Pred. No. 8.1e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGAGCCCTCTCCA 20  
|||||  
Db 54 GCGGAGCCCTCTCCA 37

RESULT 4  
LOCUS BU861576 91 bp mRNA linear EST 16-OCT-2002  
DEFINITION S003H06 Populus imbed seed cDNA library Populus tremula cDNA 5  
prime, mRNA sequence.  
ACCESSION BU861576  
VERSION BU861576.1 GI:24047636  
KEYWORDS EST.

SOURCE Populus tremula  
ORGANISM Populus tremula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosoids; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 91)  
Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
The poplar tree transcriptome: Analysis of expressed sequence tags

JOURNAL  
COMMENT

from multiple libraries  
Unpublished (2002)  
Contact: BHALERAO RUPALI R.  
Umea Plant Science Center  
Department of Plant Physiology  
University of Umea, 901 87 Umea, Sweden  
Tel: +46 90 786 5279  
Fax: +46 90 786 6676  
Email: rupali.bhalerao@plantphys.umu.se.

## FEATURES

source

1. .91  
/organism="Populus tremula"  
/mol\_type="rRNA"  
/db\_xref="taxon:113636"  
/tissue\_type="imbibed seed"  
/clone\_lib="Populus imbibed seed cDNA library"

## ORIGIN

Query Match 74.0%; Score 14.8; DB 5; Length 91;  
Best Local Similarity 88.9%; Pred. No. 8e+04; 2; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AGCGGACGCCCCCTCTCC 19  
2 AGCGGACGCTCTCTCC 19

DB

## RESULT 5

CD672055/c 82 bp mRNA linear EST 24-JUN-2003  
LOCUS f609f02.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone  
DEFINITION CD672055.1 GI:32173786

ACCESSION CD672055.1 GI:32173786  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 82)  
Wietow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of adult human iris for the NEIBank  
Project: steroid-response factors and similarities with retinal  
pigment epithelium  
Mol. Vis. 8 (4), 185-195 (2002)  
12107412

## COMMENT

Contact: Wietow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: gwaeme@helix.nih.gov  
Plate: 09 row: f column: 02  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers

## FEATURES

source

1. .82  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="f609f02"  
/tissue\_type="Iris"  
/dev\_stage="Adult"  
/lab\_host="EMD10B"  
/clone\_lib="Human Iris cDNA (Normalized): fg"  
/note="Organ: Eye; Vector: pCMTSPORT6. A human iris  
library (bx) was normalized by self-subtraction. One  
portion of double stranded plasmid DNA representing the  
library was linearized by NotI. This NotI digested library  
was used as a template for biotinylated RNA synthesis  
using SP6 RNA polymerase. Another portion of the double

## ORIGIN

Query Match 72.0%; Score 14.4; DB 6; Length 82;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CGGACGCCCCCTCTCC 19  
16 CGGACGCCCCCTCTCC 1

DB

## RESULT 6

AU107434 50 bp mRNA linear EST 28-JAN-2004  
LOCUS AU107434 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION LNC15774.1 mRNA sequence.

ACCESSION AU107434.1 GI:13556955  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tanoda,T., Mizushima-Sugano,J., Sese,J.,  
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,  
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
11375929

REFERENCE AU107434 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
AUTHORS Suzuki,Y., Taira,H., Tanoda,T., Mizushima-Sugano,J., Sese,J.,  
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,  
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
TITLE Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
PUBMED 11375929

COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1 Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and  
Sugano,S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).  
Location/Qualifiers

## FEATURES

source

1. .50  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="LNC15774"  
/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 1; Length 50;  
Best Local Similarity 84.2%; Pred. No. 1.5e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAGGCGACGCCCCCTCTCC 19  
13 GAGGCGAGCGCCTCTCC 31

DB

## RESULT 7

A1123506 58 bp mRNA linear EST 01-OCT-1998  
LOCUS A1123506 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone  
DEFINITION g601009.x1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone  
IMAGE:163616.3 similar to SW:DNA DROME P48608 DIAPHANOUS PROTEIN.  
;contains element MSRI repetitive element ;, mRNA sequence.

stranded plasmid library was converted to single-stranded  
circles in vitro using Gene II and Exonuclease III (Life  
Technologies). Single-stranded DNA (1 mg) was hybridized  
(Cot 500) with 41 mg of Bio-RNA and vector blocking  
oligonucleotides. The hybridized Bio-RNA/ss-circles were  
removed by streptavidin:phenol extraction. EST analysis  
was performed on the library at the NIH Intramural  
Sequencing Center (NISC)."

ACCESSION A1123506  
 VERSION A1123506.1 GI:3539272  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 58)  
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgaabs-remail.nih.gov  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

FEATURES  
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 Trace considered overall poor quality  
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 /db\_xref="taxon:9606"  
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 /dev\_stage="adult"  
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 /clone\_11b="Soares parathyroid tumor MBHPA"  
 /note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 5'-TGTTCACATCTGAAGTGGAGCGCCGACCAATTTTTTTTTTTTTTTT  
 TTTT-3'1, double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN  
 Query Match 71.0%; Score 14.2; DB 1; Length 58;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+05;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCTCTCCA 20  
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 Db 10 AGCCGAGCCCTCTCCA 28

RESULT 8  
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 DEFINITION SALK\_084890.49.05.x Arabidopsis thaliana TDNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_084890.49.05.x, genomic survey sequence.  
 ACCESSION BH855612  
 VERSION BH855612  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE  
 AUTHORS Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
 TITLE A sequence-indexed library of insertion mutations in the Arabidopsis genome  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Joseph R. Ecker  
 The Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: eckere@salk.edu  
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g31410. Class: TDNA tagged.

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 /mol\_type="genomic DNA"  
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 /clone\_11b="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

ORIGIN  
 Query Match 71.0%; Score 14.2; DB 9; Length 59;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+05;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTCTCC 19  
 |||||  
 Db 45 GAGCGGAGCTCTCTCTCC 27

RESULT 9  
 LOCUS CX001505 62 bp mRNA linear EST 03-DEC-2004  
 DEFINITION iv41d08.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,  
 mRNA sequence.  
 ACCESSION CX001505  
 VERSION CX001505.1 GI:56272921  
 KEYWORDS EST.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE  
 AUTHORS Baliga,V.S., Nascento,L.U. and McCombie,W.R.  
 TITLE ESTs from Canis familiaris left cardiac ventricle (dog)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mcombie@cshl.org

FEATURES  
 source  
 Location/Qualifiers  
 1..62  
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 /mol\_type="mRNA"







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 Db 35 AGCGCAGCCTTCTCTTA 53

RESULT 15  
 CG716533/c  
 LOCUS 1119045G02.x1 1119 - RescuerMu Grid AA Zea mays genomic, genomic  
 DEFINITION survey sequence.

ACCESSION CG716533  
 VERSION CG716533.1 GI:37744943  
 KEYWORDS GSS.

SOURCE  
 ORGANISM Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 60)  
 Walbot,V.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Maize genomic sequences found using engineered RescuerMu transposon  
 unpublished (2001)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu

Possible ligation site so sequence was trimmed. Post-ligation  
 sequence submitted separately.  
 Plate: 1119045 row: G column: 02  
 Class: transposon-tagged.  
 Location/Qualifiers

## FEATURES

source

1..60  
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 /db\_xref="taxon:4577"  
 /issue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="1119 - RescuerMu Grid AA"  
 /note="Organ: leaf; Vector: RescuerMu (engineered from  
 pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
 RescuerMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescuerMu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'RescuerMu.' Grid AA was grown at UC San Diego in 2002. DNA  
 was extracted from leaf strips, double digested using  
 BamHI and BglII, and ligated to form circular plasmids.  
 DH10B cells were transformed and then screened on LB  
 plates with ampicillin."

## ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 60;  
 Best Local Similarity 88.2%; Pred. No. 2.1e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 4 CGGCAGCCCCCTCTCCA 20  
 |||||  
 Db 19 CGGCAGCCCCCTCTCCA 3

Search completed: December 24, 2005, 18:28:12  
 Job time : 1577 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 seconds  
(without alignments)  
739.111 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20

Sequence: 1 gagcgagcagccctccca 20

Scoring table: IDENTITY\_NUC

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCITUS\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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C 1	14.8	74.0	60	9	5252465-13
2	14.4	72.0	55	3	US-09-887-469-13
3	13.6	68.0	50	3	US-10-131-827-169
4	13.6	68.0	55	3	US-09-357-740-16
5	13.6	68.0	92	3	US-09-513-999C-11657
6	13.2	65.0	30	6	PCT-US95-07372-3
7	13	65.0	93	3	US-09-513-999C-23015
8	12.8	64.0	20	3	US-09-120-853-19
9	12.8	64.0	42	3	US-09-120-853-3
10	12.8	64.0	47	3	US-09-422-978-3328
11	12.8	64.0	48	3	US-09-400-653A-49
12	12.8	64.0	54	2	US-08-311-486C-1107
13	12.8	64.0	55	3	US-09-357-740-18
14	12.8	64.0	79	3	US-09-407-605-56
15	12.8	64.0	83	3	US-09-621-976-17097
16	12.8	64.0	91	2	US-07-752-101A-53
17	12.8	64.0	91	2	US-09-513-999C-27692
18	12.8	64.0	93	3	US-08-976-413A-420
19	12.8	64.0	100	3	US-09-861-893-41
20	12.6	63.0	21	2	US-08-465-590-136
21	12.6	63.0	21	3	US-08-711-417C-136
22	12.6	63.0	21	3	US-09-177-650-42
23	12.6	63.0	21	3	US-09-723-909-136
24	12.6	63.0	21	6	PCT-US93-08743-136

25	12.6	63.0	25	3	US-08-772-512A-18	Sequence 18, Appl
26	12.6	63.0	25	3	US-09-396-196G-66325	Sequence 66325, A
27	12.6	63.0	25	3	US-09-396-196G-66326	Sequence 66326, A
28	12.6	63.0	25	3	US-09-396-196G-66337	Sequence 66337, A
29	12.6	63.0	25	3	US-09-396-196G-86053	Sequence 86053, A
30	12.6	63.0	25	9	5504194-3	Patent No. 5504194
31	12.6	63.0	26	3	US-09-271-013-1	Sequence 1, Appl
32	12.6	63.0	35	2	US-07-832-905B-48	Sequence 48, Appl
33	12.6	63.0	35	2	US-08-700-757-48	Sequence 48, Appl
34	12.6	63.0	36	3	US-10-012-070A-16	Sequence 16, Appl
35	12.6	63.0	39	3	US-09-046-158A-9	Sequence 9, Appl
36	12.6	63.0	41	3	US-09-214-151-5	Sequence 5, Appl
37	12.6	63.0	41	3	US-09-908-660-5	Sequence 4, Appl
38	12.6	63.0	42	2	US-07-982-712-4	Sequence 47, Appl
39	12.6	63.0	44	2	US-07-832-905B-47	Sequence 47, Appl
40	12.6	63.0	44	2	US-08-700-757-47	Sequence 47, Appl
41	12.6	63.0	69	2	US-07-609-716-29	Sequence 29, Appl
42	12.6	63.0	69	2	US-08-175-155-27	Sequence 27, Appl
43	12.6	63.0	69	2	US-08-477-509B-62	Sequence 62, Appl
44	12.6	63.0	69	3	US-08-482-085B-62	Sequence 62, Appl
45	12.6	63.0	69	3	US-08-475-411A-29	Sequence 29, Appl

## ALIGNMENTS

```
RESULT 1
5252465-13/C
; Patent No. 5252465
; APPLICANT: NIGON, VICTOR-MARC;VERDIER, GERARD;CHEBLONNE,
; YAHIA;COSSET, FRANCOIS-LOIC;LEGRAS, CATHERINE;REYS-BRION,
; ASRID;BELAKHEI, MUSTAPHA;MALLET, FRANCOIS;SAVATIER, PIERRE,
; THORAVALL, PIERICK;SAMAKUT, JACQUES;PONCET, DIDIER;BAGNAT,
; CLAUDE;BENCHAIBI, MILOUD
; TITLE OF INVENTION: AVIAN ERYTHROBLASTOSIS VIRUS VECTORS FOR
; INTEGRATION AND EXPRESSION OF HETEROLOGOUS GENES IN AVIAN CELLS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/477, 833
; FILING DATE: 03-OCT-1988
; SEQ ID NO:13:
; LENGTH: 60
5252465-13

Query Match      74.0%; Score 14.8; DB 9; Length 60;
Best Local Similarity 88.9%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      2  AGCGGAGAGCCGCTCTCC 19
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RESULT 2
US-09-887-469-13
; Sequence 13, Application US/09887469
; Patent No. 6923971
; GENERAL INFORMATION:
; APPLICANT: Krempf, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; FILE REFERENCE: 15280-424-IUS
; CURRENT APPLICATION NUMBER: US/09/887, 469
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213, 708
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
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LENGTH: 55  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Artificial  
OTHER INFORMATION: Respiratory Syncytial Virus  
US-09-887-469-13

Query Match 72.0%; Score 14.4; DB 3; Length 55;  
Best Local Similarity 93.8%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGCGAGCCCCCTCTC 18  
Db 22 GCGGCGAGCCCCCTCTC 37

RESULT 3  
US-10-131-827-169  
Sequence 169, Application US/10131827  
Patent No. 6905827  
GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
FILE REFERENCE: 506612000120  
CURRENT APPLICATION NUMBER: US/10/131,827  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 9090  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 169  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-131-827-169

Query Match 68.0%; Score 13.6; DB 3; Length 50;  
Best Local Similarity 80.0%; Pred. No. 8.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 6 GAACGAAAGCCCCCTCTCA 25

RESULT 4  
US-09-357-740-16/c  
Sequence 16, Application US/09357740  
Patent No. 6348596  
GENERAL INFORMATION:  
APPLICANT: Lee, Linda G.  
APPLICANT: Graham, Ronald J.  
APPLICANT: Mullah, Khairuzzaman B.  
APPLICANT: Haxo, Francis T.  
TITLE OF INVENTION: ASYMMETRIC CYANINE DYE QUENCHERS  
FILE REFERENCE: 9584-007  
CURRENT APPLICATION NUMBER: US/09/357,740  
CURRENT FILING DATE: 1999-07-20  
EARLIER APPLICATION NUMBER: 09/012,525  
EARLIER FILING DATE: 1998-01-23  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 55  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide  
US-09-357-740-16

Query Match 68.0%; Score 13.6; DB 3; Length 55;  
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Qy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 52 GATGGCGAGCCCCCAGTCCA 33

RESULT 5  
US-09-513-999C-11657/C  
Sequence 11657, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59,US2,REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 11657  
LENGTH: 92  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-11657

Query Match 68.0%; Score 13.6; DB 3; Length 92;  
Best Local Similarity 80.0%; Pred. No. 8e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 34 GAGCGGCGCGCGCTCGCCA 15

RESULT 6  
PCT-US95-07372-3  
Sequence 3, Application PC/TUS9507372  
GENERAL INFORMATION:  
APPLICANT: Oklahoma Medical Research Foundation  
TITLE OF INVENTION: Calcium Binding Recombinant  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07372  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.

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; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP106CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-07372-3

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Best Local Similarity 83.3%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AGCGGAGCCCTCTCC 19
Db      2 AGCGGAGCCCTCTCC 19

RESULT 7
US-09-513-999C-23015
; Sequence 23015, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 23015
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-23015

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GCAGGCCCTCTC 18
Db      62 GCAGGCCCTCTC 74

RESULT 8
US-09-120-853-19/c
; Sequence 19, Application US/09120853
; Patent No. 6057437
; GENERAL INFORMATION:
; APPLICANT: Kamiya, Kiyoa
; APPLICANT: Matsuda, Yoko
; APPLICANT: Uchida, Kiyooshi
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND
; FILE REFERENCE: 07898/030001
; CURRENT APPLICATION NUMBER: US/09/120,853
; CURRENT FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: JP 213838/1997
; EARLIER FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-120-853-19

Query Match      64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CGGAGCCCTCTCC 19
Db      20 CTGGGAGCCCTCTCC 5

RESULT 9
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; Sequence 3, Application US/09120853
; Patent No. 6057437
; GENERAL INFORMATION:
; APPLICANT: Kamiya, Kiyoa
; APPLICANT: Matsuda, Yoko
; APPLICANT: Uchida, Kiyooshi
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND
; FILE REFERENCE: 07898/030001
; CURRENT APPLICATION NUMBER: US/09/120,853
; CURRENT FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: JP 213838/1997
; EARLIER FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-120-853-3

Query Match      64.0%; Score 12.8; DB 3; Length 42;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CGGAGCCCTCTCC 19
Db      42 CTGGGAGCCCTCTCC 27

RESULT 10
US-09-422-978-3328
; Sequence 3328, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSRT.020CD1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3328
; LENGTH: 47
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TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 99-3335-53 : polymorphic base C or T  
US-09-422-978-3328

Query Match  
Best Local Similarity 64.0%; Score 12.8; DB 3; Length 47;  
Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGCAGCCCCCTCTCA 20  
DB 30 GCCAGCCCCCTCTCA 45

RESULT 11  
US-09-400-653A-49  
Sequence 49, Application US/09400653A  
Patent No. 6348311  
GENERAL INFORMATION:  
APPLICANT: Kaetan, Michael  
APPLICANT: Canman, Christine  
APPLICANT: Kim, Seong-Tae  
APPLICANT: Lim, Dae-Sik  
APPLICANT: St. Jude Children's Research Hospital  
TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies  
FILE REFERENCE: 24271/F142  
CURRENT FILING DATE: 1999-09-21  
PRIOR APPLICATION NUMBER: 09/248,061  
PRIOR FILING DATE: 1999-02-10  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 49  
LENGTH: 48  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR primer  
US-09-400-653A-49

Query Match  
Best Local Similarity 64.0%; Score 12.8; DB 3; Length 48;  
Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTC 16  
DB 7 GAGCGGAGCCCCCTC 22

RESULT 12  
US-08-311-486C-1107/C  
Sequence 1107, Application US/08311486C  
Patent No. 5811300  
GENERAL INFORMATION:  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth Draper  
APPLICANT: Kevin Kieich  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McWiggen  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: TNF-  
NUMBER OF SEQUENCES: 1157  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California

COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,486C  
FILING DATE: September 23, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/166  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-311-486C-1107

Query Match  
Best Local Similarity 64.0%; Score 12.8; DB 2; Length 54;  
Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGCAGCCCCCTCTCA 20  
DB 21 GGTAGCCCCCTCTCA 6

RESULT 13  
US-09-357-740-18/C  
Sequence 18, Application US/09357740  
Patent No. 6348596  
GENERAL INFORMATION:  
APPLICANT: Lee, Linda G.  
APPLICANT: Graham, Ronald J.  
APPLICANT: Mullah, Khairuzaman B.  
APPLICANT: Haxo, Francis T.  
TITLE OF INVENTION: ASYMMETRIC CYANINE DYE QUENCHERS  
FILE REFERENCE: 9584-007  
CURRENT APPLICATION NUMBER: US/09/357,740  
CURRENT FILING DATE: 1999-07-20  
EARLIER APPLICATION NUMBER: 09/012,525  
EARLIER FILING DATE: 1998-01-23  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 18  
LENGTH: 55  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide  
US-09-357-740-18

Query Match  
Best Local Similarity 64.0%; Score 12.8; DB 3; Length 55;  
Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



OY 5 GGCAGCCCCCTCTCCA 20  
|||||  
Db 48 GGCAGCCCCCTCTCCA 33

RESULT 14  
US-09-407-605-56  
; Sequence 56, Application US/09407605  
; Patent No. 6924365  
; GENERAL INFORMATION:  
; APPLICANT: Selden, Richard F.  
; APPLICANT: Miller, Allan M.  
; APPLICANT: Treco, Douglas A.  
; TITLE OF INVENTION: OPTIMIZED MESSENGER RNA  
; FILE REFERENCE: 10278-009001  
; CURRENT APPLICATION NUMBER: US/09/407,605  
; CURRENT FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/130,241  
; PRIOR FILING DATE: 1999-04-20  
; PRIOR APPLICATION NUMBER: 60/102,239  
; PRIOR FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56  
; LENGTH: 79  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-407-605-56

Query Match 64.0%; Score 12.8; DB 3; Length 79;  
Best Local Similarity 87.5%; Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCCCCTC 16  
|||||  
Db 48 GAGCGGAGCCCCCTC 63

RESULT 15  
US-09-621-976-17097/C  
; Sequence 17097, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17097  
; LENGTH: 83  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-17097

Query Match 64.0%; Score 12.8; DB 3; Length 83;  
Best Local Similarity 77.8%; Pred. No. 1.7e+04;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 AGCGGAGCCCCCTCTCC 19  
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Db 58 AGCGGAGCCCCCTCTCC 41

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Job time : 48.1 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 : Search time 337.6 Seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20  
Sequence: 1 gagcgagcagccctctcca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:

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4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBSCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBSCOMB.seq:\*  
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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBSCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBSCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBSCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBSCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-1
2	20	100.0	35	6	US-10-263-162-56
3	15.4	77.0	57	6	US-10-258-825-9
4	15.2	76.0	25	6	US-10-056-229-218
5	14.8	74.0	25	7	US-10-719-956-427632
6	14.8	74.0	25	8	US-10-719-900-598148
7	14.8	74.0	81	7	US-10-468-252-18
8	14.4	72.0	55	3	US-09-887-469-13
9	14.4	72.0	55	3	US-09-887-469-13
10	14.4	72.0	55	9	US-10-704-116-13
11	14.4	72.0	60	6	US-10-258-825-12
12	14.2	71.0	25	7	US-10-719-956-54800
13	14.2	71.0	25	8	US-10-719-900-467299
14	14.2	71.0	25	9	US-10-956-157-282024
15	14.2	71.0	51	8	US-10-865-478-484
16	14.2	71.0	70	3	US-09-994-228-64
17	14.2	71.0	71	3	US-09-994-228-63
18	13.8	69.0	25	7	US-10-719-956-630092
19	13.8	69.0	25	10	US-11-036-317-815857
20	13.8	69.0	65	3	US-09-908-975-25620
21	13.6	68.0	25	7	US-10-719-956-265585
22	13.6	68.0	25	7	US-10-719-956-603362
23	13.6	68.0	25	8	US-10-719-900-481600

24	13.6	68.0	25	8	US-10-719-900-481601	Sequence 481601,
25	13.6	68.0	25	8	US-10-719-900-708812	Sequence 708812,
26	13.6	68.0	25	8	US-10-719-900-863112	Sequence 863112,
27	13.6	68.0	25	8	US-10-719-900-880696	Sequence 880696,
28	13.6	68.0	25	9	US-10-956-157-210521	Sequence 210521,
29	13.6	68.0	25	9	US-10-956-157-226246	Sequence 226246,
30	13.6	68.0	25	9	US-10-956-157-244559	Sequence 244559,
31	13.6	68.0	25	9	US-10-956-157-276761	Sequence 276761,
32	13.6	68.0	25	10	US-11-036-317-75400	Sequence 75400, A
33	13.6	68.0	25	10	US-11-036-317-76950	Sequence 76950, A
34	13.6	68.0	25	10	US-11-036-317-170159	Sequence 170159,
35	13.6	68.0	25	10	US-11-036-317-205561	Sequence 205561,
36	13.6	68.0	25	10	US-11-036-317-232211	Sequence 232211,
37	13.6	68.0	25	10	US-11-036-317-346344	Sequence 346344,
38	13.6	68.0	25	10	US-11-036-317-410480	Sequence 410480,
39	13.6	68.0	25	10	US-11-036-317-421744	Sequence 421744,
40	13.6	68.0	25	10	US-11-036-317-449511	Sequence 449511,
41	13.6	68.0	25	10	US-11-036-317-815913	Sequence 815913,
42	13.6	68.0	34	6	US-10-203-821-30	Sequence 30, Appl
43	13.6	68.0	50	6	US-10-131-827-169	Sequence 169, Appl
44	13.6	68.0	65	3	US-09-908-975-30360	Sequence 30360, A
45	13.6	68.0	70	9	US-10-957-432-258	Sequence 258, App

#### ALIGNMENTS

RESULT 1  
US-09-296-264-1  
Sequence 1, Application US/09296264  
Publication No. US20030083274A1  
GENERAL INFORMATION:  
APPLICANT: WRIGHT, Jim A.  
APPLICANT: YOUNG, Aiping H.  
TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND  
TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH  
FILE REFERENCE: 032396-043  
CURRENT APPLICATION NUMBER: US/09/296,264  
CURRENT FILING DATE: 1999-04-22  
EARLIER APPLICATION NUMBER: US 60/082,791  
EARLIER FILING DATE: 1998-04-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Human  
US-09-296-264-1

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGCGGAGCCCTCTCCA 20  
Db 1 GAGCGGAGCCCTCTCCA 20

RESULT 2  
US-10-263-162-56/C  
Sequence 56, Application US/10263162  
Publication No. US20030186868A1  
GENERAL INFORMATION:  
APPLICANT: Rosenbaum, et al.  
TITLE OF INVENTION: Anti-Angiogenic Peptides  
FILE REFERENCE: REG 810  
CURRENT APPLICATION NUMBER: US/10/263,162  
CURRENT FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: 60/326,712  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 56  
LENGTH: 35  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-263-162-56

Query Match 100.0%; Score 20; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTCCA 20  
|||||  
DB 31 GAGCGGAGCCCCCTCTCCA 12

RESULT 3  
US-10-258-825-9  
Sequence 9, Application US/10258825  
Publication No. US20030133911A1  
GENERAL INFORMATION:  
APPLICANT: Conzelmann, Karl-Klaus  
TITLE OF INVENTION: Pneumovirus NS Proteins Antagonising the Interferon (IFN) Response  
FILE REFERENCE: AML00751  
CURRENT APPLICATION NUMBER: US/10/258,825  
CURRENT FILING DATE: 2002-10-25  
PRIOR APPLICATION NUMBER: PCT/EP01/04740  
PRIOR FILING DATE: 2001-04-26  
PRIOR APPLICATION NUMBER: DE 100 20 505.4  
PRIOR FILING DATE: 2000-04-26  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 9  
LENGTH: 57  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Primer hns1-No. US20030133911A115  
US-10-258-825-9

Query Match 77.0%; Score 15.4; DB 6; Length 57;  
Best Local Similarity 94.1%; Pred. No. 2.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTC 18  
|||||  
DB 6 AGCGGAGCCCCCTCTC 22

RESULT 4  
US-10-056-229-218/c  
Sequence 218, Application US/10056229  
Publication No. US20030198943A1  
GENERAL INFORMATION:  
APPLICANT: Remacle, Josee  
APPLICANT: Hamels, Sandrine  
APPLICANT: Zammateo, Nathalie  
APPLICANT: Lockman, Laurence  
APPLICANT: Dufour, Sophie  
APPLICANT: Alexandre, Isabelle  
APPLICANT: De Longueville, Francoise  
TITLE OF INVENTION: IDENTIFICATION OF A LARGE NUMBER OF  
TITLE OF INVENTION: BIOLOGICAL (MICRO)ORGANISMS GROUPS AT DIFFERENT  
TITLE OF INVENTION: LEVELS BY THEIR DETECTION ON A SAME ARRAY  
FILE REFERENCE: VAMW213-001CPI  
CURRENT APPLICATION NUMBER: US/10/056,229  
CURRENT FILING DATE: 2002-01-23  
PRIOR APPLICATION NUMBER: EP 00870055.1  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: EP 00870204.5  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: US 09/817,014  
PRIOR FILING DATE: 2001-03-23  
NUMBER OF SEQ ID NOS: 321

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 218  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Streptococcus pneumoniae  
US-10-056-229-218

Query Match 76.0%; Score 15.2; DB 6; Length 25;  
Best Local Similarity 85.0%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTCCA 20  
|||||  
DB 22 GAGCGGAGCACTATCTCCA 3

RESULT 5  
US-10-719-956-427632  
Sequence 427632, Application US/10719956  
Publication No. US20040146910A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
FILE REFERENCE: 3527.1  
CURRENT APPLICATION NUMBER: US/10/719,956  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,836  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 699466  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 427632  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-10-719-956-427632

Query Match 74.0%; Score 14.8; DB 7; Length 25;  
Best Local Similarity 88.9%; Pred. No. 5.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTC 18  
|||||  
DB 2 GAGCGGAGCTCTCTTTC 19

RESULT 6  
US-10-719-900-598148  
Sequence 598148, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 598148  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-598148

Query Match 74.0%; Score 14.8; DB 8; Length 25;  
Best Local Similarity 88.9%; Pred. No. 5.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTC 18  
|||||  
DB 2 GAGCGGAGCTCTCTTTC 19

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RESULT 7
US-10-468-252-18/C
; Sequence 18, Application US/10468252
; Publication No. US20040166560A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corporation
; TITLE OF INVENTION: Expression of recombinant proteinase K from
; TITLE OF INVENTION: Tetrachlam album in yeast
; FILE REFERENCE: RDID 01011
; CURRENT APPLICATION NUMBER: US/10/468,252
; CURRENT FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-468-252-18

Query Match          74.0%; Score 14.8; DB 7; Length 81;
Best Local Similarity 88.9%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGAGCCCTCTCCA 20
DB 75 GCGGAGCAGCCGCTCA 58

RESULT 8
US-09-887-469-13
; Sequence 13, Application US/09887469
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Krempf, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; FILE REFERENCE: 15280-424-1US
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-887-469-13

Query Match          72.0%; Score 14.4; DB 3; Length 55;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGAGCCCTCTC 18
DB 22 GCGGCGCCCTCTC 37

RESULT 9
US-09-887-469-13
; Sequence 13, Application US/09887469
; Publication No. US20040258714A9
; GENERAL INFORMATION:
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; APPLICANT: Krempf, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; FILE REFERENCE: 15280-424-1US
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-887-469-13

Query Match          72.0%; Score 14.4; DB 3; Length 55;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGAGCCCTCTC 18
DB 22 GCGGCGCCCTCTC 37

RESULT 10
US-10-704-116-13
; Sequence 13, Application US/10704116
; Publication No. US20050158338A1
; GENERAL INFORMATION:
; APPLICANT: BUCHHOLZ, URSULA
; APPLICANT: COLLINS, PETER L.
; APPLICANT: MURPHY, BRIAN R.
; APPLICANT: WHITEHEAD, STEPHEN S.
; TITLE OF INVENTION: PRODUCTION OF ATTENUATED, HUMAN-BOVINE CHIMERIC
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUSES FOR USE IN IMMUNOGENIC
; FILE REFERENCE: 2303-022-05
; CURRENT APPLICATION NUMBER: US/10/704,116
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 09/887,469
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/602,212
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/143,132
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Bovine respiratory syncytial virus
US-10-704-116-13

Query Match          72.0%; Score 14.4; DB 9; Length 55;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGAGCCCTCTC 18
DB 22 GCGGCGCCCTCTC 37
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RESULT 11
US-10-258-825-12
; Sequence 12, Application US/10258825
; Publication No. US20030133911A1
; GENERAL INFORMATION:
; APPLICANT: Conzelmann, Karl-Klaus
; TITLE OF INVENTION: Pneumovirus NS Proteins Antagonising the Interferon (IFN) Response
; FILE REFERENCE: AM100751
; CURRENT APPLICATION NUMBER: US/10/258,825
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/EP01/04740
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: DE 100 20 505.4
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer mns1-No. US20030133911A1FCORV5
US-10-258-825-12

Query Match          72.0%; Score 14.4; DB 6; Length 60;
Best Local Similarity 93.8%; Pred. No. 6.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GCGGCAGCCCCCTCTC 18
        ||||| ||||| |||||
Db       10 GCGGCAGCCCCCTCTC 25

RESULT 12
US-10-719-956-54800/c
; Sequence 54800, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 54800
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-54800

Query Match          71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 9.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AGCGGACGCCCCCTCTCCA 20
        ||||| ||||| |||||
Db       23 AGCAGAGACTCCCTCTCCA 5

RESULT 13
US-10-719-900-467299/c
; Sequence 467299, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
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; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 467299
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-467299

Query Match          71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 84.2%; Pred. No. 9.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GAGCGCAGCCCCCTCTCC 19
        ||||| ||||| |||||
Db       25 GAGTGCAGCCACTTCTCC 7

RESULT 14
US-10-956-157-282024/c
; Sequence 282024, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 282024
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-282024

Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 9.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AGCGGCAGCCCCCTCTCCA 20
        ||||| ||||| |||||
Db       21 AGCGGCATCCCCCTCTCA 3

RESULT 15
US-10-865-478-484/c
; Sequence 484, Application US/10865478
; Publication No. US20040235041A1
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: c53single Nucleotide Polymorphisms for Known Genes
; FILE REFERENCE: 15966-534-CIP1
; CURRENT APPLICATION NUMBER: US/10/865,478
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 09/443,199
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/442,129
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/442,849
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 484
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg40310734
US-10-865-478-484

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Query Match      71.0%; Score 14.2; DB 8; Length 51;
Best Local Similarity 84.2%; Pred. No. 8.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      1 GAGCGGACGCCCCCTCTCC 19
DB      19 GAGCGGACGCCCCCTCTCC 1

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 Job time : 338.6 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds  
(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20

Sequence: 1 gagcgagcagccctctcca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:

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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/ECT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length	ID	Description
C 1	14.2	71.0	25	US-11-121-849-233495	Sequence 233495,
C 2	14.2	71.0	25	US-11-121-849-278074	Sequence 278074,
C 3	13.8	69.0	25	US-11-121-849-151184	Sequence 151184,
C 4	13.8	69.0	25	US-11-121-849-464194	Sequence 464194,
C 5	13.6	68.0	25	US-11-121-849-151553	Sequence 151553,
C 6	13.6	68.0	25	US-11-121-849-315834	Sequence 315834,
C 7	13.6	68.0	25	US-11-121-849-315891	Sequence 315891,
C 8	13.6	68.0	25	US-11-121-849-409754	Sequence 409754,
C 9	13.6	68.0	25	US-11-121-849-409755	Sequence 409755,
C 10	13.6	68.0	25	US-11-121-849-409756	Sequence 409756,
C 11	13.6	68.0	25	US-11-121-849-409757	Sequence 409757,
C 12	13.6	68.0	25	US-11-121-849-411377	Sequence 411377,
C 13	13.6	68.0	25	US-11-121-849-411378	Sequence 411378,
C 14	13.6	68.0	25	US-11-121-849-411379	Sequence 411379,
C 15	13.6	68.0	25	US-11-121-849-411380	Sequence 411380,
C 16	13.2	66.0	25	US-11-121-849-124687	Sequence 124687,
C 17	13.2	66.0	25	US-11-121-849-124773	Sequence 124773,
C 18	13.2	66.0	25	US-11-121-849-124774	Sequence 124774,
C 19	13.2	66.0	25	US-11-121-849-233496	Sequence 233496,
C 20	12.8	64.0	25	US-11-121-849-13520	Sequence 13520, A
C 21	12.8	64.0	25	US-11-121-849-19002	Sequence 19002, A
C 22	12.8	64.0	25	US-11-121-849-264750	Sequence 264750,
C 23	12.8	64.0	25	US-11-121-849-264751	Sequence 264751,

24	12.8	64.0	25	7	US-11-121-849-265503	Sequence 265503,
25	12.8	64.0	25	7	US-11-121-849-307663	Sequence 307663,
26	12.8	64.0	25	7	US-11-121-849-307664	Sequence 307664,
C 27	12.8	64.0	25	7	US-11-121-849-426195	Sequence 426195,
C 28	12.8	64.0	34	6	US-10-525-710-60	Sequence 60, App1
C 29	12.6	63.0	20	7	US-11-040-468-7	Sequence 7, App1
C 30	12.6	63.0	25	7	US-11-121-849-28975	Sequence 28975, A
C 31	12.6	63.0	25	7	US-11-121-849-32420	Sequence 32420, A
C 32	12.6	63.0	25	7	US-11-121-849-38350	Sequence 38350, A
C 33	12.6	63.0	25	7	US-11-121-849-178326	Sequence 178326,
C 34	12.6	63.0	25	7	US-11-121-849-193304	Sequence 193304,
C 35	12.6	63.0	25	7	US-11-121-849-219241	Sequence 219241,
C 36	12.6	63.0	25	7	US-11-121-849-219492	Sequence 219492,
C 37	12.6	63.0	25	7	US-11-121-849-363351	Sequence 363351,
C 38	12.6	63.0	25	7	US-11-121-849-363352	Sequence 363352,
C 39	12.6	63.0	25	7	US-11-121-849-364925	Sequence 364925,
C 40	12.6	63.0	25	7	US-11-121-849-364926	Sequence 364926,
C 41	12.6	63.0	25	7	US-11-121-849-371701	Sequence 371701,
C 42	12.6	63.0	25	7	US-11-121-849-409753	Sequence 409753,
C 43	12.6	63.0	25	7	US-11-121-849-411376	Sequence 411376,
C 44	12.6	63.0	25	7	US-11-121-849-511145	Sequence 511145,
C 45	12.6	63.0	25	7	US-11-121-849-514701	Sequence 514701,

## ALIGNMENTS

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RESULT 1
US-11-121-849-233495/c
; Sequence 233495, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 233495
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-121-849-233495

Query Match      71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      2  AGCGGAGCCCTCTCCA 20
Db      22 AGCGTAGCCTCTCTCCA 4

RESULT 2
US-11-121-849-278074/c
; Sequence 278074, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 278074
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LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-278074

Query Match 71.0%; Score 14.2; DB 7; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTCCA 20  
DB 23 AGCGGAGCCACCTCTCCA 5

RESULT 3  
US-11-121-849-151184/C  
Sequence 151184, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 151184  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-151184

Query Match 69.0%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 2.6e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGAGCCCCCTCTCC 19  
DB 17 GCGGAGGTCCTCTCC 1

RESULT 4  
US-11-121-849-464194  
Sequence 464194, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 464194  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-464194

Query Match 69.0%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 2.6e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGGAGCCCCCTCTCCA 20  
DB 9 GAGGAGCCTCTCTCCA 25

RESULT 5  
US-11-121-849-151553  
Sequence 151553, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 151553  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-151553

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGAGCCCCCTCTCCA 20  
DB 5 GAGGAGAGCCCCCTCTCCA 24

RESULT 6  
US-11-121-849-315834/C  
Sequence 315834, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 315834  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-315834

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGAGCCCCCTCTCCA 20  
DB 20 GAGGAGGTCCTCTCCA 1

RESULT 7  
US-11-121-849-315891  
Sequence 315891, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 315891  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-315891

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 3 GAGCTGAGTCCCGCTCCA 22

RESULT 8  
US-11-121-849-409754/c  
Sequence 409754, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 409754  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-409754

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 24 GAGCGGCTGCTCCACTTCA 5

RESULT 9  
US-11-121-849-409755/c  
Sequence 409755, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 409755  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-409755

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 23 GAGCGGCTGCTCCACTTCA 4

RESULT 10  
US-11-121-849-409756/c  
Sequence 409756, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 409756  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-409756

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 22 GAGCGGCTGCTCCACTTCA 3

RESULT 11  
US-11-121-849-409757/c  
Sequence 409757, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 409757  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-409757

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GAGCGGAGCCCCCTCTCCA 20  
Db 21 GAGCGGCTGCTCCACTTCA 2

RESULT 12  
US-11-121-849-411377/c  
Sequence 411377, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 411377  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-411377

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FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411377
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-411377

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGCGAGCCCCCTCTCCA 20
DB 24 GAGCGGCGTCTCCCACTTCA 5

RESULT 13
US-11-121-849-411378/c
; Sequence 411378, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411378
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-411378

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGCGAGCCCCCTCTCCA 20
DB 23 GAGCGGCGTCTCCCACTTCA 4

RESULT 14
US-11-121-849-411379/c
; Sequence 411379, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-411379
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Query Match
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGCGAGCCCCCTCTCCA 20
DB 22 GAGCGGCGTCTCCCACTTCA 3

RESULT 15
US-11-121-849-411380/c
; Sequence 411380, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411380
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-411380

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGCGAGCCCCCTCTCCA 20
DB 21 GAGCGGCGTCTCCCACTTCA 2

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Job time : 135.3 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds  
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1953.383 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20  
Sequence: 1 cgagcagcgccgagcagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ha: \*  
2: gb\_in: \*  
3: gb\_env: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pr: \*  
9: gb\_ro: \*  
10: gb\_scs: \*  
11: gb\_sy: \*  
12: gb\_un: \*  
13: gb\_vl: \*  
14: gb\_htg: \*  
15: gb\_pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211659
2	15.4	77.0	99	6	AX435605
3	15.2	76.0	27	6	AX356224
4	15.2	76.0	87	6	E27048
5	14.8	74.0	100	6	AX93844
6	14.4	72.0	21	6	A91560
7	14.4	72.0	21	6	AR441815
8	14.4	72.0	21	6	AR477004
9	14.4	72.0	21	6	AX454812
10	14.4	72.0	21	6	BD023342
11	14.2	71.0	50	6	AX156996
12	14.2	71.0	51	6	AR444342
13	14.2	71.0	51	6	AX156995
14	14.2	71.0	100	9	RATMAP
15	13.8	69.0	37	6	ARI70305
16	13.8	69.0	37	6	E51079
17	13.8	69.0	37	6	AX007133
18	13.8	69.0	65	6	COS60111

19	13.8	69.0	100	6	AX989123	AX989123 Sequence
20	13.8	69.0	100	6	AX989124	AX989124 Sequence
21	13.6	68.0	23	6	ARI12201	ARI12201 Sequence
22	13.6	68.0	23	6	ARI45243	ARI45243 Sequence
23	13.6	68.0	27	6	I27230	I27230 Sequence
24	13.6	68.0	27	6	AR364785	AR364785 Sequence
25	13.6	68.0	30	6	AX611269	AX611269 Sequence
26	13.6	68.0	35	6	A07810	A07810 Sequence
27	13.6	68.0	43	6	A07815	A07815 Sequence
28	13.6	68.0	45	6	AR012045	AR012045 Sequence
29	13.6	68.0	45	6	AR062287	AR062287 Sequence
30	13.6	68.0	50	6	BD205008	BD205008 Sequence
31	13.6	68.0	50	6	AX014759	AX014759 Sequence
32	13.6	68.0	60	6	I25129	I25129 Sequence
33	13.6	68.0	60	6	AX613020	AX613020 Sequence
34	13.6	68.0	60	6	AX613021	AX613021 Sequence
35	13.6	68.0	60	6	AX613022	AX613022 Sequence
36	13.6	68.0	60	6	AX613023	AX613023 Sequence
37	13.6	68.0	65	6	C0556568	C0556568 Sequence
38	13.6	68.0	75	6	AR078717	AR078717 Sequence
39	13.6	68.0	75	6	I25146	I25146 Sequence
40	13.6	68.0	75	6	ARI98697	ARI98697 Sequence
41	13.6	68.0	75	15	MZEMTATP92	MZEMTATP92 Sequence
42	13.6	68.0	78	6	AR365016	AR365016 Sequence
43	13.6	68.0	81	6	A10907	A10907 Sequence
44	13.6	68.0	81	6	BD205009	BD205009 Sequence
45	13.6	68.0	81	6	AX014760	AX014760 Sequence

#### ALIGNMENTS

RESULT 1  
BD211659  
LOCUS  
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.  
ACCESSION BD211659.1 GI:33021429  
VERSION JP 2002512793-A/2.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.  
TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation  
JOURNAL Patent: JP 2002512793-A 2 08-MAY-2002;  
GENESENSE TECHNOLOGIES INC  
OS Homo sapiens (human)  
COMMENT  
PN JP 2002512793-A/2  
PD 08-MAY-2002  
PR 23-APR-1998 JP 2000545999  
PI JIM A WRIGHT, AIPING H YOUNG, YOON S LEE  
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC  
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

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FT key  
FT source  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGAGCAGCGCGCAGAGGAGC 20

RESULT 2  
AX435605  
LOCUS Sequence 4020 from Patent WO0229113. 99 bp DNA linear PAT 28-JUN-2002  
DEFINITION  
ACCESSION AX435605  
VERSION AX435605.1 GI:21660413  
KEYWORDS  
SOURCE Bacillus licheniformis  
ORGANISM Bacillus licheniformis  
REFERENCE 1 Berka, R. and Clausen, I. G.  
AUTHORS Methods for monitoring multiple gene expression  
TITLE Patent: WO 0229113-A 4020 11-APR-2002;  
JOURNAL Novozymes Biotech, Inc. (US); Novozymes A/S (DK)  
FEATURES  
source 1. .99  
/organism="Bacillus licheniformis"  
/mol\_type="unassigned DNA"  
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Query Match 77.0%; Score 15.4; DB 6; Length 99;  
Best Local Similarity 94.1%; Pred. No. 7.2e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCACGCGCGCAGAGGAGC 20  
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Db 31 GCACGCGCGCAGAGGAGC 47

RESULT 3  
AX356224  
LOCUS Sequence 18 from Patent WO0200905. 27 bp DNA linear PAT 06-FEB-2002  
DEFINITION  
ACCESSION AX356224  
VERSION AX356224.1 GI:18620731  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 Conner, T. W., Dubois, P., Malven, M. and Maseucci, J. D.  
AUTHORS Plant regulatory sequences for selective control of gene expression  
TITLE Patent: WO 0200905-A 18 03-JAN-2002;  
JOURNAL Monsanto Technology LLC (US)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
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/note="Synthetic"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 27;  
Best Local Similarity 85.0%; Pred. No. 1.1e+05;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGGAGC 20  
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Db 7 CGAGCAGCGCGCAAGAGGATC 26

RESULT 4  
E27048  
LOCUS 87 bp DNA linear PAT 18-JUN-2001

DEFINITION Novel receptor protein and utilization of the same.  
ACCESSION E27048  
VERSION E27048.1 GI:13026378  
KEYWORDS JP 1999152300-A/3.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 87)  
AUTHORS Kazunori, N., Yasushi, A. and Takashi, H.  
TITLE Novel receptor protein and utilization of the same  
JOURNAL Patent: JP 1999152300-A 3 08-JUN-1999;  
COMMENT  
TAKEDA CHEM IND LTD  
OS Unidentified  
PN JP 1999152300-A/3  
PD 08-JUN-1999  
PF 24-APR-1998 JP 1998114450  
PR  
PI KAZUNORI NISHI, YASUSHI ARAI, TAKASHI HORIGUCHI PC  
C07K14/715, A61K45/00, C07K16/28, C12N15/09, C12P21/02, PC  
C1201/02//A61K48/00,  
PC C12N5/10, (C12N15/09, C12R1:91), (C12P21/02, C12R1:91), C12N15/00,  
PC C12N5/00,  
PC (C12N15/00, C12R1:91)  
CC Strandedness: Double;  
CC Topology: linear;  
FH Key  
FT source 1. .87  
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Location/Qualifiers

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Query Match 76.0%; Score 15.2; DB 6; Length 87;  
Best Local Similarity 85.0%; Pred. No. 8.8e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGGAGC 20  
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Db 64 CGAGCAGCGCGCAGAGGAGC 45

RESULT 5  
AX93844  
LOCUS Sequence 5307 from Patent EP1260592. 100 bp DNA linear PAT 16-JAN-2004  
DEFINITION  
ACCESSION AX93844  
VERSION AX93844.1 GI:41000190  
KEYWORDS  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
REFERENCE 1 Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Escherichia.  
AUTHORS Donner, H., Drescher, B., Huber, A. and Weber, J.  
TITLE Biochip  
JOURNAL Patent: EP 1260592-A 5307 27-NOV-2002;  
MWG -Biotech AG (DE)  
FEATURES  
source 1. .100  
/organism="Escherichia coli"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:562"  
/note="mode mode U00096 complement (793079\_793867)"

ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 100;  
Best Local Similarity 88.9%; Pred. No. 1.2e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGGAGC 19

Db 50 GAGCGGCGCAGAGCAG 67  
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RESULT 6  
A91560  
LOCUS Sequence 87 from Patent WO9824928. 21 bp DNA linear PAT 22-JAN-2000  
DEFINITION  
ACCESSION A91560  
VERSION A91560.1 GI:6740515  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 21)  
AUTHORS Pallsgaard,N. and Hokland,P.  
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES  
JOURNAL Patent: WO 9824928-A 87 11-JUN-1998;  
PALLSGAARD NIELS (DK); HOKLAND PETER (DK)  
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Query Match 72.0%; Score 14.4; DB 6; Length 21;  
Best Local Similarity 93.8%; Pred. No. 2.4e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 3 AGCAGCGCGCAGAGGA 18  
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Db 1 AGCAGCGCGCAGAGGA 16  
RESULT 7  
AR441815/c  
LOCUS AR441815 Sequence 14 from patent US 6667164. 21 bp DNA linear PAT 20-FEB-2004  
DEFINITION  
ACCESSION AR441815  
VERSION AR441815.1 GI:42668042  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 21)  
AUTHORS Miller,M.W., Afanasieff,M. and Briles,W.E.  
TITLE Method for determining the MHC genotype of chickens  
JOURNAL Patent: US 6667164-A 14 23-DEC-2003;  
The Board of Trustees for Northern Illinois University and City of  
Hope; DeKalb, IL  
FEATURES  
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Best Local Similarity 93.8%; Pred. No. 2.4e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 5 CACGCGCGCAGAGGAGC 20  
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Db 16 CACGCGCGCAGAGGAGC 1  
RESULT 8  
AR477004/c  
LOCUS AR477004 Sequence 14 from patent US 6696253. 21 bp DNA linear PAT 14-MAY-2004  
DEFINITION  
ACCESSION AR477004  
VERSION AR477004.1 GI:47234260  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 21)  
AUTHORS Miller,M.W., Briles,W.E. and Afanasieff,M.  
TITLE Method for determining the MHC genotype of chickens  
JOURNAL Patent: US 6696253-A 14 24-FEB-2004;  
City of Hope; Duarte, CA  
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Best Local Similarity 93.8%; Pred. No. 2.4e+05;  
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OY 5 CACGCGCGCAGAGGAGC 20  
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Db 16 CACGCGCGCAGAGGAGC 1  
RESULT 9  
AX454812/c  
LOCUS AX454812 Sequence 14 from Patent WO0206535. 21 bp DNA linear PAT 06-JUL-2002  
DEFINITION  
ACCESSION AX454812  
VERSION AX454812.1 GI:21714041  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS Miller,M.W., Afanasieff,M. and Briles,W.E.  
TITLE Method for breeding disease resistant domesticated fowl  
JOURNAL Patent: WO 0206535-A 14 24-JAN-2002;  
City of Hope (US)  
FEATURES  
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/organism="synthetic construct"  
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/note="Primer for SSCP analysis of MHC B class II-beta  
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ORIGIN  
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Best Local Similarity 93.8%; Pred. No. 2.4e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 16 CACGCGCGCAGAGGAGC 1  
RESULT 10  
BD023342  
LOCUS BD023342 21 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for detecting abnormality in chromosome.  
ACCESSION BD023342  
VERSION BD023342.1 GI:22564565  
KEYWORDS JP 2001505428-A/87.  
Homo sapiens (human)  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 21)  
AUTHORS Pallsgaard,N. and Hokurando,P.  
TITLE Method for detecting abnormality in chromosome  
JOURNAL Patent: JP 2001505428-A 87 24-APR-2001;  
NIELLS PARISGAARD

COMMENT	PN	JP 2001505428-A/87
	PD	24-APR-2001
	PF	08-DEC-1997 JP 19985252090
	PI	NEILUS PARISGARD,PATER HOKURANDO
	PC	C12N15/09,C12Q1/68,G01N33/50,C12N15/00
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	CC	Topology: Linear;
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Best Local Similarity	93.8%;	Pred. No. 2.4e+05;
Matches	15; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	3 AGCAGCGCGGCAGAGA 18	
Db	1 AGCAGCGAGCAGAGA 16	
RESULT 11		
LOCUS	AX156996	50 bp DNA linear PAT 22-JUN-2001
DEFINITION	Sequence 324 from Patent WO01140521.	
ACCESSION	AX156996	
VERSION	AX156996.1 GI:14538327	
KEYWORDS	.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Homnidae; Homo.	
REFERENCE	1 Shimkets,R.A. and Leach,M.	
AUTHORS	Nucleic acids containing single nucleotide polymorphisms and	
TITLE	methods of use thereof	
JOURNAL	Patent: WO 0140521-A 324 07-JUN-2001;	
FEATURES	Curagen Corporation (us)	
source	Location/Qualifiers	
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	/organism="Homo sapiens"	
	/mol_type="unasigned DNA"	
	/db_xref="taxon:9606"	
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	/note="Nucleotide deleted between bases 25 and 26	
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Best Local Similarity	84.2%;	Pred. No. 2.4e+05;
Matches	16; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	1 CGAGCACGGCGCAGAGAG 19	
Db	30 CGAGACGGCGCGCAGAG 48	
RESULT 12		
LOCUS	AR444342	51 bp DNA linear PAT 20-FEB-2004
DEFINITION	Sequence 753 from patent US 6670464.	
ACCESSION	AR444342	
VERSION	AR444342.1 GI:42672121	
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	

REFERENCE	1 (bases 1 to 51)
AUTHORS	Shinkets,R.A. and Leach,M.
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL	Patent: US 6670464-A 753 30-DEC-2003;
FEATURES	Curagen Corporation; New Haven, CT
source	location/Qualifiers
ORIGIN	1..51
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	/mol_type="genomic DNA"
Query Match	71.0%; Score 14.2; DB 6; Length 51;
Best Local Similarity	84.2%; Pred. No. 2.4e+05;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	2 GAGCAGCGCGCAGAGGAGC 20
Db	26 GAGCAGCGGAGAGAGAGAGC 44
RESULT_13	
LOCUS	AX156995
DEFINITION	Sequence 323 from Patent WO0140521.
ACCESSION	AX156995
VERSION	AX156995.1 GI:14538326
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Homidae; Homo.
REFERENCE	1
AUTHORS	Shinkets,R.A. and Leach,M.
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL	Patent: WO 0140521-A 323 07-JUN-2001;
FEATURES	Curagen Corporation (US)
source	location/Qualifiers
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	/db_xref="taxon:9606"
	/note="1 of 2 allelic variants (324 is other entry)
	Accession number cg20436198"
misc_feature	
ORIGIN	
Query Match	71.0%; Score 14.2; DB 6; Length 51;
Best Local Similarity	84.2%; Pred. No. 2.4e+05;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 CGAGCAGCGCGCAGAGGAG 19
Db	31 CGAGCAGCGCGCGAGAGAG 49
RESULT_14	
RATMAP/c	
LOCUS	RATMAP 100 bp mRNA linear ROD 27-APR-1993
DEFINITION	Rat major acute phase protein mRNA (alpha-MP gene), partial cds.
ACCESSION	M26758
VERSION	M26758.1 GI:205301
KEYWORDS	major acute phase protein.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
	Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 100)
AUTHORS	Anderson,K.P., Martin,A.D. and Heath,E.C.





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds  
(without alignments)  
777.677 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20

Sequence: 1 cgagcacgscgcagagagagc 20

Scoring table: IDENTITY\_NUC

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N GeneSeq\_21.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31432
2	20	100.0	20	3	ADA74684
3	19	95.0	29	12	ADO48591
4	15.8	79.0	50	13	ADU24833
5	15.8	79.0	50	13	ADU22300
6	15.4	77.0	99	6	ABK76729
7	15.2	76.0	27	6	ABK27825
8	14.8	74.0	48	1	AAH80520
9	14.8	74.0	52	6	ADG69851
10	14.8	74.0	54	11	ADN88873
11	14.8	74.0	100	8	ACD74037
12	14.4	72.0	20	10	ADC38589
13	14.4	72.0	21	6	AAV40985
14	14.4	72.0	21	6	ABK8264
15	14.4	72.0	21	6	ADD29196
16	14.4	72.0	42	10	ADC38571
17	14.2	71.0	27	12	ADN06162
18	14.2	71.0	42	9	ADB39065
19	14.2	71.0	48	9	ADB39064

20	14.2	71.0	50	4	AAI73383
21	14.2	71.0	51	3	AAI73382
22	14.2	71.0	51	4	AAI73382
23	14.2	71.0	63	8	ACF57081
24	14.2	71.0	63	12	ADBE3198
25	14.2	71.0	63	13	ADU81373
26	14.2	71.0	63	14	ABE44262
27	14.2	71.0	75	9	ADB39116
28	14.2	71.0	96	9	ADB39117
29	13.8	69.0	20	13	ADR86867
30	13.8	69.0	20	13	ADR82422
31	13.8	69.0	23	14	ADZ84685
32	13.8	69.0	37	3	AAZ57918
33	13.8	69.0	65	6	ABN56988
34	13.8	69.0	80	13	ADY5949
35	13.8	69.0	100	8	ACD69317
36	13.8	69.0	100	8	ACD69316
37	13.6	68.0	23	2	AAZ24557
38	13.6	68.0	23	2	AAZ24649
39	13.6	68.0	23	9	ACD45012
40	13.6	68.0	23	12	ADU46207
41	13.6	68.0	27	3	AAQ34929
42	13.6	68.0	28	3	AAZ49806
43	13.6	68.0	28	3	AAZ49806
44	13.6	68.0	45	2	AAI38929
45	13.6	68.0	45	2	AAI39278

## ALIGNMENTS

RESULT 1  
AAZ31432  
ID AAZ31432 standard; DNA; 20 BP.  
AC AAZ31432;  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Human neuropilin mRNA specific antisense oligo GTT3602.  
XX  
KW Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;  
XX papilloma; diabetic retinopathy; antisense; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN W0955855-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 23-APR-1999; 99WO-CA000324.  
XX  
PR 23-APR-1998; 98US-0082791P.  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
PI Wright JA, Young AH, Lee YS;  
XX WPI; 2000-023357/02.  
XX  
PT Antisense oligonucleotides that inhibit neuropilin expression, useful for  
PT treating cancer.  
XX  
PS Claim 4; Page 16; 57pp; English.  
XX  
CC Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit  
CC human neuropilin expression. The antisense oligonucleotides can be used  
CC to inhibit the growth or metastasis of a mammalian tumor and inhibit  
CC neovascularisation. The oligonucleotides may be used to treat various  
CC forms of cancers or tumors, such as sarcomas, melanomas, adenomas,  
CC carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of  
CC the mouth, throat, larynx and lung, genitourinary cancers such as

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
 CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
 CC cancer, head and neck cancers, and nervous system cancers, as well as  
 CC benign lesions such as papillomas. The methods may be used to treat  
 CC neovascularisation disorders such as diabetic retinopathy, and  
 CC retinopathy of prematurity and age related macular degeneration  
 XX  
 SQ Sequence 20 BP; 5 A; 6 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGGAGC 20  
 DB 1 CGAGCAGCGCGCAGAGGAGC 20

RESULT 2  
 ADA74684  
 ID ADA74684 standard; DNA; 20 BP.  
 AC ADA74684;  
 XX  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE GT13602 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
 KM cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;  
 KM GT13602; antisense; human; ss.  
 XX  
 OS Homo sapiens.

FN US2003083274-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 XX 22-APR-1999; 99US-00296264.  
 XX  
 PR 23-APR-1998; 98US-0082791P.

XX (WRIGHT) WRIGHT J A.  
 PA (YOUNG) YOUNG A H.  
 PA (LEERY) LEE Y S.  
 XX  
 PI Wright JA, Young AH, Lee YS;  
 XX  
 DR WPI; 2003-576622/54.

PT New antisense oligonucleotide that inhibits neuropilin expression, useful  
 PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
 PT mammalian tumor.  
 PT  
 PS Claim 1; Page 5; 27pp; English.

XX The invention relates to a novel antisense oligonucleotide that inhibits  
 CC the expression of neuropilin, also known as VEGF165R (vascular  
 CC endothelial growth factor receptor). The oligonucleotide of the invention  
 CC demonstrates cytostatic activity and may be useful for inhibiting the  
 CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in  
 CC mammals. Furthermore, the oligonucleotide may be utilized during gene  
 CC therapy. The current sequence is that of the GT13602 antisense  
 CC oligonucleotide of the invention which is targeted to human neuropilin  
 CC mRNA.  
 XX  
 SQ Sequence 20 BP; 5 A; 6 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGGAGC 20

DB 1 CGAGCAGCGCGCAGAGGAGC 20

RESULT 3  
 ADO48591/C  
 ID ADO48591 standard; DNA; 29 BP.  
 XX  
 AC ADO48591;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human neuropilin 1 (NRP1) PCR primer #48.

XX human; melanoma; single nucleotide polymorphism; SNP; neuropilin 1; NRP1;  
 KM mannose receptor C type 2; MRC2; PCR; primer; ss; genotyping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200404163-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 06-NOV-2003; 2003WO-US035876.  
 XX  
 PR 06-NOV-2002; 2002US-0424475P.  
 PR 23-JUL-2003; 2003US-0489703P.

XX (SEQU-) SEQUENOM INC.  
 XX  
 PI Roth RB, Nelson MR, Braun A, Kammerer SM;  
 XX  
 DR WPI; 2004-411720/38.  
 XX  
 PT Identifying a subject at risk of melanoma, useful for treating melanoma,  
 PT comprises detecting the presence or absence of one or more polymorphic  
 PT variations associated with melanoma in a nucleic acid sample from a  
 PT subject.  
 XX  
 PS Example 3; Page 76; 176pp; English.

XX The invention comprises a method for identifying a subject at risk of  
 CC melanoma. The invention involves detecting the presence or absence of one  
 CC or more polymorphic variations associated with melanoma in the neuropilin  
 CC 1 (NRP1) or mannose receptor C type 2 (MRC2) genes. The method of the  
 CC invention is useful for identifying subjects at risk and treating  
 CC melanoma. The present DNA sequence represents a PCR primer that was used  
 CC to detect single nucleotide polymorphisms within human NRP1.  
 XX  
 SQ Sequence 29 BP; 2 A; 10 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GAGCAGCGCGCAGAGGAGC 20  
 DB 29 GAGCAGCGCGCAGAGGAGC 11

RESULT 4  
 ADU24833/C  
 ID ADU24833 standard; DNA; 50 BP.  
 XX  
 AC ADU24833;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE Retroelement consensus sequence identifier oligonucleotide #203.

XX Expression pattern; transposable element; developmental potential;  
 KM stem cell; cellular differentiation induction factor;  
 KM methylation pattern; chromatin status pattern; endogenous retrovirus;

KM ERV; short interspersed nuclear element; SINE;  
 XX long interspersed nuclear element; LINE; retroelement; ss.  
 OS Synthetic.  
 XX WO2004097005-A2.  
 XX 11-NOV-2004.  
 PD 29-APR-2004; 2004WO-US013667.  
 XX 29-APR-2004; 2003US-0466801P.  
 PR 29-APR-2003; 2003US-0466801P.  
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA Mcdonald JF;  
 XX WPI; 2004-804756/79.  
 DR WPI; 2004-804756/79.  
 XX  
 PT Assigning an expression pattern of transposable elements to the level of  
 PT developmental potential of a cell comprises determining expression of one  
 PT or more families of transposable elements, and assigning the expression  
 PT pattern.  
 PS Disclosure; SEQ ID NO 303; 50pp; English.  
 XX  
 CC The invention relates to a method of assigning an expression pattern of  
 CC transposable elements to the level of developmental potential of a cell.  
 CC The method comprises determining the expression of one or more families  
 CC of transposable elements, and assigning the expression pattern obtained  
 CC to the level of developmental potential of a cell. Also disclosed are a  
 CC method of determining the developmental potential of a stem cell, a  
 CC method of identifying a cellular differentiation induction factor, a  
 CC method of identifying a factor that increases the developmental potential  
 CC of a cell, a method of assigning a methylation pattern of transposable  
 CC elements to the level of developmental potential of a cell, and a method  
 CC of assigning a chromatin status pattern of transposable elements to the  
 CC level of developmental potential of a cell. In assigning an expression  
 CC pattern of transposable elements to the level of developmental potential  
 CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem  
 CC cell, or a differentiated cell. The expression pattern is determined by  
 CC microarray analysis. One or more of the families of transposable elements  
 CC are retroelement families, or DNA element families. One or more of the  
 CC families of retroelements is selected from the group consisting of  
 CC endogenous retroviruses (ERVs), a family of short interspersed nuclear  
 CC elements (SINEs) and a family of long interspersed nuclear elements  
 CC (LINEs). The expression of the transposable elements is measured by  
 CC assaying for the mRNA transcribed from the genes or proteins translated  
 CC from an mRNA transcribed from the genes. The expression of two or more  
 CC families of transposable elements is determined and used to form the  
 CC pattern of expression. The methylation of the transposable element genes  
 CC is monitored by enzymatic means, microarray analysis, or methylation-  
 CC specific PCR. The methylation pattern is determined by microarray  
 CC analysis. The methods of the invention are useful for assigning an  
 CC expression pattern of transposable elements to the level of developmental  
 CC potential of a cell. This sequence represents an oligonucleotide  
 CC identifier of a retroelement consensus sequence.  
 XX  
 SQ Sequence 50 BP; 8 A; 22 C; 6 G; 14 T; 0 U; 0 Other;  
 QY Query Match 79.0%; Score 15.8; DB 13; Length 50;  
 DB Best Local Similarity 89.5%; Pred. NO. 3.1e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 2 GAGCAGCGCGCAGAGAGC 20  
 |||||  
 26 GAGCAGCGCGAGAGAGC 8

AC ADU22300;  
 XX 27-JAN-2005 (first entry)  
 DT  
 XX Human transposable element representative sequence, SEQ ID 303.  
 DE  
 XX Human transposable element; DNA methylation; chromatin; cancer;  
 KM LINE; long interspersed nuclear element; SINE;  
 KM short interspersed nuclear element; HERV; human endogenous retrovirus;  
 XX microarray.  
 OS Homo sapiens.  
 XX WO2004096021-A2.  
 XX 11-NOV-2004.  
 PD 29-APR-2004; 2004WO-US013522.  
 XX 29-APR-2004; 2003US-0466798P.  
 PR 29-APR-2003; 2003US-0466798P.  
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA Mcdonald JF;  
 XX WPI; 2004-804580/79.  
 DR WPI; 2004-804580/79.  
 XX  
 PT Determining expression, methylation or chromatin status pattern of  
 PT families of transposable elements in a sample e.g. for diagnosing cancer,  
 PT comprises determining the expression, methylation or chromatin status of  
 PT the elements.  
 XX  
 PS Disclosure; SEQ ID NO 303; 68pp; English.  
 XX  
 CC The invention relates to determining expression, methylation or chromatin  
 CC status pattern of one or more families of transposable elements in a  
 CC sample comprising determining expression, methylation or chromatin status  
 CC of one or more families of transposable elements. Also included are a  
 CC method of assigning an expression pattern of transposable elements to a  
 CC type of cancerous cell in a sample, a method of diagnosing cancer, a  
 CC method of determining the effectiveness of an anti-cancer therapeutic in  
 CC a subject, a method of assigning a methylation pattern of one or more  
 CC families of transposable elements to a type of cancerous cell in a sample  
 CC and a method of assigning a chromatin status pattern of transposable  
 CC elements to a type of cancerous cell in a sample. The method is useful in  
 CC determining an expression, methylation or chromatin status pattern of one  
 CC or more families of transposable elements (e.g. LINE, long interspersed  
 CC nuclear element, SINE, short interspersed nuclear element, or HERV, human  
 CC endogenous retrovirus) in a sample for diagnosing cancer or determining  
 CC the effectiveness of an anti-cancer therapeutic. The present sequence is  
 CC a representative sequence for a human transposable element, used in a  
 CC microarray to study the expression, methylation or chromatin status  
 CC pattern of the transposable elements.  
 XX  
 SQ Sequence 50 BP; 8 A; 22 C; 6 G; 14 T; 0 U; 0 Other;  
 QY Query Match 79.0%; Score 15.8; DB 13; Length 50;  
 DB Best Local Similarity 89.5%; Pred. NO. 3.1e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 2 GAGCAGCGCGCAGAGAGC 20  
 |||||  
 26 GAGCAGCGCGAGAGAGC 8

RESULT 5  
 ADU22300/c  
 ID ADU22300 standard; DNA; 50 BP.  
 XX

RESULT 6  
 ABK76729  
 ID ABK76729 standard; DNA; 99 BP.  
 XX  
 AC ABK76729;  
 XX 13-AUG-2002 (first entry)  
 XX

DE	Bacillus licheniformis genomic sequence tag (GST) #4020.
XX	
KM	Differential gene expression; genomic sequenced tag; GST;
KW	altered culture condition; environmental stress;
KW	physiological provocation; ds.
XX	
OS	Bacillus licheniformis.
XX	
PN	WO200229113-A2.
XX	
PD	11-APR-2002.
XX	
PF	05-OCT-2001; 2001WO-US031437.
XX	
PR	06-OCT-2000; 2000US-00680598.
XX	
PR	27-MAR-2001; 2001US-0279526P.
XX	
PA	(NOVO ) NOVOZYMES BIOTECH INC.
XX	(NOVO ) NOVOZYMES AS.
XX	
PI	Berka R, Clausen IG;
XX	
DR	WPI; 2002-416684/44.
XX	
PT	Monitoring differential expression of several genes in first Bacillus
XX	cell relative to expression of same genes in one or more second Bacillus
PT	cells, by using substrate containing Bacillus genomic sequenced tag
XX	array.
XX	
PS	Claim 4; SEQ ID NO 4020; 200pp; English.
XX	
CC	The invention describes a method of monitoring differential expression of
XX	genes in a first Bacillus cell relative to expression of the genes in
CC	other Bacillus cells, comprising hybridising labelled nucleic acid probes
XX	isolated from Bacillus cells to a substrate containing array of Bacillus
CC	genomic sequenced tags (GST), examining the array, and determining
XX	relative gene expression by an observed hybridisation reporter signal of
CC	a spot in the array. The method is useful for measuring the expression of
XX	genes in a first Bacillus cell relative to expression of the same genes
CC	in one or more second Bacillus cells. The method is useful for monitoring
XX	global expression of several genes from a Bacillus cell, discovering new
CC	genes, identifying possible functions of unknown open reading frames and
XX	monitoring gene copy number variation and stability. Monitoring changes
CC	in expression of genes may be used to provide a representation of the way
XX	in which Bacillus cells adapt to changes in culture conditions,
CC	CC environmental stress or other physiological provocation. Extensive follow
CC	up characterisation is unnecessary, when one spot on an array equals one
XX	gene or one open reading frame, since sequence information is available.
CC	This sequence represents a genomic sequence tag (GST) used in the method
XX	of the invention. Note: The sequence data for this patent did not form
CC	part of the printed specification, but was obtained in electronic format
XX	directly from WIPO at fcp.wipo.int/pub/published_pat_sequences
XX	
SO	Sequence 99 BP; 32 A; 26 C; 20 G; 20 T; 0 U; 1 Other;
	Query Match 77.0%; Score 15.4; DB 6; Length 99;
	Best Local Similarity 94.1%; Pred. No. 4.5e+03;
	Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	4 GCACGCCGACGAGAGC 20
Db	31 GCACGCCGACGAGAGC 47
RESULT 7	
ABK27825	
ID	ABK27825 standard; DNA; 27 BP.
XX	
AC	ABK27825;
XX	
DT	09-APR-2002 (first entry)
XX	
DE	Corn male reproductive tissue promoter, PCR primer #15.

XX	Corn; male reproductive tissue; promoter; plant; gene stacking;
KM	fertility; insect; pathogen; herbicide tolerance; primer; ss.
XX	
OS	Zea mays.
PN	MO200200905-A2.
XX	
PD	03-JAN-2002.
XX	
PF	26-JUN-2001; 2001WO-US020658.
XX	
PR	28-JUN-2000; 2000US-0214357P.
XX	
PA	(MONS ) MONSANTO TECHNOLOGY LLC.
XX	
PI	Conner TW, Dubois P, Malven M, Masucci JD;
XX	
DR	WPI; 2002-147890/19.
XX	
PT	New plant regulatory sequences or promoters and nucleic acids encoding
PT	them, useful for regulating gene expression, especially in male
PT	reproductive tissues.
XX	
PS	Example 3; Page 96; 131pp; English.
XX	
CC	The invention relates to an isolated nucleic acid (I) promoter capable of
CC	regulating transcription of an operably linked DNA sequence. The promoter
CC	sequences may be used for selectively modulating expression of any
CC	operatively linked gene and provide additional regulatory element
CC	diversity in a plant expression vector in gene stacking approaches, and
CC	for regulating gene expression in male reproductive tissues or gene
CC	transcription of any target gene (e.g. for controlling fertility, insect,
CC	pathogen or herbicide tolerance). The nucleic acids are useful as
CC	hybridisation probes or primers in hybridisation assays of other plant
CC	tissues to identify closely related or homologous genes and associated
CC	regulatory sequences. ABK27808-ABK27918 represent corn male reproductive
CC	tissue promoter sequences and PCR primers of the invention
XX	
SQ	Sequence 27 BP; 8 A; 6 C; 11 G; 2 T; 0 U; 0 Other;
	Query Match 76.0%; Score 15.2; DB 6; Length 27;
	Best Local Similarity 85.0%; Pred. No.5.6e+03;
	Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0
OY	1 CGAGCAGCGCGCAGAGGAGC 20
DB	7 CGAGGACGCGCGAAGGATC 26
RESULT 8	
AA080520	
ID	AA080520 standard; DNA; 48 BP.
XX	
AC	AA080520;
XX	
DT	25-MAR-2003 (revised)
DT	03-OCT-2002 (revised)
DT	11-DEC-1990 (first entry)
XX	
DE	Synthetic oligonucleotide used in prodn. of hybrid gene.
XX	
KW	Synthetic oligonucleotide; hybrid gene; RESA 3' repeat;
KW	Plasmodium falciparum; malaria; vaccine.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	1..24
FT	/*tag= a
FT	/note= "claimed peptide"
XX	
XX	WO8802757-A.

```

XX 21-APR-1988.
PD
XX
XX 16-OCT-1987; 87WO-AU000352.
PF
XX
XX 17-OCT-1986; 86AU-00008551.
PR
XX 17-OCT-1986; 87AU-00081506.
XX
PA (SARA-) SARAFANE PTY LTD.
PA (LANG/) LANGFORD C J.
XX
XX Langford CJ, Edwards SJ;
XX
XX WPI; 1988-119462/17.
DR
XX P-PSDB; AAP80519.
XX
PT New hybrid protein or polypeptide - contg. epitope(s) or mimotope(s) of
PT several antigens esp. useful as antimalarial vaccines.
XX
XX
XX Disclosure; Page ?; 37pp; English.
XX
XX
XX several antigens esp. useful as antimalarial antigens. The
CC oligonucleotide encodes an epitope of a P.falciparum antigen. The peptide
CC can be used in an antimalarial vaccine. (Updated on 03-OCT-2002 to add
CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 48 BP; 14 A; 12 C; 20 G; 2 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 1; Length 48;
Best Local Similarity 88.9%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCAGCGCGCAGAGAG 19
   |||||
   |||||
   |||||
Db 13 GAGCAGCAGCGCGCAGAG 30

RESULT 9
ADG69851
ID ADG69851 standard; DNA; 52 BP.
XX
XX ADG69851;
XX
XX 11-MAR-2004 (first entry)
XX
XX Rat saliv1 transferase (RST) related PCR primer RST-FlB.
XX
XX transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic acid;
KW plant; cell wall; improved digestibility; biomass conversion;
KW highly fermentable carbohydrate; PCR primer; ss.
XX
XX Synthetic.
OS
XX Rattus sp.
XX
XX WO200268666-A1.
XX
XX 06-SEP-2002.
XX
XX 16-NOV-2001; 2001WO-US043588.
XX
XX 17-NOV-2000; 2000US-0249608P.
XX
XX (GEMV ) GENENCOR INT INC.
XX
XX Dunn-Coleman N, Langdon T, Morris P;
XX
XX WPI; 2002-698675/75.
XX
XX New transgenic plant comprising an expression cassette with a promoter
PT operably linked to a ferulic acid esterase encoding polynucleotide,
PT useful in improving digestibility for livestock and enhancing biomass
PT conversion.
XX

```

```

PS Example 2; Page 34; 208pp; English.
XX
XX The present invention describes a transgenic plant (I) comprising an
CC expression cassette with a promoter operably linked to a ferulic acid
CC esterase encoding polynucleotide. Also described: (1) controlling (M1)
CC the level of phenolic acids in plant cell walls of a transgenic plant by
CC introducing into the plant an expression cassette comprising a promoter
CC operably linked to a ferulic acid esterase encoding polynucleotide; and
CC (2) a transgenic plant (II) produced by (M1). The transgenic plants are
CC useful in improving digestibility for livestock and enhancing biomass
CC conversion. The method is useful for enhancing the production of more
CC highly fermentable carbohydrates in plants, especially forage grasses.
CC The expression cassette is useful for controlling the level of phenolic
CC acids in plant cell walls of a transgenic plant. The present sequence is
CC used in the exemplification of the present invention.
XX
XX
SQ Sequence 52 BP; 19 A; 6 C; 21 G; 6 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 6; Length 52;
Best Local Similarity 88.9%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCAGCGCGCAGAGAG 19
   |||||
   |||||
   |||||
Db 6 GATCAGCGCGCAGAGAG 23

RESULT 10
ADN88873
ID ADN88873 standard; DNA; 54 BP.
XX
XX ADN88873;
XX
XX 01-JUN-2004 (first entry)
XX
XX RST-FlB PCR primer.
XX
XX Transgenic plant; ferulic acid esterase; fermentable carbohydrate;
KW animal feed; phenolic acid; PCR; primer; ss.
XX
XX Synthetic.
OS
XX WO2003043411-A2.
XX
XX 30-MAY-2003.
XX
XX 21-MAY-2002; 2002WO-US016239.
XX
XX 16-NOV-2001; 2001US-00991209.
XX
XX 16-NOV-2001; 2001WO-US043588.
XX
XX (GEMV ) GENENCOR INT INC.
XX
XX Dunn-Coleman N, Langdon T, Morris P;
XX
XX WPI; 2003-457563/43.
XX
XX New transgenic plant comprising an expression cassette with a promoter
PT operably linked to ferulic acid esterase encoding polynucleotide, useful
PT for enhancing availability of fermentable carbohydrates as feed for grass
PT -fed animals.
XX
XX Example 2; Page 32; 190pp; English.
XX
XX The present invention relates to transgenic plants comprising an
CC expression cassette having a promoter operably linked to a ferulic acid
CC esterase (FAE) encoding polynucleotide. The transgenic plants are useful
CC for enhancing the availability of fermentable carbohydrates as feed for
CC grass-fed animals. The methods are useful for reducing the levels of
CC phenolic acids in the cell walls available for cross-linking either by
CC directly disrupting ester bonds linking phenolics and lignins to cell
CC wall polysaccharides or by preventing excessive fermentation of cell wall
CC carbohydrates. The present sequence is a primer used to illustrate the

```





```

XX DE Primer TELAML1:1216L21 for abnormality detection.
XX XX
XX XX PCR primer: chromosomal abnormality; abnormality detection; leukaemia;
XX XX lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
XX XX medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX FN WO9824928-A2.
XX XX
XX PD 11-JUN-1998.
XX XX
XX PF 08-DEC-1997; 97WO-DK000556.
XX XX
XX PR 06-DEC-1996; 96DK-00001401.
XX XX
XX PA (PALL/) PALLISGAARD N.
XX XX
XX PI Pallsgaard N, Hokland P;
XX XX
XX DR WPI; 1998-333344/29.
XX XX
XX PT Detection of chromosomal abnormalities - by subjecting patient sample
XX PT nucleic acids to a multiplex molecular amplification procedure using
XX PT primers specific for characteristic nucleic acid sequence.
XX XX
XX PS Claim 73; Page 85; 126pp; English.
XX XX
XX CC This sequence represents a primer used in the method of the invention for
XX CC the detection of the presence or absence of chromosomal abnormalities,
XX CC each abnormality being associated with a condition in a subject and each
XX CC method defined by at least one characteristic nucleic acid sequence. The
XX CC method comprises: (a) obtaining a sample of nucleic acids derived from a
XX CC subject which may harbour one of the chromosomal abnormalities; (b)
XX CC subjecting the sample to a multiplex molecular amplification (MMA)
XX CC procedure, where a number of the characteristic sequences, if present in
XX CC a sufficient amount, will be amplified; (c) retrieving the product(s)
XX CC from step (b), and detecting the presence and/or absence of an amplicon
XX CC characteristic of the abnormal sequences to detect the presence or
XX CC absence of corresponding chromosomal abnormalities; where the MMA
XX CC procedure comprises the use of at least 7 mutually distinct primers (MDP)
XX CC in one single reaction mixture, each of the primers defining an end of at
XX CC least one characteristic nucleic acid sequence, and where at least one of
XX CC the primers defines the first end of at least two characteristic nucleic
XX CC acid sequences, the characteristic nucleic acid sequences each being
XX CC determined in their opposite ends by MDP selected from the remainder of
XX CC the MDP. The method can be used for detecting chromosomal abnormalities
XX CC associated with diseases including numerous leukaemia's, lymphoma's,
XX CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
XX CC medullablastoma, malignant melanoma, and malignant neoplastic conditions
XX XX
XX SQ Sequence 21 BP; 7 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
XX XX
XX Query Match 72.0%; Score 14.4; DB 2; Length 21;
XX Best Local Similarity 93.8%; Pred. No. 1.2e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX QY 3 AGCAGCGCGCAGAGGA 18
XX Db 1 AGCAGCGAGCAGAGGA 16
XX XX
XX RESULT 14
XX ABR8264/C
XX ID ABR8264 standard; DNA; 21 BP.
XX AC ABR8264;
XX XX
XX DT 07-OCT-2002 (first entry)
XX XX
XX DE Exon 2 (alpha domain) of chicken class I gene PCR primer RV69BL.

```

```

XX XX
XX XX Chicken: exon 2; alpha domain; class I gene; Rfp-Y; B-F; B-L; B-G;
XX XX major histocompatibility complex; MHC; domesticated fowl;
XX XX Marek's disease; genetic disease resistance; PCR; primer; ss.
XX XX
XX OS Gallus sp.
XX OS
XX PN US2002083482-A1.
XX XX
XX PD 27-JUN-2002.
XX XX
XX PF 22-JUN-2001; 2001US-00886607.
XX XX
XX PR 19-JUL-2000; 2000US-00619758.
XX XX
XX PA (MILL/) MILLER M M.
XX PA (BRIL/) BRILES W E.
XX PA (AFAN/) AFANASSIEFF M.
XX XX
XX PI Miller MM, Briles WE, Afanasieff M;
XX XX
XX DR WPI; 2002-557335/59.
XX XX
XX PT Determining the major histocompatibility complex genotypes of a
XX PT domesticated fowl useful for selecting fowl, particularly chickens,
XX PT genetically resistant to a variety of diseases, particularly Marek's
XX PT disease.
XX XX
XX PS Claim 14; Page 7; 22pp; English.
XX XX
XX CC The present invention relates to a new method for determining the major
XX CC histocompatibility complex (MHC) genotypes of a domesticated fowl. The
XX CC method of the invention involves amplifying and denaturing nucleic acid
XX CC from the fowl which contains a region with a sequence corresponding to an
XX CC Rfp-Y, B-F, B-L or B-G region of the genome and separating the denatured
XX CC products electrophoretically to produce a pattern characteristic to the
XX CC genotype of the fowl. The method is useful for determining the MHC
XX CC genotypes of domestic fowl. The method may be used to select for domestic
XX CC fowl, particularly chickens, genetically resistant to a variety of
XX CC diseases, particularly Marek's disease. The methods of the invention are
XX CC useful for producing offspring that carry genetic resistance to disease.
XX CC The present nucleic acid sequence represents an exon 2 (alpha domain) of
XX CC chicken class I gene PCR primer that was used in the methods of the
XX CC invention for MHC genotyping
XX XX
XX SQ Sequence 21 BP; 4 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX XX
XX Query Match 72.0%; Score 14.4; DB 6; Length 21;
XX Best Local Similarity 93.8%; Pred. No. 1.2e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX QY 5 CACGCGCGCAGAGGAGC 20
XX Db 16 CACGCGCAGAGGAGC 1
XX XX
XX RESULT 15
XX AAD29196/C
XX ID AAD29196 standard; DNA; 21 BP.
XX AC AAD29196;
XX XX
XX DT 07-MAY-2002 (first entry)
XX XX
XX DE Fowl MHC B class II-beta genotype analysing PCR primer, RV69BL.
XX XX
XX KW Fowl; haplotyping; breeding; domesticated fowl; disease resistance;
XX KW major histocompatibility; MHC; Marek's disease; PCR primer; ss.
XX XX
XX OS Gallus sp.
XX OS
XX PN WO200206535-A2.
XX XX

```

```

PD 24-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US022519.
XX
XX 19-JUL-2000; 2000US-00619758.
XX
XX (CITY ) CITY OF HOPE.
XX
XX Miller MM, Afanasieff M, Briles WE;
XX
XX WPI, 2002-171822/22.
XX
XX Determining major histocompatibility complex genotypes of domesticated
XX fowl for breeding disease resistant fowl by comparing B and Rfp-Y systems
XX of genome from the fowl to corresponding known genotypes.
XX
XX Claim 14; Page 16; 37pp; English.
XX
XX The invention relates to a method for haplotyping and breeding
XX domesticated fowl for increased disease resistance. Disease resistance in
XX domesticated fowl has been associated with the B and Rfp-Y systems of
XX major histocompatibility (MHC) genes. The method is useful for
XX determining the Mhc genotypes of a domesticated fowl. The method is
XX useful in selecting domesticated fowl which are resistant to a
XX preselected disease preferably Marek's disease by determining a genotype
XX of Rfp-Y, B-F, B-L or B-G genes of the domesticated fowl, correlating the
XX determined genotypes with resistance to the preselected disease and
XX selecting a domesticated fowl having a determined genotype which
XX correlates with resistance to the preselected disease. The method is also
XX useful for breeding domesticated fowl to produce an offspring resistant
XX to a preselected disease by selecting a first domesticated fowl of a
XX gender which is resistant to a preselected disease, and mating the first
XX domesticated fowl with a second domesticated fowl of the opposite gender
XX to produce offspring. The present sequence is a PCR primer used for
XX genotyping fowl Mhc region
XX
XX Sequence 21 BP; 4 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 72.0%; Score 14.4; DB 6; Length 21;
XX Best Local Similarity 93.8%; Pred. No. 1.2e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CACGGCGCAGAGAGC 20
DB 16 CACGGCGCAGAGAGC 1

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Search completed: December 24, 2005, 12:28:52  
 Job time : 173.4 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds  
(without alignment)  
595.256 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20  
Sequence: 1 cgagcagcgcgcagagagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	94	1	AA197619
2	15.8	79.0	52	1	AM693858
3	15.8	79.0	95	10	CM456343
4	15.2	76.0	55	2	BI250613
5	15.2	76.0	90	2	BI104703
6	15.2	76.0	100	7	CF954727
7	15.2	76.0	100	11	CL954628
8	14.8	72.0	68	7	CV304081
9	14.4	72.0	87	4	AK185845
10	14.4	72.0	87	4	AK185845
11	14.4	72.0	100	10	AG195654
12	14.2	71.0	55	3	BH643795
13	14.2	71.0	79	3	BQ167594
14	14.2	71.0	84	7	CO911144
15	14.2	71.0	95	10	CM118187
16	13.8	69.0	40	10	CG715520
17	13.8	69.0	62	10	CG650832
18	13.8	69.0	63	10	CG728306
19	13.8	69.0	92	9	AZ595307
20	13.8	69.0	93	11	CNS03900
21	13.8	69.0	95	9	BH173450
22	13.8	69.0	98	3	BI768381

23	13.6	68.0	46	1	AA082876
24	13.6	68.0	50	1	AU104090
25	13.6	68.0	67	10	BX987261
26	13.6	68.0	69	8	CM456343
27	13.6	68.0	71	10	CM115297
28	13.6	68.0	72	6	CD949020
29	13.6	68.0	74	7	CV589750
30	13.6	68.0	75	10	CL266096
31	13.6	68.0	81	3	BH490089
32	13.6	68.0	81	9	BH849516
33	13.6	68.0	86	9	BH796584
34	13.6	68.0	87	9	AZ918012
35	13.6	68.0	88	10	CZ233884
36	13.6	68.0	91	10	CG785229
37	13.6	68.0	92	5	B0564305
38	13.6	68.0	95	4	AK189242
39	13.6	68.0	100	6	CB212828
40	13.4	67.0	25	9	AZ374695
41	13.4	67.0	47	10	BX224384
42	13.4	67.0	74	1	AA492659
43	13.4	67.0	88	1	AA574321
44	13.2	66.0	23	6	CF277473
45	13.2	66.0	38	10	CZ551355

#### ALIGNMENTS

RESULT 1  
AA197619  
LOCUS  
DEFINITION AA197619 94 bp mRNA linear EST 19-FEB-1997  
5', mRNA sequence.  
ACCESSION  
AA197619 GI:1793270  
VERSION  
AA197619  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
MUS MUSCULUS  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 94)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Schellenger, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
Teisberg, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
TITLE  
The WashU-HMI Mouse EST Project  
JOURNAL  
Unpublished (1996)  
COMMENT  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:391812  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 81.  
FEATURES  
Location/Qualifiers  
1..94  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:639820"  
/sex="male"  
/issue\_type="Thymus"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_1lb="Soares\_thymus\_2NBWT"



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
1 (bases 1 to 55)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

## FEATURES

source  
1. 55  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="mix FVB/N, C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5149483"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NciI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lothar Hennighausen/Robin Humphreys,  
NIH"  
High quality sequence stop: 55.  
Location/Qualifiers

## ORIGIN

Query Match 76.0%; Score 15.2; DB 2; Length 55;  
Best Local Similarity 85.0%; Pred. No. 3.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCCGACAGAGC 20  
|||  
Db 41 CGGCACGCGACGAGCAGC 22

RESULT 5  
BI104703/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BI104703 90 bp mRNA linear EST 26-JUN-2001  
602891614F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:5036690 5',  
mRNA sequence.  
BI104703  
BI104703.1 GI:14555596  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Mus.  
1 (bases 1 to 90)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: LLM1101 row: 1 column: 03  
High quality sequence stop: 90.  
Location/Qualifiers

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## source

1. 90  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
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/clone="IMAGE:5036690"  
/tissue\_type="spontaneous tumor, metastatic to mammary.  
stem cell origin"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NciI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Gilbert Smith, NIH"

## ORIGIN

Query Match 76.0%; Score 15.2; DB 2; Length 90;  
Best Local Similarity 85.0%; Pred. No. 3.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCCGACAGAGC 20  
|||  
Db 75 CGGCACGCGACGAGCAGC 56

RESULT 6  
CP954727  
LOCUS  
DEFINITION  
ACCESSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

CP954727 100 bp mRNA linear EST 15-JAN-2004  
5246r6icb 10479.y1 Oryza sativa cv. PA64s leaf cDNA library Oryza  
sativa (indica cultivar-group) cDNA 5', mRNA sequence.  
CP954727  
CP954727.1 GI:38470596  
EST.  
Oryza sativa (indica cultivar-group)  
Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretoidae; Oryzaceae; Oryza.  
1 (bases 1 to 100)  
Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,  
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,  
Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,  
Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, O.,  
Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,  
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,  
Wu, S. and Liu, J.  
The Genomes of Oryza sativa: A History of Duplications  
PLoS Biol. 3 (2), e38 (2005)  
15685292  
Contact: Yan Zhou  
Bioinformatics Department  
Hangzhou Genomics Institute  
No. 51 Zhijiang Road, Hangzhou 310008, China  
Tel: 86-571-56805886  
Fax: 86-571-56805884  
Email: [zhouyan@genomics.org.cn](mailto:zhouyan@genomics.org.cn)  
Seq primer: M13 Forward  
High quality sequence stop: 100  
POLYA=yes.  
Location/Qualifiers

## FEATURES

## source

1. 100  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="PA64s"  
/db\_xref="taxon:39946"  
/tissue\_type="leaf"  
/dev\_stage="trfcol1"  
/clone\_lib="Oryza sativa cv. PA64s leaf cDNA library"

## ORIGIN

Query Match 76.0%; Score 15.2; DB 7; Length 100;  
Best Local Similarity 85.0%; Pred. No. 3.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CGAGCAGCGCGCAGAGAGC 20  
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48 CGAGCAGCGAGAGAGAGAGC 67

RESULT 7  
LOCUS CL954628  
DEFINITION OsrRUA002883 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL954628  
VERSION CL954628.1 GI:52366637  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 100)  
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G., K. S., Deng, X. M., and Wang, J.  
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis  
Unpublished (2004)  
Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Classes: exon-trapped.  
Location/Qualifiers  
1..100  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:39946"  
/clone\_lib="Oryza sativa Express Library"  
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN  
Query Match 76.0%; Score 15.2; DB 10; Length 100;  
Best Local Similarity 85.0%; Pred. No. 3.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CGAGCAGCGCGCAGAGAGC 20  
|||||  
48 CGAGCAGCGAGAGAGAGAGC 67

Db 48 CGAGCAGCGAGAGAGAGAGC 67

RESULT 8  
GGA270142/c 96 bp DNA linear GSS 08-JUL-2000  
LOCUS GGA270142  
DEFINITION Gallus gallus anonymous sequence from Cosmid mapping to chromosome 5 (Cosmid 27 - Contig 43), genomic survey sequence.  
ACCESSION AJ231913.1 GI:3451731  
VERSION AJ231913.1  
KEYWORDS GSS; genome survey sequence.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 96)  
Smith, J., Bruley, C. K., Paton, I. R., Dunn, I., Jones, C. T., Windsor, D., Morris, D. R., Law, A. S., Masabanda, J., Sazanov, A., Waddington, D., Fries, R., and Burt, D. W.  
Differences in gene density on chicken macrochromosomes and microchromosomes  
Anim. Genet. 31 (2), 96-103 (2000)

REFERENCE  
AUTHORS

TITLE

JOURNAL

PUBMED 10782207  
REFERENCE 2 (bases 1 to 96)  
AUTHORS Smith, J., Bruley, C. K., Paton, I. R., Law, A. S., Masabanda, J., Waddington, D., Fries, R., and Burt, D. W.  
TITLE Direct Submission  
JOURNAL Submitted (12-AUG-1998) Division of Molecular Biology, Roslin Institute, Roslin, Midlothian EH25 9PS, Scotland, UK  
FEATURES  
source  
1..96  
/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9031"  
/chromosome="5"  
/map="5q"

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Best Local Similarity 88.9%; Pred. No. 5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 AGCAGCGCGCAGAGAGC 20  
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36 AGCAGCGAGCAGAGAGC 19

Db 36 AGCAGCGAGCAGAGAGC 19

RESULT 9  
CV304081 68 bp mRNA linear EST 23-SEP-2004  
LOCUS CV304081/c  
DEFINITION t988d01.g7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA sequence.  
ACCESSION CV304081  
VERSION CV304081.1 GI:52621414  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 68)  
Dike, S., Ballja, V. S., Nascimento, L. U., Xuan, Z., Ou, J., Zutavern, T., Palmer, L. B., Hannon, G., Zhang, M. O., and McCombie, W. R.  
The mouse genome: Experimental examination of gene predictions and transcriptional start sites  
Genome Res. 14 (12), 2424-2429 (2004)  
Contact: Ballja VS  
McCombie Laboratory  
Cold Spring Harbor Laboratory  
500 Sunnyside Blvd, Woodbury, NY 11797, USA  
Fax: 516 422 4109  
Email: ballja@cshl.org.  
Location/Qualifiers  
1..68  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone\_lib="Mouse 5' RACE clones"  
/note="Vector: PCR-TOPO.1; Cloned 5' RACE fragments amplified from 5' RACE cDNA generated from 15 pooled mouse tissues and stages: 7, 11, 15, & 17-day total embryo, whole brain, eye, kidney, liver, lung, prostate, submaxillary gland, smooth muscle, spleen, testes and uterus."

ORIGIN  
Query Match 72.0%; Score 14.4; DB 7; Length 68;  
Best Local Similarity 93.8%; Pred. No. 7.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 AGCAGCGCGCAGAGAGC 18  
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35 AGCAGCGCAGAGAGC 20

Db 35 AGCAGCGCAGAGAGC 20

RESULT 10  
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LOCUS  
DEFINITION  
AK185845  
AK185845.1 GI:56010022  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
ORIGIN  
FEATURES  
SOURCE  
Db  
Query Match  
Best Local  
Matches  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
AG195654  
AG195654.1 GI:45227830

87 bp mRNA linear HTC 23-NOV-2004  
Mus musculus cDNA, clone: Y0G0135G22, strand: minus,  
reference: ENSEMBL: Mouse-Transcript-ENST: ENSMUST0000070400, based  
on BLAT search.  
AK185845  
AK185845.1 GI:56010022  
HTC; ASSETS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
Watabiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,  
Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,  
Hayashizaki, Y., and Carninci, P.  
Libraries enriched for alternatively spliced exons reveal splicing  
patterns in melanocytes and melanomas  
Nat. Methods 1, 233-239 (2004)  
2 (bases 1 to 87)  
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N.,  
Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M.,  
Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watabiki, A. and  
Hayashizaki, Y.  
Direct Submission  
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama,  
Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,  
URL: http://genome.gsc.riken.jp, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
Alternative Splicing Libraries (ASLs) are prepared by: Preparing  
of single-stranded DNA using a RNA template from full length cDNA  
libraries, hybridizing of  
single-stranded DNAs, removing of remaining single-stranded DNA,  
digesting of regions comprising double-stranded DNA by a set of 4  
bp-cutters, capturing of DNA hybrids with loop structures  
(alternative spliced exon), ligation of Y-shaped primers to  
isolated DNA hybrids with loop structures, PCR amplification of  
ligation products and their cloning into pUC1 vector. (Reference).  
Location/Qualifiers  
1..87  
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/cell\_type="mixture of melanoma cell and melanocyte cell"  
/clone\_lib="Alternative Splicing Library L2"  
/note="strand: minus, reference: ENSEMBL: Mouse-Transcript-  
ENST: ENSMUST0000070400, based on BLAT search"

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
ORIGIN  
FEATURES  
SOURCE  
Db  
Query Match  
Best Local  
Matches  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
AG195654  
AG195654.1 GI:45227830

GSS.  
Pan troglodytes (chimpanzee)  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Pan.  
1  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
BAC end sequences of library RP-43  
Unpublished  
2 (bases 1 to 100)  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
Direct Submission  
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);  
52, Oun-dong, Yusong-gu, Daegu 705-333, Korea  
(E-mail: redstone@mail.kribb.re.kr, URL: http://pne.grc.kribb.re.kr/  
Tel: 82-42-866-7181, Fax: 82-42-866-4409)  
Clones are derived from the chimpanzee BAC library RP-43 This BAC  
end was generated during the R&D process and may have higher chance  
of clone tracking errors.  
PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBAC3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.  
Location/Qualifiers  
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RESULT 12  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
AG195654  
AG195654.1 GI:18672592

55 bp DNA linear GSS 14-FEB-2002  
1008060C01.2EL.Y1 1008 - RescueMu Grid I Zea mays genomic, genomic  
survey sequence.  
BH643795  
BH643795.1 GI:18672592  
GSS.  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 55)  
Walbot, V.  
Maize genomic sequences found using engineered RescueMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1008060 row: 21  
Class: transposon-tagged.  
Location/Qualifiers

## FEATURES

source

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1..55
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/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI, Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmhd.iastate.edu and follow the links for 'RescueMu'. Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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## ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 55;  
Best Local Similarity 84.2%; Pred. No. 9.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCAGCGCGCAGAGGAGC 20  
|||||  
35 GAGCAGCGCAGCAGCAGC 17

RESULT 13  
B0167594/C

LOCUS B0167594 79 bp mRNA linear EST 20-MAY-2003  
DEFINITION WHE0077\_H03\_P05ZK Cheyenne wheat endosperm cDNA library Triticum aestivum cDNA clone WHE0077\_H03\_P05, mRNA sequence.

ACCESSION B0167594  
VERSION B0167594.1 GI:20312113

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticaceae; Triticum.

REFERENCE 1 (bases 1 to 79)  
Altenbach S., Anderson O.D., Chao S., Crossman C., Galili G., Laudencia-Chinganco D., Lazo G.R., Rausch C.U., Stamova B. and Vela S.

TITLE The structure and function of the expressed portion of the wheat genomes - Cheyenne endosperm cDNA library

JOURNAL Unpublished (2003)  
COMMENT Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818

FEATURES

source

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/note="Vector: Lambda ZAP II, excised phagemid; Site_1: EcoRI; Seeds collected, Cheyenne endosperm isolated, and RNA prepared by Susan Altenbach. Library constructed by Stratagene, Inc. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab."
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## ORIGIN

Query Match 71.0%; Score 14.2; DB 3; Length 79;  
Best Local Similarity 84.2%; Pred. No. 9.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCAGCGCGCAGAGGAGC 20  
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58 GAGCGCGCGCAGAGGAGC 40

RESULT 14

LOCUS C0911144

DEFINITION B03015E02 B03 Capsicum annuum cDNA 5', mRNA sequence.  
ACCESSION C0911144  
VERSION C0911144.1 GI:51301447

KEYWORDS EST.

SOURCE Capsicum annuum

ORGANISM Capsicum annuum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 84)  
Song W.Y., Jeon W.B., Kim K.S., Lee H.H., Ko M.K., Kim Y.S., Hong J.C. and Oh B.J.  
Generation of Hot Pepper (Capsicum annuum) ESTs (Express Sequence Tags) from Red Ripe Fruit (Song, et al.)

TITLE Unpublished (2004)

JOURNAL Contact: Boun-Jun Oh  
Jeonnam Biotechnology Research Center  
Namyang Bld. #603, 10-4 Gwangsan-dong, Dong-gu, Gwangju 501-180, Korea

FEATURES  
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ORIGIN

Query Match 71.0%; Score 14.2; DB 7; Length 84;  
Best Local Similarity 84.2%; Pred. No. 9.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 64 CGAGCAGCGCAGAGG 82

RESULT 15



CM118187/c 95 bp DNA linear GSS 29-OCT-2004  
 LOCUS 104 494 11108068 148 34621 006 Sorghum methylation filtered library  
 DEFINITION (LibID:104) Sorghum bicolor genomic clone 11108068, genomic survey  
 sequence.  
 ACCESSION CM118187  
 VERSION CM118187.1 GI:54810734  
 KEYWORDS GSS.  
 SOURCE Sorghum bicolor (sorghum)  
 ORGANISM Sorghum bicolor (sorghum)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 95)  
 Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,  
 Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,  
 McNameamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korf,I.F.,  
 Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and  
 Martienssen,R.A.  
 Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)  
 15660154  
 TITLE Sorghum genome sequencing by methylation filtration  
 JOURNAL PUBMED  
 COMMENT Contact: Bedell JA  
 Oxion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@oxiongenomics.com  
 Plate: 494 row: k column: 04  
 Seq primer: SWfor Forward  
 Class: methylation filtered  
 High quality sequence stop: 95.  
 Location/Qualifiers  
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 /organism="Sorghum bicolor"  
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 /db\_xref="taxon:4558"  
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 /clone\_lib="Sorghum methylation filtered library (LibID:  
 104)"  
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA  
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 kb fraction, ligated into HincII-digested pBCSK(-) vector  
 and electroporated into E. coli cells. This is a  
 methylation filtered library."  
 ORIGIN  
 Query Match 71.0%; Score 14.2; DB 10; Length 95;  
 Best Local Similarity 84.2%; Pred. No. 9.2e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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 Db 59 GGGCAGCGCTCACAGAGC 41  
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 Job time : 1576 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 : Search time 48.1 Seconds  
(without alignments)  
739.111 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20

Sequence: 1 cgcagcagcgagcagcagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Issued Patents NA: \*  
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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCUS\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.4	72.0	21	3	US-09-619-758-14 Sequence 14, Appl
C 2	14.4	72.0	21	3	US-09-886-607-14 Sequence 14, Appl
C 3	14.2	71.0	25	3	US-09-396-196G-65948 Sequence 65948, A
4	14.2	71.0	25	3	US-09-396-196G-65949 Sequence 65949, A
5	14.2	71.0	25	3	US-09-396-196G-65950 Sequence 65950, A
6	14.2	71.0	25	3	US-09-396-196G-65951 Sequence 65951, A
7	14.2	71.0	25	3	US-09-396-196G-71454 Sequence 71454, A
C 8	14.2	71.0	25	3	US-09-396-196G-71470 Sequence 71470, A
C 9	14.2	71.0	25	3	US-09-396-196G-71471 Sequence 71471, A
10	14.2	71.0	51	3	US-09-443-199C-753 Sequence 753, App
11	13.8	69.0	25	3	US-09-396-196G-46316 Sequence 46316, A
12	13.8	69.0	25	3	US-09-396-196G-46317 Sequence 46317, A
13	13.8	69.0	25	3	US-09-396-196G-46318 Sequence 46318, A
14	13.8	69.0	25	3	US-09-396-196G-46319 Sequence 46319, A
15	13.8	69.0	25	3	US-09-396-196G-46320 Sequence 46320, A
16	13.8	69.0	37	3	US-09-344-888A-19 Sequence 19, Appl
17	13.6	68.0	23	3	US-09-032-894-90 Sequence 90, Appl
18	13.6	68.0	23	3	US-09-031-626-90 Sequence 90, Appl
19	13.6	68.0	27	2	US-08-170-095B-36 Sequence 36, Appl
20	13.6	68.0	27	2	5428007-6 Patent No. 5428007
21	13.6	68.0	45	2	US-08-785-448-6 Sequence 6, Appl
22	13.6	68.0	45	2	US-08-925-927-6 Sequence 6, Appl
23	13.6	68.0	45	2	US-08-875-154-8 Sequence 8, Appl
24	13.6	68.0	45	3	US-09-120-576-6 Sequence 6, Appl

25	13.6	68.0	50	3	US-09-673-274C-14 Sequence 14, Appl
C 26	13.6	68.0	60	2	US-08-009-265-17 Sequence 17, Appl
C 27	13.6	68.0	75	2	US-08-009-265-42 Sequence 42, Appl
C 28	13.6	68.0	75	2	US-08-322-679-10 Sequence 10, Appl
C 29	13.6	68.0	75	3	US-08-686-993A-22 Sequence 22, Appl
C 30	13.6	68.0	78	9	5457037-7 Patent No. 5457037
C 31	13.6	68.0	81	3	US-09-673-274C-15 Sequence 15, Appl
C 32	13.2	66.0	25	3	US-09-396-196G-23837 Sequence 23837, A
C 33	13.2	66.0	25	3	US-09-396-196G-23838 Sequence 23838, A
C 34	13.2	66.0	25	3	US-09-396-196G-92823 Sequence 92823, A
35	13.2	66.0	25	3	US-09-396-196G-92824 Sequence 92824, A
36	13.2	66.0	25	3	US-09-396-196G-92825 Sequence 92825, A
37	13.2	66.0	25	3	US-09-396-196G-93601 Sequence 93601, A
C 38	13.2	66.0	25	3	US-09-396-196G-107012 Sequence 107012, A
C 39	13.2	66.0	25	3	US-09-396-196G-108063 Sequence 108063, A
C 40	13.2	66.0	40	3	US-09-548-797B-157 Sequence 157, App
41	13.2	66.0	43	3	US-09-380-190A-46 Sequence 46, Appl
C 42	13.2	66.0	44	3	US-09-380-420C-13 Sequence 13, Appl
C 43	13.2	66.0	44	3	US-09-899-642A-13 Sequence 13, Appl
44	13.2	66.0	51	3	US-09-443-199C-754 Sequence 754, App
45	13.2	66.0	92	2	US-08-487-141B-109 Sequence 109, App

#### ALIGNMENTS

RESULT 1  
US-09-619-758-14/c  
Sequence 14, Application US/09619758  
Patent No. 6667164  
GENERAL INFORMATION:  
APPLICANT: Miller, Marcia M  
APPLICANT: Afanasieff, Marielle  
TITLE OF INVENTION: Methods for Breeding Disease-resistant Domestic Fowl  
FILE REFERENCE: 1954-322  
CURRENT FILING DATE: 1954-12-27  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: US 09/244,093  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: US 08/744,025  
PRIOR FILING DATE: 1996-12-27  
PRIOR APPLICATION NUMBER: US 07/865,662  
PRIOR FILING DATE: 1995-01-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer for  
OTHER INFORMATION: SSCP analysis of Mhc B class II-beta genotype of  
OTHER INFORMATION: fowl  
US-09-619-758-14  
Query Match 72.0%; Score 14.4; DB 3; Length 21;  
Best Local Similarity 93.8%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 5 CACGGCGCAGAGGAGC 20  
16 CACGGTCAGAGGAGC 1  
RESULT 2  
US-09-886-607-14/c  
Sequence 14, Application US/09886607  
Patent No. 6696253  
GENERAL INFORMATION:  
APPLICANT: Miller, Marcia  
APPLICANT: Afanasieff, Marielle  
APPLICANT: Briles, W. Elwood

```
; TITLE OF INVENTION: Method for Breeding Disease Resistant Domesticated Fowl
; FILE REFERENCE: 1954-376
; CURRENT APPLICATION NUMBER: US/09/886,607
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 09/244,093
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/619,757
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 08/774,025
; PRIOR FILING DATE: 1996-12-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Gallus sp.
US-09-886-607-14
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Query Match          72.0%; Score 14.4; DB 3; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      5 CACGGCGCAGAGGAGC 20
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Db       16 CACGGTGCAGAGAGC 1
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RESULT 3
US-09-396-196G-65948
; Sequence 65948, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65948
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Query Match          71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 CGAGCAGCGCGCAGAGAG 19
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Db       7 CCAGAGGCGCGCAGAGAG 25
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RESULT 4
US-09-396-196G-65949
; Sequence 65949, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65949
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Query Match          71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 CGAGCAGCGCGCAGAGAG 19
         |||||
Db       6 CCAGAGGCGCGCAGAGAG 24
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```
RESULT 5
US-09-396-196G-65950
; Sequence 65950, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65950
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Query Match          71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGAGCAGCGCGCAGAGAG 19
         |||||
Db       5 CCAGAGGCGCGCAGAGAG 23
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```
RESULT 6
US-09-396-196G-65951
; Sequence 65951, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65951
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Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CGAGCAGCGCGCAGAGAGC 19  
Db 3 CCAGAAAGCGCGCAGAGAGC 21

## RESULT 7

US-09-396-196G-71454/c  
; Sequence 71454, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71454  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-71454

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGCGCGCAGAGAGC 20  
Db 19 GAGCAGCTTGCGAGAGAGC 1

## RESULT 8

US-09-396-196G-71470/c  
; Sequence 71470, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71470  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-71470

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGCGCGCAGAGAGC 20  
Db 23 GAGCAGCTTGCGAGAGAGC 5

RESULT 9  
US-09-396-196G-71471/c  
; Sequence 71471, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71471  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-71471

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGCGCGCAGAGAGC 20  
Db 21 GAGCAGCTTGCGAGAGAGC 3

RESULT 10  
US-09-443-199C-753  
; Sequence 753, Application US/09443199C  
; Patent No. 6670464  
; GENERAL INFORMATION:  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Leach, Martin  
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide  
; FILE REFERENCE: 15966-534A  
; CURRENT APPLICATION NUMBER: US/09/443,199C  
; CURRENT FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 60/109,024  
; PRIOR FILING DATE: 1998-11-17  
; NUMBER OF SEQ ID NOS: 1272  
; SOFTWARE: Curagen Patent Formatter Version 0.9  
; SEQ ID NO 753  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (26)...(0)  
; OTHER INFORMATION: 1 of 2 allelic variants (754 is other entry)  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Accession number cg43921619  
US-09-443-199C-753

Query Match 71.0%; Score 14.2; DB 3; Length 51;  
Best Local Similarity 84.2%; Pred. No. 4.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGCGCGCAGAGAGC 20  
Db 26 GAGCAGGAGAGAGAGAGC 44

RESULT 11  
US-09-396-196G-46316  
; Sequence 46316, Application US/09396196G

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/ Patent No. 6821724
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196G
/ CURRENT FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 46316
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196G-46316
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Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 4 GCACGGCGCAGAGAGC 20
    |||||
Db 8 GCACGCGCGAGATGAGC 24
```

```
RESULT 12
US-09-396-196G-46317
/ Sequence 46317, Application US/09396196G
/ Patent No. 6821724
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196G
/ CURRENT FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 46317
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196G-46317
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```
Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 GCACGGCGCAGAGAGC 20
    |||||
Db 7 GCACGCGCGAGATGAGC 23
```

```
RESULT 13
US-09-396-196G-46318
/ Sequence 46318, Application US/09396196G
/ Patent No. 6821724
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196G
```

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/ CURRENT FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 46318
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196G-46318
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Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 GCACGGCGCAGAGAGC 20
    |||||
Db 5 GCACGCGCGAGATGAGC 21
```

```
RESULT 14
US-09-396-196G-46319
/ Sequence 46319, Application US/09396196G
/ Patent No. 6821724
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196G
/ CURRENT FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 46319
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196G-46319
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```
Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 4 GCACGGCGCAGAGAGC 20
    |||||
Db 4 GCACGCGCGAGATGAGC 20
```

```
RESULT 15
US-09-396-196G-46320
/ Sequence 46320, Application US/09396196G
/ Patent No. 6821724
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196G
/ CURRENT FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 46320
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
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US-09-396-196G-46320

Query Match

Best Local Similarity 69.0%; Score 13.8; DB 3; Length 25;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCACGCGCGCAGAGAGC 20  
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 Db 2 GCACGCGCGCAGAGAGC 18

Search completed: December 24, 2005, 18:36:19  
 Job time : 49.1 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20

Sequence: 1 cgagcagcgccgagagagc 20

Scoring table: IDENTITY\_NUC

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
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6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-2
2	19	95.0	29	9	US-10-703-817-104
3	15.4	77.0	99	3	US-09-974-300-4020
4	15.2	76.0	25	7	US-10-719-956-362544
5	15.2	76.0	27	3	US-09-894-633A-18
6	14.8	74.0	25	10	US-11-036-317-855094
7	14.8	74.0	55	3	US-09-991-209-72
8	14.4	72.0	21	3	US-09-886-607-14
9	14.2	71.0	25	7	US-10-719-956-601919
10	14.2	71.0	25	9	US-10-809-189-65948
11	14.2	71.0	25	9	US-10-809-189-65949
12	14.2	71.0	25	9	US-10-809-189-65950
13	14.2	71.0	25	9	US-10-809-189-65951
14	14.2	71.0	25	9	US-10-809-189-71454
15	14.2	71.0	25	9	US-10-809-189-71470
16	14.2	71.0	25	9	US-10-809-189-71471
17	14.2	71.0	27	6	US-10-186-157-6
18	14.2	71.0	42	6	US-10-353-678-35
19	14.2	71.0	48	6	US-10-353-678-35
20	14.2	71.0	63	6	US-10-174-394-41
21	14.2	71.0	63	8	US-10-435-087-27
22	14.2	71.0	63	9	US-10-980-764-13
23	14.2	71.0	63	9	US-10-980-659-13

24	14.2	71.0	63	9	US-10-980-695-13	Sequence 13, Appl
25	14.2	71.0	75	6	US-10-353-678-65	Sequence 65, Appl
26	14.2	71.0	96	6	US-10-353-678-65	Sequence 66, Appl
27	13.8	69.0	20	9	US-10-800-350-165	Sequence 165, Appl
28	13.8	69.0	20	9	US-10-800-077-165	Sequence 165, Appl
29	13.8	69.0	23	9	US-10-980-002-7	Sequence 7, Appl1
30	13.8	69.0	25	8	US-10-719-900-109231	Sequence 309231,
31	13.8	69.0	25	8	US-10-719-900-109231	Sequence 309231,
32	13.8	69.0	25	9	US-10-809-189-46316	Sequence 46316, A
33	13.8	69.0	25	9	US-10-809-189-46317	Sequence 46317, A
34	13.8	69.0	25	9	US-10-809-189-46318	Sequence 46318, A
35	13.8	69.0	25	9	US-10-809-189-46319	Sequence 46319, A
36	13.8	69.0	25	9	US-10-809-189-46320	Sequence 46320, A
37	13.8	69.0	65	3	US-09-908-975-29746	Sequence 29746, A
38	13.6	68.0	23	3	US-09-778-152-80	Sequence 90, Appl
39	13.6	68.0	23	3	US-10-023-610-50	Sequence 90, Appl
40	13.6	68.0	23	7	US-10-212-848-50	Sequence 90, Appl
41	13.6	68.0	25	7	US-10-719-956-194261	Sequence 194261,
42	13.6	68.0	25	7	US-10-719-956-194262	Sequence 194262,
43	13.6	68.0	25	7	US-10-719-956-194262	Sequence 194262,
44	13.6	68.0	25	8	US-10-719-900-949166	Sequence 949166,
45	13.6	68.0	25	10	US-11-036-317-95368	Sequence 95368, A

## ALIGNMENTS

RESULT 1  
US-09-296-264-2  
; Sequence 2, Application US/09296264  
; Publication No. US20030083274A1  
; GENERAL INFORMATION:  
; APPLICANT: WRIGHT, Jim A.  
; APPLICANT: YOUNG, Aiping H.  
; APPLICANT: LEE, Yoon S.  
; TITLE OF INVENTION: NEUROPILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND  
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH  
; FILE REFERENCE: 032396-043  
; CURRENT APPLICATION NUMBER: US/09/296,264  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: US 60/082,791  
; EARLIER FILING DATE: 1998-04-23  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-296-264-2

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGAGC 20  
Db 1 CGAGCAGCGCGCAGAGAGC 20

RESULT 2  
US-10-703-817-104/C  
; Sequence 104, Application US/10703817  
; Publication No. US20050118117A1  
; GENERAL INFORMATION:  
; APPLICANT: ROTH, RICHARD B.  
; APPLICANT: NELSON, MATTHEW ROBERTS  
; APPLICANT: KAMMERER, STEFAN M.  
; APPLICANT: BRAUN, ANDREAS  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: SEQ-4061-UT  
; CURRENT APPLICATION NUMBER: US/10/703,817  
; CURRENT FILING DATE: 2003-11-06

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/ PRIOR APPLICATION NUMBER: 60/489,703
/ PRIOR FILING DATE: 2003-07-23
/ PRIOR APPLICATION NUMBER: 60/424,475
/ PRIOR FILING DATE: 2002-11-06
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 104
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
US-10-703-817-104

Query Match          95.0%; Score 19; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  GAGCAGCGCGCAGAGAGC 20
        |||||
Db      29 GAGCAGCGCGCAGAGAGC 11

RESULT 3
US-09-974-300-4020
/ Sequence 4020, Application US/09974300
/ Patent No. US20020146721A1
/ GENERAL INFORMATION:
/ APPLICANT: Berka, Randy M.
/ APPLICANT: Clausen, Ib Groth
/ TITLE OF INVENTION: Methode For Monitoring Multiple Gene
/ FILE REFERENCE: 10085,500-US
/ CURRENT APPLICATION NUMBER: US/09/974,300
/ CURRENT FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 09/680,598
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/279,526
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 8481
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4020
/ LENGTH: 99
/ TYPE: DNA
/ ORGANISM: Bacillus licheniformis
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(99)
/ OTHER INFORMATION: n = A,T,C or G
US-09-974-300-4020

Query Match          77.0%; Score 15.4; DB 3; Length 99;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4  GCACGCGCGCAGAGAGC 20
        |||||
Db      31 GCACGCGCGCAGAGAGC 47

RESULT 4
US-10-719-956-362544/c
/ Sequence 362544, Application US/10719956
/ Publication No. US20040146910A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methode of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002-11-20
/ NUMBER OF SEQ ID NOS: 699466
```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 362544
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-719-956-362544

Query Match          76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CGAGCAGCGCGCAGAGAGC 20
        |||||
Db      20 CGAGCAGCGCGCAGAGAGC 1

RESULT 5
US-09-894-633A-18
/ Sequence 18, Application US/09894633A
/ Patent No. US20020124285A1
/ GENERAL INFORMATION:
/ APPLICANT: Comer, Timothy
/ APPLICANT: Dubois, Patrice
/ APPLICANT: Malven, Marianne
/ APPLICANT: Masucci, James
/ TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSION
/ FILE REFERENCE: 38-21(1585)B
/ CURRENT APPLICATION NUMBER: US/09/894,633A
/ CURRENT FILING DATE: 2001-06-28
/ PRIOR APPLICATION NUMBER: 60/214,357
/ PRIOR FILING DATE: 2000-06-28
/ PRIOR APPLICATION NUMBER: 09/894,633
/ PRIOR FILING DATE: 2000-06-28
/ NUMBER OF SEQ ID NOS: 111
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18
/ LENGTH: 27
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(27)
/ OTHER INFORMATION: synthetic primer sequence
US-09-894-633A-18

Query Match          76.0%; Score 15.2; DB 3; Length 27;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CGAGCAGCGCGCAGAGAGC 20
        |||||
Db      7  CGAGCAGCGCGCAGAGAGC 26

RESULT 6
US-11-036-317-855094
/ Sequence 855094, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 855094
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
```

US-11-036-317-855094

Query Match 74.0%; Score 14.8; DB 10; Length 25;

Best Local Similarity 88.9%; Pred. No. 4.4e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGAG 19

Db 8 GAGCAGCGCGCAGAGAG 25

RESULT 7

US-09-991-209-72

Sequence 72, Application US/09991209

Publication No. US20030024009A1

GENERAL INFORMATION:

APPLICANT: Dunn-Coleman, Nigel

APPLICANT: Langdon, Timothy

APPLICANT: Morse, Phillip

TITLE OF INVENTION: Manipulation of the Phenolic Acid

TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted

FILE REFERENCE: GC648-2

CURRENT APPLICATION NUMBER: US/09/991,209

CURRENT FILING DATE: 2002-07-02

PRIOR APPLICATION NUMBER: US 60/249,608

PRIOR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 72

LENGTH: 55

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: primer

US-09-991-209-72

Query Match 74.0%; Score 14.8; DB 3; Length 55;

Best Local Similarity 88.9%; Pred. No. 3.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGAG 19

Db 6 GATCAGCGCGAAGAGAG 23

RESULT 8

US-09-886-607-14/C

Sequence 14, Application US/09886607

Patent No. US20020083482A1

GENERAL INFORMATION:

APPLICANT: Miller, Marcia

APPLICANT: Afanasieff, Marielle

APPLICANT: Biles, W. Elwood

TITLE OF INVENTION: Method for Breeding Disease Resistant Domesticated Fowl

FILE REFERENCE: 1954-376

CURRENT APPLICATION NUMBER: US/09/886,607

CURRENT FILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: US 09/244,093

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: US 09/619,757

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: US 08/774,025

PRIOR FILING DATE: 1996-12-27

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.0

SEQ ID NO 14

LENGTH: 21

TYPE: DNA

ORGANISM: Gallus sp.

Query Match

72.0%; Score 14.4; DB 3; Length 21;

Best Local Similarity 93.8%; Pred. No. 6.9e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CACGCCGCGCAGAGAGC 20

Db 16 CACGTCGCGCAGAGAGC 1

RESULT 9

US-10-719-956-601919/C

Sequence 601919, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR FILING DATE: 2002.11.20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 601919

LENGTH: 25

TYPE: DNA

ORGANISM: Rattus norvegicus

US-10-719-956-601919

Query Match 71.0%; Score 14.2; DB 7; Length 25;

Best Local Similarity 84.2%; Pred. No. 8.2e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGAGC 20

Db 24 GAGCCGCGCGCAGAGAGC 6

RESULT 10

US-10-809-189-65948

Sequence 65948, Application US/10809189

Publication No. US20050048531A1

GENERAL INFORMATION:

APPLICANT: Michael Miltmann

APPLICANT: David Lockhart

APPLICANT: Atymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/10/809,189

CURRENT FILING DATE: 2004-03-25

PRIOR APPLICATION NUMBER: US/09/396,196

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 65948

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-10-809-189-65948

Query Match 71.0%; Score 14.2; DB 9; Length 25;

Best Local Similarity 84.2%; Pred. No. 8.2e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGAG 19

Db 7 CGAGAGCGCGCGCAGAGAG 25

RESULT 11

US-10-809-189-65949

```
; Sequence 65949, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-65949
```

```
Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGAGCAGCGCGCAGAGGAG 19
         |||||
Db       6 CCGAAGAGCGCGCAGAGGAG 24
```

```
RESULT 12
US-10-809-189-65950
; Sequence 65950, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-65950
```

```
Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGAGCAGCGCGCAGAGGAG 19
         |||||
Db       5 CCGAAGAGCGCGCAGAGGAG 23
```

```
RESULT 13
US-10-809-189-65951
; Sequence 65951, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
```

```
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-65951
```

```
Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGAGCAGCGCGCAGAGGAG 19
         |||||
Db       3 CCGAAGAGCGCGCAGAGGAG 21
```

```
RESULT 14
US-10-809-189-71454/C
; Sequence 71454, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71454
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-71454
```

```
Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GAGCAGCGCGCGCAGAGGAG 20
         |||||
Db       19 GAGCAGCGTTGCGAGAGAGC 1
```

```
RESULT 15
US-10-809-189-71470/C
; Sequence 71470, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
```

```

? CURRENT FILING DATE: 2004-03-25
? PRIOR APPLICATION NUMBER: US/09/396,196
? PRIOR FILING DATE: 1999-09-15
? PRIOR APPLICATION NUMBER: 60/100,678
? PRIOR FILING DATE: 1998-09-17
? NUMBER OF SEQ ID NOS: 127806
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 71470
? LENGTH: 25
? TYPE: DNA
? ORGANISM: mus musculus
US-10-809-189-71470

```

Query Match	71.0%	Score 14.2	DB 9	Length 25
Best Local Similarity	84.2%	Pred. No. 8.2e+03		
Matches	16	Conservative	0	Mismatches 3, Indels 0, Gaps 0
OY	2	GAGCAGCGCGCAGAGAGAC	20	
Db	23	GAGCAGCGTTCGAGAGAGAC	5	

Search completed: December 25, 2005, 04:14:20  
Job time : 338.6 secs

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```

; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 27
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(63)
US-10-842-206-27
```

```

Query Match          71.0%; Score 14.2; DB 6; Length 63;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      2 GAGCAGCGCGCAGAGAGC 20
        ||| ||| ||| ||| ||| |||
DB      30 GAGCGCGCGCGAGCGGAGC 48
```

RESULT 3

```

US-10-980-459-13
; Sequence 13, Application US/10980459
; Publication No. US20050256042A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
```

```

; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Jeffers, Michael B.
; APPLICANT: LaRochele, William J.
; APPLICANT: Lichenstein, Henri
; APPLICANT: Namdev, Pradyumna Kumar
; APPLICANT: Valax, Pascal
; APPLICANT: Yim, Zachary
; APPLICANT: Hahne, William
; TITLE OF INVENTION: Methods of Preventing and Treating Alimentary Mucositis
```

```

; FILE REFERENCE: Cura-57 AM
; CURRENT APPLICATION NUMBER: US/10/980,459
; PRIOR APPLICATION NUMBER: 2004-11-03
; PRIOR FILING DATE: 2003-5-9
; PRIOR APPLICATION NUMBER: 10/842,179
; PRIOR FILING DATE: 2004-5-10
; PRIOR APPLICATION NUMBER: 60/541,728
; PRIOR FILING DATE: 2004-2-4
; PRIOR APPLICATION NUMBER: 60/545,278
; PRIOR FILING DATE: 2004-2-18
; PRIOR APPLICATION NUMBER: 60/
; PRIOR FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: CuraseqList version 0.1
```

```

; SEQ ID NO 13
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(63)
US-10-980-459-13
```

```

Query Match          71.0%; Score 14.2; DB 6; Length 63;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      2 GAGCAGCGCGCAGAGAGC 20
        ||| ||| ||| ||| ||| |||
DB      30 GAGCGCGCGCGAGCGGAGC 48
```

RESULT 4

```

US-10-949-720-165
; Sequence 165, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
```

```

; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-949-720-165
```

```

Query Match          69.0%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      4 GCACGCGCGCAGAGAGC 20
        ||| ||| ||| ||| ||| |||
DB      4 GCAGGCGCGCACAGAGC 20
```

RESULT 5

```

US-11-121-849-366542
; Sequence 366542, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366542
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

```

US-11-121-849-366542
```

```

Query Match          69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      4 GCACGCGCGCAGAGAGC 20
        ||| ||| ||| ||| ||| |||
DB      4 GCTCGCGCGCAGAGAGC 20
```

RESULT 6

```

US-11-121-849-213468/c
; Sequence 213468, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
```



CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 213468  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-213468

Query Match  
Best Local Similarity 80.0%; Score 13.6; DB 7; Length 25;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGAGC 20  
DB 20 CGAACACGCGCGAGAGCATC 1

RESULT 7  
US-11-121-849-213523/c  
Sequence 213523, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 213523  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-213523

Query Match  
Best Local Similarity 80.0%; Score 13.6; DB 7; Length 25;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGAGC 20  
DB 20 CGAACACGCGCGAGAGCATC 1

RESULT 8  
US-11-121-849-357209/c  
Sequence 357209, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 357209  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-357209

Query Match 68.0%; Score 13.6; DB 7; Length 25;

Best Local Similarity 80.0%; Pred. No. 3.3e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGAGC 20  
DB 21 CGGCACGACGCGCTGAGCATC 2

RESULT 9  
US-10-939-294A-15531  
Sequence 15531, Application US/10939294A  
Publication No. US20050266417A1  
GENERAL INFORMATION:  
APPLICANT: Barany, Francis  
APPLICANT: Turner, Daniel  
APPLICANT: Pingle, Maneesh  
TITLE OF INVENTION: Methods for identifying target nucleic acid molecules  
FILE REFERENCE: 19603/4121 (CRF D-2995-02)  
CURRENT APPLICATION NUMBER: US/10/939,294A  
CURRENT FILING DATE: 2004-09-10  
PRIOR APPLICATION NUMBER: US 60/502/731  
PRIOR FILING DATE: 2003-09-12  
NUMBER OF SEQ ID NOS: 38895  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 15531  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-15531

Query Match  
Best Local Similarity 80.0%; Score 13.6; DB 6; Length 32;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGAGC 20  
DB 7 CGGGAATGCGCGCAGCGAGC 26

RESULT 10  
US-10-939-294A-15856  
Sequence 15856, Application US/10939294A  
Publication No. US20050266417A1  
GENERAL INFORMATION:  
APPLICANT: Barany, Francis  
APPLICANT: Turner, Daniel  
APPLICANT: Pingle, Maneesh  
TITLE OF INVENTION: Methods for identifying target nucleic acid molecules  
FILE REFERENCE: 19603/4121 (CRF D-2995-02)  
CURRENT APPLICATION NUMBER: US/10/939,294A  
CURRENT FILING DATE: 2004-09-10  
PRIOR APPLICATION NUMBER: US 60/502/731  
PRIOR FILING DATE: 2003-09-12  
NUMBER OF SEQ ID NOS: 38895  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 15856  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-15856

Query Match  
Best Local Similarity 80.0%; Score 13.6; DB 6; Length 32;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGAGCAGCGCGCAGAGAGC 20

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Db          7 CCAGCGTGGCGAGCGAGC 26

RESULT 11
US-11-121-849-20944
; Sequence 20944, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 20944
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-20944

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          3 AGCAGCGCGCAGAGAGC 20
            |||||
Db          2 AGCAGCGCTGAAGAGAGC 19

RESULT 12
US-11-121-849-34121
; Sequence 34121, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 34121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-34121

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          3 AGCAGCGCGCAGAGAGC 20
            |||||
Db          5 AGCGCTGGCGAGAGAGC 22

RESULT 13
US-11-121-849-258042
; Sequence 258042, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 258042
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-258042

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          3 AGCAGCGCGCAGAGAGC 20
            |||||
Db          5 AGCGCTGGCGAGAGAGC 22

RESULT 14
US-11-121-849-356175
; Sequence 356175, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 356175
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-356175

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          2 GAGCAGCGCGCAGAGAG 15
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Db          3 GAGCAGCGCGCAGAGAGC 20

RESULT 15
US-11-121-849-360121/C
; Sequence 360121, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 360121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-360121

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db	19	CAAGCAGCTTGCAGAGGA	2						

Search completed: December 25, 2005, 04:37:02  
 Job time : 136.3 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds  
(without alignments)  
1953.383 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20

Sequence: 1 ggcagcagcgagcagcagcg 20

Scoring table: IDENTITY\_NUC

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_in: \*  
3: gb\_env: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pr: \*  
9: gb\_ro: \*  
10: gb\_scs: \*  
11: gb\_sy: \*  
12: gb\_un: \*  
13: gb\_vi: \*  
14: gb\_htg: \*  
15: gb\_pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211660
2	16.8	84.0	51	6	AX15695
3	15.2	76.0	96	6	CQ745222
4	15.2	76.0	99	6	A23183
5	14.8	74.0	100	6	AX997929
6	14.8	74.0	100	6	AX997930
7	14.2	71.0	26	6	AB559751
8	14.2	71.0	26	6	AX146654
9	14.2	71.0	40	6	AX490799
10	14.2	71.0	45	6	AX128401
11	14.2	71.0	45	6	AX429834
12	14.2	71.0	65	6	AR038667
13	14.2	71.0	66	6	AR038665
14	14.2	71.0	78	13	AF362846
15	14.2	71.0	78	13	AF362847
16	14.2	71.0	78	13	AF362848
17	13.8	69.0	60	6	AR009383
18	13.8	69.0	78	6	A67678

19	13.6	68.0	30	6	AR063475	AR063475 Sequence
20	13.6	68.0	30	6	I28155	I28155 Sequence 12
21	13.6	68.0	37	6	AX356235	AX356235 Sequence
22	13.6	68.0	49	10	AL823803	AL823803 Arabidops
23	13.6	68.0	51	6	CQ005836	CQ005836 Sequence
24	13.6	68.0	51	6	CQ005837	CQ005837 Sequence
25	13.6	68.0	64	8	HUMMACU	L37707 Homo saplen
26	13.6	68.0	86	6	AX236733	AX236733 Sequence
27	13.6	68.0	90	6	AX236627	AX236627 Sequence
28	13.6	68.0	97	11	AF430188	AF430188 Synthetic
29	13.6	68.0	100	2	AB182402	AB182402 Ceratina
30	13.6	68.0	100	10	AF235063	AF235063 Mus muscu
31	13.4	67.0	50	6	AR410670	AR410670 Sequence
32	13.4	67.0	50	6	AR439034	AR439034 Sequence
33	13.4	67.0	50	6	AR473054	AR473054 Sequence
34	13.4	67.0	50	6	AR527040	AR527040 Sequence
35	13.4	67.0	50	6	AR566073	AR566073 Sequence
36	13.4	67.0	50	6	AR592091	AR592091 Sequence
37	13.4	67.0	50	6	AR604365	AR604365 Sequence
38	13.4	67.0	50	6	AR604951	AR604951 Sequence
39	13.4	67.0	50	6	AR613616	AR613616 Sequence
40	13.4	67.0	50	6	AR635787	AR635787 Sequence
41	13.4	67.0	50	6	AR650516	AR650516 Sequence
42	13.4	67.0	50	6	AR657457	AR657457 Sequence
43	13.4	67.0	50	6	AX697498	AX697498 Sequence
44	13.4	67.0	60	6	COS37981	COS37981 Sequence
45	13.2	66.0	21	6	A86893	A86893 Sequence 3

#### ALIGNMENTS

RESULT 1  
BD211660  
LOCUS  
DEFINITION  
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION  
BD211660.1 GI:33021430  
VERSION  
JP 2002512793-A/3.  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 20)  
Wright,J.A., Young,A.H. and Lee,Y.S.  
TITLE  
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation  
JOURNAL  
Patent: JP 2002512793-A 3 08-MAY-2002;  
GENENSENSE TECHNOLOGIES INC

COMMENT  
OS Homo sapiens (human)  
PN JP 2002512793-A/3  
PD 08-MAY-2002

PR 23-APR-1998 JP 2000545999  
PI 23-APR-1998 US 60/082791  
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC  
Antisense oligonucleotide sequence of neuropilin and method of using the  
CC same for controlling cell proliferation  
FH Key Location/Qualifiers  
FT source 1..20  
FT Location/Qualifiers  
1..20  
Location/Qualifiers  
/organism="Homo sapiens (human)".  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

#### ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCG 20  
|||||  
Db 1 GGACGAGGCGGACGACGCG 20

RESULT 2  
AX156995  
LOCUS A23183/c 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 323 from Patent WO0140521.  
ACCESSION AX156995  
VERSION AX156995.1 GI:14538326  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Shimkova, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
METHODS methods of use thereof  
PATENT: WO 0140521-A 323 07-JUN-2001;  
Curegen Corporation (US)  
LOCATION/Qualifiers

FEATURES  
source 1..51  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 26  
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Accession number CG20436198"

ORIGIN  
Query Match 84.0%; Score 16.8; DB 6; Length 51;  
Best Local Similarity 90.0%; Pred. No. 7e+04;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCG 20  
|||||  
Db 22 GGACGCGGCGGACGACGCG 41

RESULT 3  
CQ745222/c 96 bp DNA linear PAT 03-FEB-2004  
LOCUS CQ745222  
DEFINITION Sequence 31156 from Patent WO02068579.  
ACCESSION CQ745222  
VERSION CQ745222.1 GI:42362958  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
PATENT: WO 02068579-A 31156 06-SEP-2002;  
PE Corporation (NY) (US)  
LOCATION/Qualifiers

FEATURES  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 76.0%; Score 15.2; DB 6; Length 96;  
Best Local Similarity 85.0%; Pred. No. 2.2e+05;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCG 20  
|||||  
Db 31 GGCTGAGGCGGACGCGCG 12

RESULT 4  
A23183 99 bp DNA linear PAT 11-JAN-1995  
LOCUS A23183/c  
DEFINITION Artificial DNA for DNA adapter (4d. 7).  
ACCESSION A23183  
VERSION A23183.1 GI:833251  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct

REFERENCE  
AUTHORS Stern, A., Hagemann, I. and Ziegler-Landeburger, D.  
TITLE Method of introduction of nucleic acids in cells  
PATENT: EP 0544292-A 7 02-JUN-1993;  
BOEHRINGER MANNHEIM GMBH  
LOCATION/Qualifiers

FEATURES  
source 1..99  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

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Query Match 76.0%; Score 15.2; DB 6; Length 99;  
Best Local Similarity 85.0%; Pred. No. 2.2e+05;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCG 20  
|||||  
Db 88 GGACGAGGCGGACGACGCG 69

RESULT 5  
AX997929 100 bp DNA linear PAT 16-JAN-2004  
LOCUS AX997929  
DEFINITION Sequence 9392 from Patent EP1260592.  
ACCESSION AX997929  
VERSION AX997929.1 GI:41004275  
KEYWORDS  
SOURCE  
ORGANISM Escherichia coli

REFERENCE  
AUTHORS Donner, H., Drescher, B., Huber, A. and Weber, J.  
TITLE Biochip  
PATENT: EP 1260592-A 9392 27-NOV-2002;  
MWG - Biotech AG (DE)  
LOCATION/Qualifiers

FEATURES  
source 1..100  
/organism="Escherichia coli"  
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/db\_xref="taxon:562"  
/note="D1832 D1832 U00096 complement(1913655\_\_1914206)"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 100;  
Best Local Similarity 88.9%; Pred. No. 3.1e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGACGCG 19  
|||||  
Db 15 GACGAGGCGGACGACGCG 32

RESULT 6  
AX997930 100 bp DNA linear PAT 16-JAN-2004  
LOCUS AX997930

DEFINITION Sequence 9393 from Patent EP1260592.  
ACCESSION AX997930  
VERSION AX997930.1 GI:41004276  
KEYWORDS  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE 1  
AUTHORS Donner, H., Dreischer, B., Huber, A. and Weber, J.  
TITLE Biochip  
JOURNAL Patent: EP 1260592-A 9393 27-NOV-2002;  
MMG - Biotech AG (DE)  
FEATURES  
source Location/Qualifiers  
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/organism="Escherichia coli"  
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/db\_xref="taxon:562"  
/note="b1832 b1832 U00096 complement(1913655\_1914206)"

ORIGIN  
Query Match 74.0%; Score 14.2; DB 6; Length 100;  
Best Local Similarity 88.9%; Pred. No. 3.1e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GACGAGGCGGACGCGC 19  
Db 79 GACGAGGCGGACGCGC 96

RESULT 7  
AR559751/c  
LOCUS AR559751 26 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 5 from patent US 6750380.  
ACCESSION AR559751.  
VERSION AR559751.1 GI:53969849  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Johal, G.S. and Mulsanti, D.S.  
TITLE Isolated nucleic acid molecules encoding the Dw3 P-glycoprotein of sorghum and methods of modifying growth in transgenic plants therewith  
JOURNAL Patent: US 6750380-A 5 15-JUN-2004;  
Pioneer Hi-Bred International, Inc. and The Curators of the University of Missouri; Des Moines, IA  
FEATURES  
source Location/Qualifiers  
1..26  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 26;  
Best Local Similarity 84.2%; Pred. No. 6.6e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACGAGGCGGACGCGC 20  
Db 24 GACGAGGCGGACGCGC 6

RESULT 8  
AX146654/c  
LOCUS AX146654 26 bp DNA linear PAT 31-MAY-2001  
DEFINITION Sequence 5 from Patent WO0134818.  
ACCESSION AX146654  
VERSION AX146654.1 GI:14285047  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Johal, G.S. and Mulsanti, D.S.  
TITLE Sorghum dwarfing genes and methods of use  
JOURNAL Patent: WO 0134818-A 5 17-MAY-2001;  
Johal, Gurmukh S. (US); Mulsanti, Dilbag S. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer designed from sequence of Zea mays Br2 gene"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 26;  
Best Local Similarity 84.2%; Pred. No. 6.6e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACGAGGCGGACGCGC 20  
Db 24 GACGAGGCGGACGCGC 6

RESULT 9  
AX490799/c  
LOCUS AX490799 40 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 13 from Patent WO0246400.  
ACCESSION AX490799  
VERSION AX490799.1 GI:22323749  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Kranz, D.M., Starwalt, S. and Bluestone, J.A.  
TITLE Mutated class II major histocompatibility proteins  
JOURNAL Patent: WO 0246400-A 13 13-JUN-2002;  
The Board of Trustees of the University of Illinois (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic nucleotide primer"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 40;  
Best Local Similarity 84.2%; Pred. No. 6e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACGAGGCGGACGCGC 20  
Db 39 GACGAGGCGGACGCGC 21

RESULT 10  
AX128401  
LOCUS AX128401 45 bp DNA linear PAT 15-MAY-2001  
DEFINITION Sequence 62 from Patent WO0130843.  
ACCESSION AX128401  
VERSION AX128401.1 GI:14134909  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Barbas, C.F., Kadon, M. and Beerli, R.  
TITLE Ligand activated transcriptional regulator proteins  
JOURNAL Patent: WO 0130843-A 62 03-MAY-2001;  
Novartis AG (CH); The Scripps Research Institute (US)  
FEATURES  
source Location/Qualifiers  
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ORIGIN /mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Recombinant molecule"

Query Match 71.0%; Score 14.2; DB 6; Length 45;  
Best Local Similarity 84.2%; Pred. No. 5.9e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGGCGGCGACGGC 19  
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Db 3 GGAGAGGGCGGCGCGCGC 21

RESULT 11  
LOCUS AX429834 45 bp DNA linear PAT 21-JUN-2002  
DEFINITION Sequence 26 from Patent WO0206463.  
ACCESSION AX429834  
VERSION AX429834.1 GI:21541010  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Beerli, R., Schopfer, U. and Barbas, C.F.  
TITLE Regulation of gene expression using single-chain, monomeric, ligand  
JOURNAL dependent polypeptide switches  
Patent: WO 0206463-A 26 24-JAN-2002;  
The Scripps Research Institute (US)  
LOCATION/Qualifiers  
1. .45  
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/note="Synthesized"

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Query Match 71.0%; Score 14.2; DB 6; Length 45;  
Best Local Similarity 84.2%; Pred. No. 5.9e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGGCGGCGACGGC 19  
||| ||||| ||| |||  
Db 3 GGAGAGGGCGGCGCGCGC 21

RESULT 12  
LOCUS AR038667 65 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5807675.  
ACCESSION AR038667  
VERSION AR038667.1 GI:5958030  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 65)  
AUTHORS Davalian, D., Singh, R. and Ullman, E.F.  
TITLE Fluorescent oxygen channeling immunoassays  
JOURNAL Patent: US 5807675-A 5 15-SEP-1998;  
FEATURES Location/Qualifiers  
1. .65  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 65;  
Best Local Similarity 84.2%; Pred. No. 5.4e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGGCGGCGACGGCG 20  
||| ||||| ||| |||

Db 3 GAAGCGGGCGGCGATGGCG 21

RESULT 13  
LOCUS AR038665/c 66 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5807675.  
ACCESSION AR038665  
VERSION AR038665.1 GI:5958028  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 66)  
AUTHORS Davalian, D., Singh, R. and Ullman, E.F.  
TITLE Fluorescent oxygen channeling immunoassays  
JOURNAL Patent: US 5807675-A 3 15-SEP-1998;  
FEATURES Location/Qualifiers  
1. .66  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 66;  
Best Local Similarity 84.2%; Pred. No. 5.4e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGGCGGCGACGGCG 20  
||| ||||| ||| |||  
Db 28 GAAGCGGGCGGCGATGGCG 10

RESULT 14  
LOCUS AF362846 78 bp RNA linear VRL 09-MAY-2001  
DEFINITION HIV-1 isolate 3040P1 from USA envelope glycoprotein, V3 region  
(env) gene, partial cde.  
ACCESSION AF362846  
VERSION AF362846  
KEYWORDS  
SOURCE Human immunodeficiency virus 1 (HIV-1)  
ORGANISM Human immunodeficiency virus 1  
REFERENCE 1  
AUTHORS Viruses; Retro-transcribing viruses; Retroviridae;  
Orthoretrovirinae; Lentiviruses; Primate lentivirus group.  
TITLE 1 (bases 1 to 78)  
AUTHORS Freel, S.A., Williams, J.M., Nelson, J.A., Patton, L.L., Fiscus, S.A.,  
Swanstrom, R. and Shugars, D.C.  
JOURNAL Characterization of human immunodeficiency virus type 1 in saliva  
and blood plasma by V3-specific heteroduplex tracking assay and  
genotype analyses  
J. Virol. 75 (10), 4936-4940 (2001)  
11312368  
2 (bases 1 to 78)  
REFERENCE 2  
AUTHORS Freel, S.A., Williams, J.M., Nelson, J.A., Patton, L.L., Fiscus, S.A.,  
Swanstrom, R. and Shugars, D.C.  
TITLE Direct Submission  
JOURNAL Submitted (21-MAR-2001) Dentistry and Microbiology, University of  
North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA  
LOCATION/Qualifiers  
1. .78  
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1. .>78  
/gene="env"  
1. .>78  
/gene="env"  
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/codon\_start=1



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## ORIGIN

Query Match 71.0%; Score 14.2; DB 13; Length 78;  
 Best Local Similarity 84.2%; Pred. No. 5.2e+05;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGAGGGCGACGCGC 19  
 |||||  
 Db 31 GGACCGAGGAGCATGCGC 49

## RESULT 15

AF362847

LOCUS

DEFINITION HIV-1 isolate 3040P2 from USA envelope glycoprotein, V3 region

(env) gene, partial cds.

ACCESSION

AF362847

VERSION

AF362847.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL PUBMED  
 11312368  
 2 (bases 1 to 78)  
 Freil,S.A., Williams,J.M., Nelson,J.A., Patton,L.L., Fiscus,S.A.,  
 Swansstrom,R. and Shugars,D.C.  
 Characterization of human immunodeficiency virus type 1 in saliva  
 and blood plasma by V3-specific heteroduplex tracking assay and  
 genotype analyses  
 J. Virol. 75 (10), 4936-4940 (2001)

REFERENCE

AUTHORS

TITLE

JOURNAL

SUBMITTED

North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA

FEATURES

source

1..78  
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 /mol\_type="genomic RNA"  
 /isolate="3040P2"  
 /db\_xref="taxon:11676"  
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 /country="USA"  
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 /note="V3 region"  
 /codon\_start=1  
 /product="envelope glycoprotein"  
 /protein\_id="AAK51974.1"  
 /db\_xref="GI:14010378"  
 /translation="NNNTRRSIQIGPGRAMHTTRIIGDIR"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 13; Length 78;  
 Best Local Similarity 84.2%; Pred. No. 5.2e+05;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGAGGGCGACGCGC 19  
 |||||  
 Db 31 GGACCGAGGAGCATGCGC 49

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds  
(without alignments)  
777.677 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20  
Sequence: 1 gacgagggcgagcagcagcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390996

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_21.\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31433 Human neu
2	20	100.0	20	9	ADA74685 GT13603 a
3	16.8	84.0	51	4	AA173382 Human sil
4	15.4	77.0	27	10	ADD95271 Acalligene
5	15.2	76.0	51	12	ADP85110 PCR prime
6	15.2	76.0	95	2	AAQ42957 Encodes 8
7	14.8	74.0	100	8	ACD78116 E. coli K
8	14.8	74.0	100	8	ACD78117 E. coli K
9	14.2	71.0	26	4	AAAD06342 Sorghum d
10	14.2	71.0	30	3	AAZ98666 Escherich
11	14.2	71.0	30	3	AAZ98642 Probe for
12	14.2	71.0	40	6	ABN84043 Single ch
13	14.2	71.0	45	4	AAAD06100 Drosophi
14	14.2	71.0	45	6	AA172470 D. melano
15	14.2	71.0	45	8	ACA02214 D. melano
16	14.2	71.0	50	3	AAZ98665 Escherich
17	14.2	71.0	50	3	AAZ98641 E. coli K
18	14.2	71.0	60	4	AAZ48615 Pseudomon
19	14.2	71.0	60	4	AAZ48592 Pseudomon

C 20	14.2	71.0	60	8	ACA15641	ACA15641 Prokaryot
C 21	14.2	71.0	60	8	ACA15759	ACA15759 Prokaryot
C 22	14.2	71.0	66	2	AAQ85876	AAQ85876 "CTAATC-3
C 23	13.8	69.0	21	13	ADU43614	ADU43614 Knock-dow
C 24	13.8	69.0	27	10	ADD95213	Add95213 Acalligene
C 25	13.8	69.0	33	14	ADZ64744	Adz64744 Bmal1 pro
C 26	13.8	69.0	45	14	ADM67731	Adm67731 IBD SNP d
C 27	13.8	69.0	50	6	ABZ03249	Abz03249 Human leu
C 28	13.8	69.0	50	6	ABZ04801	Abz04801 Human leu
C 29	13.8	69.0	50	10	ADG33513	Adg33513 Human DNA
C 30	13.8	69.0	60	2	AAV60517	AAV60517 Cloned Pa
C 31	13.8	69.0	78	2	AAV19397	AAV19397 Signal se
C 32	13.6	68.0	22	14	AE828666	Aeb28666 RT-PCR pr
C 33	13.6	68.0	30	2	AA747994	Aat747994 Herpes si
C 34	13.6	68.0	30	2	AAV72560	AAV72560 Herpes si
C 35	13.6	68.0	31	12	AD008593	Ado08593 Positiona
C 36	13.6	68.0	32	11	ADM33284	Adm33284 PS A link
C 37	13.6	68.0	32	11	ADM33282	Adm33282 Monocag P
C 38	13.6	68.0	32	12	AD008587	Ado08587 Positiona
C 39	13.6	68.0	32	12	AD008592	Ado08592 Positiona
C 40	13.6	68.0	32	12	AD008598	Ado08598 Positiona
C 41	13.6	68.0	32	12	AD008583	Ado08583 Positiona
C 42	13.6	68.0	32	12	AD008596	Ado08596 Positiona
C 43	13.6	68.0	32	12	AD008611	Ado08611 Positiona
C 44	13.6	68.0	32	12	AD008585	Ado08585 Positiona
C 45	13.6	68.0	32	14	AE828663	Aeb28663 Oligonuci

## ALIGNMENTS

RESULT 1	AAZ31433	standard; DNA, 20 BP.
ID	AAZ31433	
AC	AAZ31433;	
XX		
DT	07-FEB-2000	(first entry)
XX		
DE	Human neuropilin mRNA specific antisense oligo GT13603.	
XX		
KW	Neuropilin; human; growth; metastasis; tumor; neovascularization; cancer;	
KW	papilloma; diabetic retinopathy; antisense; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	W0955855-A2.	
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA000324.
XX		
PR	23-APR-1998;	98US-0082791P.
XX		
PA	(GENE-) GENSENSE TECHNOLOGIES INC.	
XX		
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI; 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for	
PT	treating cancer.	
XX		
PS	Claim 4; Page 16; 57pp; English.	
CC	Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit	
CC	human neuropilin expression. The antisense oligonucleotides can be used	
CC	to inhibit the growth or metastasis of a mammalian tumor and inhibit	
CC	neovascularization. The oligonucleotides may be used to treat various	
CC	forms of cancers or tumors, such as sarcomas, melanomas, adenomas,	
CC	carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of	
CC	the mouth, throat, larynx and lung, genitourinary cancers such as	

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
CC cancer, head and neck cancers, and nervous system cancers, as well as  
CC benign lesions such as papillomas. The methods may be used to treat  
CC neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration  
SQ Sequence 20 BP; 4 A; 5 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGCGG 20  
DB 1 GGACGAGGCGGACGCGG 20

## RESULT 2

ADA74685  
ID ADA74685 standard; DNA; 20 BP.

AC ADA74685;

DT 20-NOV-2003 (first entry)

DE GT13603 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
XX cytosolic; growth; tumor metastasis; angiogenesis; gene therapy;  
XX GT13603; antisense; human; ss.

OS Homo sapiens.

FN US2003083274-A1.

PD 01-MAY-2003.

PE 22-APR-1999; 99US-00296264.

PR 23-APR-1998; 98US-0082791P.

PA (WRIGHT) WRIGHT J A.  
PA (YOUNG) YOUNG A H.  
PA (LEEVY) LEEVY S.

PI Wright JA, Young AH, Lee YS;

DR WPI; 2003-576622/54.

PT New antisense oligonucleotide that inhibits neuropilin expression, useful  
PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
PT mammalian tumor.

PS Claim 1; Page 5; 27pp; English.

CC The invention relates to a novel antisense oligonucleotide that inhibits  
CC the expression of neuropilin, also known as VEGF165R (vascular  
CC endothelial growth factor receptor). The oligonucleotide of the invention  
CC demonstrates cytostatic activity and may be useful for inhibiting the  
CC growth or metastasis of a mammalian tumor and to inhibit angiogenesis in  
CC mammals. Furthermore, the oligonucleotide may be utilized during gene  
CC therapy. The current sequence is that of the GT13603 antisense  
CC oligonucleotide of the invention which is targeted to human neuropilin  
CC mRNA.

SQ Sequence 20 BP; 4 A; 5 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGCGG 20

DB 1 GGACGAGGCGGACGCGG 20

RESULT 3  
AA173382  
ID AA173382 standard; DNA; 51 BP.

AC AA173382;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ.323.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
XX protein therapy; vaccine; probe; diagnostic assay; detection;  
XX quantitation; restorative therapy; polymorphic; db.

OS Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

PE 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

PA (CURA-) CURAGEN CORP.

PI Shinkels RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.

PS Claim 1; Page 153; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

SQ Sequence 51 BP; 5 A; 14 C; 29 G; 3 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 4; Length 51;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGCGG 20  
DB 22 GGACCGGCGGACGAGCAGCGG 41

RESULT 4  
ADD95271

```
ID ADP95271 standard; DNA; 27 BP.
XX
XX ADD95271;
AC
XX 29-JAN-2004 (first entry)
DT
XX
XX Acaligenes faecalis M3A 3-HP dehydrogenase PCR primer SEQ ID NO:19.
DE
XX
XX alanine 2; 3-aminomutase; enzyme; beta-alanine; alpha-alanine; 1;
KM
XX 3-propanediol; pantothenate; coenzyme A; CoA; cell; PCR primer; ss.
KM
XX
OS Synthetic.
OS Alcaligenes faecalis.
XX
XX WO2003062173-A2.
PN
XX
XX 31-JUL-2003.
PD
XX
XX 17-JAN-2003; 2003WO-US001635.
PF
XX
XX 18-JAN-2002; 2002US-0350727P.
BR
XX 25-APR-2002; 2002US-0375785P.
PR
XX
XX (CRGI ) CARGILL INC.
PA
XX
XX Liao HH, Gokarn RR, Gort SJ, Jessen HT, Selifonova O;
PI
XX
XX WPI; 2003-646066/61.
DR
XX
XX New cell, comprising alanine 2,3-aminomutase activity, useful for
PT producing beta-alanine from alpha-alanine, 1,3-propanediol, pantothenate,
PT CoA, HP or 1,3-propanediol.
PT
XX
XX Example 10; SEQ ID NO 19; 119pp; English.
PS
XX
XX The present invention describes a cell, comprising alanine 2,3-
CC aminomutase activity, and which produces beta-alanine from alpha-alanine.
CC Also described: (1) a polypeptide comprising alanine 2,3-aminomutase
CC activity; (2) an isolated nucleic acid comprising a sequence that encodes
CC the polypeptide; (3) a vector comprising the isolated nucleic acid; (4) a
CC recombinant nucleic acid comprising the isolated nucleic acid; (5) a cell
CC transformed with the recombinant nucleic acid; (6) a non-human transgenic
CC animal comprising the recombinant nucleic acid; (7) a transformed cell
CC comprising at least exogenous nucleic acid molecule, which encodes the
CC polypeptide; (8) a specific binding agent that specifically binds to the
CC polypeptide; (9) a method of producing the polypeptide; (10) a method of
CC making beta-alanine from alpha-alanine; (11) a method of identifying a
CC cell comprising alanine 2,3-aminomutase activity; (12) a method for
CC making 1,3-propanediol, pantothenate, CoA, 3-hydroxypropionic acid (HP);
CC (13) a method for making 1,3-propanediol from 3-HP; and (14) a transgenic
CC plant comprising the recombinant nucleic acid. The cell is useful for
CC producing beta-alanine from alpha-alanine, 1,3-propanediol, pantothenate,
CC CoA, HP or 1,3-propanediol. The present sequence represents a PCR primer
CC which is used in the exemplification of the present invention.
CC
XX
SQ Sequence 27 BP; 5 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
Query Match 77.0%; Score 15.4; DB 10; Length 27;
Best Local Similarity 94.1%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
XX
DE PCR primer used to amplify human RAMOS RA-1 VHS leader gDNA.
XX
XX hypermutating cell; in vivo nucleic acid evolution; diversity;
KM
XX RAMOS RA-1 cell; human; VHS leader; ss; PCR; primer.
KM
XX
XX Homo sapiens.
OS
XX WO2004055182-A1.
PN
XX
XX 01-JUL-2004.
PD
XX
XX 18-DEC-2003; 2003WO-AU001697.
PF
XX
XX 18-DEC-2002; 2002AU-00953381.
PR
XX
XX (DIAT-) DIATECH PTY LTD.
PA
XX
XX Irving RA, Hudson PJ, Mustafa H, Mark K, Abregu ME;
PI
XX
XX WPI; 2004-488066/46.
DR
XX
XX Producing and selecting a gene product with desired characteristics by
PT introducing into a hypermutating cell a target nucleic acid molecule
PT encoding a gene product, useful in the field of evolution of nucleic
PT acids in vivo.
PT
XX
XX Example 1; SEQ ID NO 117; 143pp; English.
PS
XX
XX The invention relates to a novel method for producing and selecting a
CC gene product with desired characteristics. The method comprises
CC introducing into a hypermutating cell, a target nucleic acid molecule
CC encoding a gene product, such that the molecule is integrated into an
CC immunoglobulin locus of the genome of the hypermutating cell, culturing
CC the hypermutating cell so the molecule undergoes hypermutation during DNA
CC and/or RNA synthesis giving rise to a population of cells expressing
CC mutant gene products and selecting a mutant gene product with desired
CC characteristics. The compositions and methods of the invention may be
CC useful in the field of evolution of nucleic acids in vivo and for
CC introducing diversity into gene products. The current sequence is that of
CC a PCR primer which was used in the exemplification of the invention.
CC
XX
SQ Sequence 51 BP; 6 A; 22 C; 10 G; 13 T; 0 U; 0 Other;
Query Match 76.0%; Score 15.2; DB 12; Length 51;
Best Local Similarity 85.0%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

DB 1 GGAGGAGGCGAGCAGCGCG 20  
40 GGAGGAGGCGAGGATGCG 21

```
XX
XX
XX RESULT 6
XX AAQ42957/C
XX ID AAQ42957 standard; DNA; 95 BP.
XX
XX AAQ42957;
AC
XX 25-MAR-2003 (revised)
DT 07-SEP-1993 (first entry)
DT
XX
XX Encodes 8 Arg C-terminal extension of G-CSF.
DE
XX
XX Granulocyte Colony Stimulating Factor; Cell-homing factor;
KM fusion protein; targeting; gene therapy; ds.
KM
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 63..86
FT misc_feature
FT
/*tag= a
/!note= "8 Arg codons - there is a 4-nucleotide overhang
```

at the 5' end of the coding strand and a 4-nt overhang (5'-AGCT-3') at the 5' end of the complementary strand"

EP544292-A2.  
02-JUN-1993.  
26-NOV-1992; 92EP-00120205.  
27-NOV-1991; 91DE-04139001.  
(BOE) BOEHRINGER MANNHEIM GMBH.  
Stern A, Hagemann I, Ziegler-Landesberger D;  
WPI; 1993-177078/22.  
Cell introduction of cell homing factor-polycation-nucleic acid complex -  
of linear genetic cell homing factor-polycation fusion having ionic  
interaction with nucleic acid, the polycation part having at least three  
lysine and arginine.  
Example 2, Page 6; 17pp; German.  
This sequence codes for the C-terminal region of G-CSF fused to 8  
Arginine residues and a proline residue. The basic nature of the  
extension ("polycation chain") results in ionic interaction of the  
protein with DNA to form a complex. The G-CSF acts to target the complex  
to e.g. NFS60 cells where the associated DNA can be taken up by those  
cells at a much higher rate than when the basic extension is not present.  
(Updated on 25-MAR-2003 to correct PN field.)

Sequence 95 BP; 12 A; 35 C; 26 G; 22 T; 0 U; 0 Other;  
Query Match 76.0%; Score 15.2; DB 2; Length 95;  
Best Local Similarity 85.0%; Pred. No. 6.2e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GGACGAGGCGGACGACGCGC 20  
88 GGACGAGGCGGACGACGCGC 69

RESULT 7  
ACD78116  
ID ACD78116 standard; DNA; 100 BP.  
ACD78116;  
19-SEP-2003 (first entry)  
E. coli K12 MG1655 biochip probe SEQ ID 9392.  
Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
Escherichia coli.  
EP1260592-A1.  
27-NOV-2002.  
17-MAY-2001; 2001EP-00112179.  
17-MAY-2001; 2001EP-00112179.  
(MMGB-) MMG-BIOTECH AG.  
Donner H, Drescher B, Huber A, Weber J;  
WPI; 2003-241155/24.  
Biochip containing probes complementary with open reading frames in  
Escherichia coli K12, useful for detecting gene expression and expression

patterns.  
Claim 3; Page 1465; 2004pp; German.  
This invention describes a novel biochip comprising probe spots, each  
containing many identical probes. The probes are nucleotide sequences of  
30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
least one includes a segment of at least 20 bases identical with, or  
complementary to, a segment of an open reading frame (orf) of Escherichia  
coli K12. The biochip is used for specific detection of gene expression  
in K12 and for determining the gene expression pattern, e.g. for  
diagnostic determination of which E. coli strains are present in the gut,  
and to determine the effects of e.g. growth media on gene expression. The  
biochip provides as comprehensive as possible detection of the K12  
genome, with simultaneous analysis of many different genes with a single  
device, and comparison of gene expression between K12 and its mutants or  
other E. coli strains in a single experiment. Apart from qualitative and  
quantitative information about gene expression, it also allows  
measurements of population densities for the various strains. The use of  
synthetic oligonucleotides for preparation of probes allows free  
variation in probe length and ensures high purity (and thus selectivity,  
reactivity and reproducibility); also synthetic probes are generally  
shorter than probes prepared by polymerase chain reaction. ACD68731 to  
ACD81540 represent oligonucleotide probes used with the biochip described  
in the invention

Sequence 100 BP; 29 A; 21 C; 27 G; 23 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 8; Length 100;  
Best Local Similarity 88.9%; Pred. No. 9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 GACGAGGCGGACGACGCGC 19  
15 GACGAGGAGCAAGCGC 32

RESULT 8  
ACD78117  
ID ACD78117 standard; DNA; 100 BP.  
ACD78117;  
19-SEP-2003 (first entry)  
E. coli K12 MG1655 biochip probe SEQ ID 9393.  
Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
Escherichia coli.  
EP1260592-A1.  
27-NOV-2002.  
17-MAY-2001; 2001EP-00112179.  
17-MAY-2001; 2001EP-00112179.  
(MMGB-) MMG-BIOTECH AG.  
Donner H, Drescher B, Huber A, Weber J;  
WPI; 2003-241155/24.  
Biochip containing probes complementary with open reading frames in  
Escherichia coli K12, useful for detecting gene expression and expression  
patterns.  
Claim 3; Page 1465; 2004pp; German.  
This invention describes a novel biochip comprising probe spots, each  
containing many identical probes. The probes are nucleotide sequences of

CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
 CC least one includes a segment of at least 20 bases identical with, or  
 CC complementary to, a segment of an open reading frame (orf) of *Escherichia*  
 CC coli K12. The biochip is used for specific detection of gene expression  
 CC in K12 and for determining the gene expression pattern, e.g. for  
 CC diagnostic determination of which *E. coli* strains are present in the gut,  
 CC and to determine the effects of e.g. growth media on gene expression. The  
 CC biochip provides as comprehensive as possible detection of the K12  
 CC genome, with simultaneous analysis of many different genes with a single  
 CC device, and comparison of gene expression between K12 and its mutants or  
 CC other *E. coli* strains in a single experiment. Apart from qualitative and  
 CC quantitative information about gene expression, it also allows  
 CC measurements of population densities for the various strains. The use of  
 CC synthetic oligonucleotides for preparation of probes allows free  
 CC variation in probe length and ensures high purity (and thus selectivity,  
 CC reactivity and reproducibility); also synthetic probes are generally  
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to  
 CC ACD81540 represent oligonucleotide probes used with the biochip described  
 CC in the invention

SO Sequence 100 BP; 23 A; 21 C; 27 G; 29 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 8; Length 100;  
 Best Local Similarity 88.9%; Pred. No. 9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACGAGCGGACACGCGC 19  
 |||||  
 DB 79 GACGAGGACGACGACGCGC 96

#### RESULT 9

AAD06342/C  
 ID AAD06342 standard; DNA; 26 BP.

XX AAD06342;

DT 10-AUG-2001 (first entry)

DE Sorghum dwarfing gene, Dw3 allele amplifying PCR primer #1.

XX Sorghum; dwarfing gene; Dw3; P-glycoprotein; transgenic plant;

KM plant growth; pathogen resistance; plant breeding; PCR primer; ss.

XX Sorghum bicolor.

XX WO200134818-A2.

XX 17-MAY-2001.

PF 10-NOV-2000; 2000WO-US030816.

PR 12-NOV-1999; 99US-0165176P.

XX (JOHA/) JOHAL G S.

PA (MUT/) MUTITANI D S.

XX Jotai GS, Multani DS;

XX WPI; 2001-329088/34.

PT Novel sorghum dwarfing genes useful for modifying the growth of the  
 PT organisms, particularly plants, such as maize, wheat, Basmati rice,  
 PT rye, millet and barley and for enhancing resistance to pathogens.

XX Example 1; Page 63; 76pp; English.

CC The present sequence is a PCR primer used for amplifying sorghum dwarfing  
 CC gene, Dw3 allele. The primer is derived from the nucleotide sequence of  
 CC maize Bz2 gene. Dw3 DNA is useful for modifying the growth of an  
 CC organism, especially reducing the height of monocotyledon plants, such as  
 CC maize, wheat, rice, Basmati rice, sorghum, rye, millet and barley. Dw3  
 CC DNA is useful for producing transgenic monocotyledon and dicotyledon

CC plants like soybean, sunflower, safflower, alfalfa, cotton, *Brassica* sp.,  
 CC peanuts or fruit trees. The Dw3 DNA is also useful for isolating the  
 CC nucleotide homologous molecules that encode P-glycoproteins, enhancing the  
 CC resistance of plants to pathogens, including bacteria, fungi, viruses,  
 CC nematodes and insects, as probes for the isolation of other P-  
 CC glycoprotein-like genes and as molecular markers. Identifying plants that  
 CC possess a mutant allele is useful in agriculture, particularly in  
 CC breeding dwarf crop plants, particularly dwarf sorghum plants

SO Sequence 26 BP; 0 A; 12 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 26;  
 Best Local Similarity 84.2%; Pred. No. 1.7e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGCGGACACGCGC 20  
 |||||  
 DB 24 GACGAGCGGACACGCGC 6

#### RESULT 10

AAZ98666/C  
 ID AAZ98666 standard; DNA; 30 BP.

XX AAZ98666;

DT 05-JUN-2000 (first entry)

DE *Escherichia coli* K12 DNAJ gene fragment probe sequence.

KM Specific binding assay; DNAJ; analyte determination; antigen; hapten;  
 KM drug; cancer marker; pesticide; chemiluminescent compound; pollutant;  
 KM probe; ss.

XX *Escherichia coli*.

XX EP984282-A2.

XX 08-MAR-2000.

PF 21-MAY-1992; 99EP-00121551.

XX 22-MAY-1991; 91US-00704569.

PR 20-JUN-1991; 91US-00718490.

PR 21-MAY-1992; 92EP-00304630.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Ullman EF, Kirakosian H, Pease JS, Wagner DB, Daniloff Y;

XX WPI; 2000-225922/20.

PT Particles containing a chemiluminescent donor and a fluorescent acceptor  
 PT are useful in specific binding assays to determine antigens, haptens,  
 PT enzymes, hormones, cancer markers or nutritional markers.

XX Example 5; Page 66; 79pp; English.

CC This sequence represents a probe for a fragment of the *Escherichia coli*  
 CC DNAJ gene. The fragment is used as an example target sequence in a method  
 CC for determining analyte in a sample using the particles of the invention.  
 CC The invention relates to particles (I) containing a compound (II) and a  
 CC fluorescent compound (III). Compound II reacts with singlet oxygen to  
 CC form a metastable intermediate that can decompose with simultaneous or  
 CC subsequent emission of light. The fluorescent compound (III) is excited  
 CC by activated compound (II) and emits at a wavelength longer than the  
 CC emission wavelength of compound (II). The particles are useful in  
 CC specific binding assays. The assays can be used to determine antigens or  
 CC haptens, e.g. blood group or HLA antigens or bacterial, fungal, protozoal  
 CC or viral antigens, other proteins e.g. immunoglobulins, cytokines,  
 CC enzymes, hormones, cancer markers or nutritional markers, microorganisms,  
 CC drugs, metabolites, pesticides, pollutants or polynucleotides. The longer  
 CC emission wavelength of (III) eliminates interference from serum

CC components when the particles are used in specific binding assays in the  
CC presence of such components  
XX  
SQ Sequence 30 BP; 2 A; 14 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 30;  
Best Local Similarity 84.2%; Pred. No. 1.7e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGGCGAGCAGCGCG 20  
DB 28 GAAGCGGGCGAGCAGTGGCG 10

RESULT 11  
AA298642/C  
ID AA298642 standard; DNA; 30 BP.

XX AA298642;  
XX  
XX  
DT 05-JUN-2000 (first entry)  
XX

DE Probe for E. coli DNAJ gene fragment target sequence.

XX Homogeneous specific binding assay; DNAJ gene; analyte determination;  
KW antigen; hapten; drug; cancer marker; pesticide; pollutant;  
KW photochemically activatable chemiluminescent compound; probe; ss.

XX Escherichia coli.

XX EP984281-A2.

XX PD 08-MAR-2000.

XX 21-MAY-1992; 99EP-00121547.

XX 22-MAY-1991; 91US-00704569.

XX 20-JUN-1991; 91US-00718490.

XX 21-MAY-1992; 92EP-00304630.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Ullman EF, Klrakossian H, Pease JS, Wagner DB, Daniloff Y;  
PI WPI; 2000-197307/18.

XX Homogeneous specific binding assay, e.g. for proteins or nucleic acids,  
PT uses photochemically activatable chemiluminescent compound.  
XX

XX Example 5; Page 66; 78pp; English.

CC This sequence represents a probe for a fragment of the Escherichia coli  
CC K12 DNAJ gene, used as an example of a target sequence in a homogeneous  
CC assay. The invention relates to a homogeneous assay for determining an  
CC analyte, comprising combining medium suspected of containing an analyte  
CC with a label reagent, and intrinsically metastable species, and  
CC determining the reaction. The label reagent comprises a suspended  
CC particle and a specific binding pair (sbp) member associated with a  
CC photochemically activatable chemiluminescent compound (PACC), the sbp is  
CC capable of binding to a second sbp or to the analyte, the second sbp  
CC being capable of binding to the analyte. The metastable species is  
CC capable of diffusing into the medium and reacts preferentially with the  
CC PACC, when brought into close proximity by the presence or absence of the  
CC analyte. The method can be used to determine antigens or haptens, e.g.  
CC blood group or HLA antigens or bacterial, fungal, protozoal or viral  
CC antigens, other proteins e.g. immunoglobulins, cytokines, enzymes,  
CC hormones, cancer markers or nutritional markers, microorganisms, drugs,  
CC metabolites, pesticides, pollutants or polynucleotides. The method is a  
CC homogeneous assay and does not require a separation step  
XX

SQ Sequence 30 BP; 2 A; 14 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 30;

Best Local Similarity 84.2%; Pred. No. 1.7e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGGCGAGCAGCGCG 20  
DB 28 GAAGCGGGCGAGCAGTGGCG 10

RESULT 12  
ABN84043/C  
ID ABN84043 standard; DNA; 40 BP.

XX ABN84043;  
XX

XX 23-SEP-2002 (first entry)  
XX

DE Single chain Class II MHC, I-Ag7 mutagenic primer 4.

XX Major histocompatibility complex; MHC; combinatorial library; I-Ag7;  
KW insulin-dependent diabetes mellitus; autoimmune disease; antidiabetic;  
KW diagnosis; mutagenesis; PCR; primer; ss.

XX Synthetic.

XX WO200246400-A2.

XX 13-JUN-2002.

XX 10-DEC-2001; 2001WO-US047830.

XX 08-DEC-2000; 2000US-0254248P.

XX (UNIT I ) UNIV ILLINOIS FOUND.

XX Krantz DM, Starwalt S, Bluestone JA;  
PI WPI; 2002-537566/57.

XX Novel isolated mutant major histocompatibility complex class II chimeric  
PT protein displayed on recombinant yeast cell surface has improved  
PT stability or T-cell receptor binding, useful for treating autoimmune  
PT disease.  
XX

XX Example 3; Page 27; 66pp; English.

XX The present sequence is mutagenic primer 3 for positions beta-56 and beta  
CC -57 of a single chain (sc) Class II major histocompatibility complex  
CC (MHC) haplotype I-Ag7 construct. A site-directed mutagenesis strategy  
CC involving PCR sewing and yeast homologous recombination was used to  
CC mutate residues beta-56 and -57. Mutant libraries of sc MHC Class II  
CC protein were generated and displayed on the cell surface of recombinant  
CC yeast cells, and stibilised I-Ag7 proteins were identified. Haplotype I-  
CC Ag7 is associated with the development of insulin-dependent diabetes  
CC mellitus (IDDM) in the non-obese (NOD) mouse model of IDDM. The present  
CC invention allows the creation and isolation of stabilised variants of  
CC Class II peptide-MHC complexes. Stabilised variants of single chain I-  
CC Ag7, in association with each of 3 peptides of interest (BDC2.5(A)),  
CC GAD65(78-95) and B9-23 (insulin), have been produced. These can be used in  
CC diagnostic tests of IDDM, in imaging tests, and in the treatment or  
CC prevention of IDDM  
XX

SQ Sequence 40 BP; 4 A; 19 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 40;  
Best Local Similarity 84.2%; Pred. No. 1.7e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGGCGAGCAGCGCG 20  
DB 39 GACGTGGCGGACTACCGCG 21

RESULT 13



```

AAD06100
ID AAD06100 standard; DNA; 45 BP.
XX
AC AAD06100;
XX
DT 31-JUL-2001 (first entry)
XX
DE Drosophila Ecr coding region amplifying primer, (Aec1)-Ecr.
XX
KW Fusion protein; nucleotide-binding domain; NBD; ligand-binding domain;
KW LBD; transcription regulating domain; TRD; zinc finger protein; ZFP;
KW ligand-activated transcriptional regulator; gene regulation;
KW gene therapy; cell proliferative disorder; cancer; psoriasis;
KW pemphigus vulgaris; Behcet's syndrome; lipid histiocytosis; Ecr;
KW PCR primer; ecdysone receptor; ss.
XX
OS Drosophila sp.
XX
PN WO200130843-A1.
XX
PD 03-MAY-2001.
XX
PF 23-OCT-2000; 2000WO-EP010430.
XX
PR 25-OCT-1999; 99US-00433042.
XX
PR 02-JUN-2000; 2000US-00586625.
XX
PA (NOVS ) NOVARTIS AG.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbae CF, Kadan M, Beerli R;
XX
DR WPI; 2001-308618/32.
XX
PT New fusion protein containing nucleotide-binding and ligand-binding
PT domains, useful e.g. in gene therapy of cancer, provides ligand-activated
PT control of gene expression.
XX
XX
PS Example 12; Page 110; 218pp; English.
XX
CC The invention relates to fusion protein comprising a nucleotide-binding
CC domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor
CC (ICR) and a transcription regulating domain (TRD). NBD is a polydactyl
CC zinc finger protein, or a modular part of it, that interacts specifically
CC with a contiguous sequence of at least 3 nucleotides. The fusion protein
CC functions as a ligand-activated transcriptional regulator. The fusion
CC protein and the nucleic acid encoding it, are used to regulate gene
CC expression, particularly in gene therapy for treating malignant cell
CC proliferative diseases (e.g. colon cancer, prostate cancer, renal-cell
CC carcinoma) and non-malignant cell proliferative diseases (e.g. psoriasis,
CC pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The
CC fusion protein and its DNA are also useful for treating diseases caused
CC by viruses in humans/plants, genetic and/or acquired diseases. The fusion
CC protein can be designed to target any selected gene (endogenous or
CC exogenous), and can be made to have different selectivity or specificity
CC for endogenous or exogenous ligands. The present sequence is Drosophila
CC ecdysone receptor (Ecr) coding region amplifying primer, (Aec1)-Ecr. This
CC primer is used to obtain LBD which is used to construct fusion protein of
CC the invention
XX
SQ Sequence 45 BP; 9 A; 14 C; 17 G; 5 T; 0 U; 0 Other;

```

```

Query Match 71.0%; Score 14.2; DB 4; Length 45;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Oy 1 GGACGAGGCGGACGCGC 19
    ||| ||||| ||| |||
Db 3 GGAGGAGGCGCGCCCGGC 21

```

```

RESULT 14
AA172470

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```

ID AA172470 standard; DNA; 45 BP.
XX
AC AA172470;
XX
DT 16-MAY-2002 (first entry)
XX
DE D. melanogaster ecdysone receptor LBD primer, EcRasc-B.
XX
KW Polymerase chain reaction; primer; amplify; PCR; reporter;
KW polypeptide gene switch; ligand binding domain; LBD; transcription;
KW nuclear hormone receptor; gene therapy; regulation; expression; ss.
XX
OS Synthetic.
XX
PN WO200206463-A2.
XX
PD 24-JAN-2002.
XX
PF 16-JUL-2001; 2001WO-EP008190.
XX
PR 18-JUL-2000; 2000US-00619063.
XX
PR (NOVS ) NOVARTIS AG.
XX
PR (NOVS ) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Beerli R, Schopfer U, Barbae CF;
XX
DR WPI; 2002-179793/23.
XX
PT Single chain, monomeric polypeptide gene switches for regulating gene
PT function, comprise two ligand binding domains derived from nuclear
PT hormone receptors operatively linked to one functional domain.
XX
XX
PS Example 1; Page 31; 63pp; English.
XX
CC The sequences given in AA172463-72 are primers which were used in the
CC generation of single chain switch which could be used in the construction
CC of a non-naturally occurring polypeptide gene switch comprising two
CC ligand binding domains (LBds) derived from nuclear hormone receptors
CC operatively linked to a first functional domain. The gene switch is
CC useful for regulating the function of a target nucleotide that contains a
CC defined sequence, by exposing the target nucleotide to the polypeptide
CC gene switch in the presence of a ligand that binds one of the LBds of the
CC polypeptide, where the DNA binding domain of the polypeptide binds the
CC defined sequence, or the functional domain of the polypeptide alters the
CC function of the target nucleotide. The gene switch is also useful in the
CC field of gene therapy and as a regulator of gene expression or
CC transcription. The advantage of the gene switches of the invention over
CC existing gene switches is the need for only a single molecular switch and
CC a single expression vector for production of that switch
XX
SQ Sequence 45 BP; 9 A; 14 C; 17 G; 5 T; 0 U; 0 Other;

```

```

Query Match 71.0%; Score 14.2; DB 6; Length 45;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Oy 1 GGACGAGGCGGACGCGC 19
    ||| ||||| ||| |||
Db 3 GGAGGAGGCGCGCCCGGC 21

```

```

RESULT 15
ACA02214
ID ACA02214 standard; DNA; 45 BP.
XX
AC ACA02214;
XX
DT 23-MAY-2003 (first entry)
XX
DE D. melanogaster ecdysone receptor LBD amplification primer EcRasc-B.
XX

```

```

KW Ecdysone receptor; ligand binding domain; LBD; PCR; primer; ss;
KM gene switch; gene regulation; fruit fly.
XX
OS Drosophila melanogaster.
OS Synthetic.
XX
PN US2002168714-A1.
XX
PD 14-NOV-2002.
XX
PF 18-JUL-2001; 2001US-00908153.
XX
PR 18-JUL-2000; 2000US-00325747.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbas CF, Beerli R, Schopfer U;
XX
DR WPI; 2003-328405/31.
XX
PT Novel polypeptide gene switch useful for regulating gene function,
PT comprises two ligand binding domains derived from nuclear hormone
PT receptors operatively linked to a functional domain.
XX
PS Example 1; Page 11; 33pp; English.
XX
CC The invention relates to a non-naturally occurring polypeptide (or
CC polypeptide gene switch) comprising two ligand binding domains derived
CC from nuclear hormone receptors operatively linked to a first functional
CC domain. The polypeptide is useful for regulating the function of a target
CC nucleotide that contains a defined sequence, by exposing the target
CC nucleotide to the polypeptide in the presence of a ligand that binds one
CC of the ligand binding domains of the polypeptide, where the DNA binding
CC domain of the polypeptide binds the defined sequence or alters the
CC function of the target nucleotide. The gene switches can be produced
CC using a single molecular switch and a single expression vector. The
CC present sequence represents a Drosophila melanogaster ecdysone receptor
CC ligand binding domain amplification primer
XX
SQ Sequence 45 BP; 9 A; 14 C; 17 G; 5 T; 0 U; 0 Other;
Query Match 71.0%; Score 14.2; DB 8; Length 45;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGACGAGGGCGGACGCGC 19
   ||| ||||| ||| |||
Db 3 GGAGGAGGGCGGCGCCGCGC 21

```

Search completed: December 24, 2005, 12:28:53  
 Job time : 172.4 secs



Query Match 79.0%; Score 15.8; DB 10; Length 88;  
Best Local Similarity 89.5%; Pred. No. 1.9e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGACGCGC 20  
|||||  
43 GACGCGGCGGACGACTGCG 25

RESULT 2  
AI000040 79 bp mRNA linear EST 05-JUN-1998  
LOCUS 0946C07.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE:1608396 3'  
DEFINITION similar to TR:O15551 O15551 RAT VENTRAL PROSTATE.1 HOMOLOG.  
; contains TAR1.b1 MSRI repetitive element ;, mRNA sequence.  
AI000040  
ACCESSION AI000040.1 GI:3190594  
VERSION Est.  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 79)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
source  
FEATURES  
source  
Trace considered overall poor quality  
Seq primer: -40m3 fwd. ET from Amerham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..79  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1608396"  
/sex="female, pooled"  
/tissue\_type="breast"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Br2"  
/note="Vector: pTR73D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from pooled bulk  
breast tumor tissue, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pTR73  
vector. This library is the normalized version of  
NCI\_CGAP Br1.1. Library was constructed by Bento Soares  
and M. Fatima Bonaldo."

ORIGIN  
Query Match 76.0%; Score 15.2; DB 1; Length 79;  
Best Local Similarity 85.0%; Pred. No. 3.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCGC 20  
|||||  
52 GGACGAGGATGACGACGCGC 71

RESULT 3

C2914888 88 bp DNA linear GSS 08-AUG-2005  
LOCUS 4013009A12.x1 4013 - RescuerMu Grid O Zea mays genomic, genomic  
survey sequence.  
DEFINITION  
VERSION C2914888  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
source  
FEATURES  
source  
Maize genomic sequences found using engineered RescuerMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: [walbot@stanford.edu](mailto:walbot@stanford.edu)  
Plate: 4013009 row: 40  
Class: transposon-tagged.  
Location/Qualifiers  
1..88  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="4013 - RescuerMu Grid O"  
/note="Organ: leaf; Vector: RescuerMu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
RescuerMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescuerMu, go to the web  
site "<http://www.multitranposon.org/project/RescuerMu/>". Grid  
O was grown at Stanford in 2001. DNA was extracted from  
leaf strips, double digested using BamHI and BglII, and  
ligated to form circular plasmids. DH10B cells were  
transformed and then screened on LB plates with  
ampicillin."

ORIGIN  
Query Match 76.0%; Score 15.2; DB 10; Length 88;  
Best Local Similarity 85.0%; Pred. No. 3.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCGC 20  
|||||  
57 GGACGAGGACGAGGACGCGC 76

RESULT 4  
CC796892 84 bp DNA linear GSS 01-JUL-2003  
LOCUS SALK\_144200.16.65.x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_144200.16.65.x, genomic  
survey sequence.  
ACCESSION CC796892  
VERSION CC796892.1 GI:32392115  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (chale crese)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
1 (bases 1 to 84)

REFERENCE

## AUTHORS

Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadinb, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shin, P., Zimmerman, J., and Ecker, J.R.

## TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

## JOURNAL COMMENT

Unpublished (2001)

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At5g05530 and 300 bases of the 5' end of At5g05540.  
Class: TDNA tagged.

## FEATURES

## source

1..84  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_14200.16.65.x"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 74.0%; Score 14.8; DB 9; Length 84;  
Best Local Similarity 88.9%; Pred. No. 5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## QY

3 ACGAGGGGACGACGCG 20  
|||||  
56 ACGAGGGGACGACGCG 73

## DB

## RESULT 5

## AM064096/c

LOCUS AM064096 87 bp mRNA linear EST 07-DEC-2000  
DEFINITION SP0522 KRIIB Human CD4 intrathymic T-cell cDNA library Homo sapiens  
CDNA 3', mRNA sequence.

## ACCESSION

AM064096  
AM064096.1 GI:8888033

## KEYWORDS

## SOURCE

## ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 87)  
Goh, S.-H., Park, J.-H., Lee, Y.-J., Lee, H.-G., Yoo, H.-S., Lee, I.-C.,  
Park, V.-H., Kim, Y.-S., and Lee, C.-C.

Gene expression profile and identification of differentially  
expressed transcripts during human intrathymic T-cell development  
by cDNA sequencing analysis

Genomics 70 (1), 1-18 (2000)

## JOURNAL

## PUBMED

## COMMENT

Contact: Sung-Ho Goh  
Genome Research Center  
Korea Research Institute of Bioscience and Biotechnology  
Oun-dong 52, Yu Sung-Gu, Daejeon 305-333, Republic of Korea

Tel: 82-42-860-4473

Fax: 82-42-860-4479

Email: gohsh@mail.kribb.re.kr

Seq primer: 77

High quality sequence stop: 87

POLYA=No.

## FEATURES

## source

Location/Qualifiers  
1..87  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cistae\_type="Thymus"  
/cell\_type="Intrathymic T-cell"  
/dev\_stage="CD3+4+8- single positive stage"  
/clone\_lib="KRIIB Human CD4 intrathymic T-cell cDNA  
library"  
/note="Vector: pGEM-T; cDNA was made from total  
cytoplasmic RNA of sorted human intrathymic CD3+4+8-  
T-cell, adaptor ligated, amplified with PCR, and cloned  
into pGEM-T vector."

## ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 87;  
Best Local Similarity 88.9%; Pred. No. 5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## QY

3 ACGAGGGGACGACGCG 20  
|||||  
38 ACGAGGGGACGACGCG 21

## DB

## RESULT 6

## A2919805/c

LOCUS A2919805 91 bp DNA linear GSS 17-DEC-2001  
DEFINITION 1006016G03.Y1 1006 - Rescuemu Grid G Zea mays genomic, genomic  
survey sequence.

## ACCESSION

A2919805

## KEYWORDS

## SOURCE

## ORGANISM

Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Maize genomic sequences found using engineered Rescuemu transposon  
Unpublished (2001)  
Contact: Walbot V.  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 1006016 row: 41  
Class: transposon-tagged.

## FEATURES

## source

Location/Qualifiers  
1..91  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/cistae\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - Rescuemu Grid G"  
/note="Organ: leaf; Vector: Rescuemu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
Rescuemu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescuemu, go to the web  
site 'www.zmdb.iastate.edu' and follow the links for  
'Rescuemu'. Grid G was grown at Stanford in 2000. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

```

ORIGIN
Query Match          74.0%; Score 14.8; DB 9; Length 91;
Best Local Similarity 88.9%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGGGCGGACGACG 18
    |||||
    34 GGACGAGGGCGGAGTACGG 17

RESULT 7
BH218633          91 bp DNA linear GSS 08-NOV-2001
LOCUS             1006080D10.x1 1006 - Rescuemu Grid G Zea mays genomic, genomic
DEFINITION        survey sequence.
ACCESSION          BH218633
VERSION            BH218633.1 GI:16811673
KEYWORDS           GSS.
SOURCE             Zea mays
ORGANISM           Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 91)
Walbot, V.
Maize genomic sequences found using engineered Rescuemu transposon
REFERENCE          Unpublished (2001)
AUTHORS            Contact: Walbot V
JOURNAL            Department of Biological Sciences
COMMENT            Stanford University
                  855 California Ave, Palo Alto, CA 94304, USA
                  Tel: 650 723 2227
                  Fax: 650 725 8221
                  Email: walbot@stanford.edu
                  Plate: 1006080 row: 28
                  Class: transposon-tagged.
FEATURES
source            1..91
                  /organism="Zea mays"
                  /mol_type="genomic DNA"
                  /cultivar="mixed Background W23/A188/B73"
                  /db_xref="taxon:4577"
                  /tissue_type="leaf"
                  /dev_stage="radult"
                  /lab_host="DH10B"
                  /clone_lib="1006 - Rescuemu Grid G"
                  /note="Organ: leaf; Vector: Rescuemu (engineered from
                  pBluescript backbone); Site 1: BamHI; Site 2: BglII;
                  Rescuemu is a 4.9 kb, modified maize Mu transposon
                  designed to allow plasmid rescue from total genomic
                  DNA. Mu elements insert preferentially into transcription
                  units. For more information on Rescuemu, go to the web
                  site 'www.zmdb.iastate.edu' and follow the links for
                  'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was
                  extracted from leaf punches, double digested using BamHI
                  and BglII, and ligated to form circular plasmids. DH10B
                  cells were transformed and then screened on LB plates with
                  ampicillin."

ORIGIN
Query Match          74.0%; Score 14.8; DB 9; Length 91;
Best Local Similarity 88.9%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACGAGGGCGGACGACG 19
    |||||
    77 GACGAGGTCGAGCAGCAGC 60

RESULT 8
A1900558/ C        64 bp mRNA linear EST 12-JUL-2004
LOCUS              A1900558

```

```

DEFINITION        sc07g10.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
                  Gm-c1012-1531 5' similar to SW:PSAF FLATR P46486 PHOTOSYSTEM I
                  REACTION CENTRE SUBUNIT III PRECURSOR ;, mRNA sequence.
ACCESSION          A1900558
VERSION            A1900558.1 GI:5606404
KEYWORDS           EST.
SOURCE             Glycine max (soybean)
ORGANISM           Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
Glycine.
1 (bases 1 to 64)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Streptoc, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,
Schurk, R., Riltter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
TITLE              Public Soybean EST Project
JOURNAL            Contact: Shoemaker R/Public Soybean EST Project
COMMENT            Public Soybean EST Project
                  Washington University School of Medicine
                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                  Tel: 314 286 1800
                  Fax: 314 286 1810
                  Email: est@watson.wustl.edu
                  When it has been determined, an EST from the other end of this
                  clone is listed in the 'Other ESTs on clone' field. Trace
                  considered overall poor quality Possible reversed clone: similarity
                  on wrong strand This clone is available through: Biogenetic
                  Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
                  4163; email: info@biogeneticservices.com)
                  Seq primer: -40RP from Gibco
                  High quality sequence stop: 1.
FEATURES
source            1..64
                  /organism="Glycine max"
                  /mol_type="mRNA"
                  /cultivar="Williams"
                  /db_xref="taxon:3847"
                  /clone="GENOME SYSTEMS CLONE ID: Gm-c1012-1531"
                  /tissue_type="Apical shoot tips, 9-10 day old etiolated
                  seedlings"
                  /lab_host="XLI0-Gold"
                  /clone_lib="Gm-c1012"
                  /note="Vector: pBluescript II XR; Site 1: EcoRI, Site 2:
                  XhoI; This cDNA library was constructed from mRNA isolated
                  from the apical shoots of 9 to 10 day old etiolated
                  seedlings. The shoot tips including any emerged leaves
                  were harvested for mRNA isolation. The cDNA library was
                  prepared using the Stratagene pBluescript II XR cDNA
                  library construction kit. Complementary DNA was
                  synthesized from mRNA using a primer consisting of a poly
                  (dT) sequence with a XhoI restriction site. EcoRI adapters
                  were ligated to the blunt-ended cDNA fragments followed by
                  XhoI digestion. The cDNA fragments were directionally
                  cloned into the EcoRI-XhoI restriction site of the
                  pBluescript vector. The ligated cDNA fragments were
                  transformed into XLI0-Gold host cells. This library was
                  constructed by Dr. Randy Shoemaker and Dr. John
                  Erpelting."

ORIGIN
Query Match          72.0%; Score 14.4; DB 1; Length 64;
Best Local Similarity 93.8%; Pred. No. 7.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGGGCGGACGCGGCG 20
    |||||
    34 GAGGGCGGACGCGGCG 19

DB 34 GAGGGCGGACGCGGCG 19

```

RESULT 9  
BH226921/c 84 bp DNA linear GSS 08-NOV-2001  
LOCUS 1006135G08.2EL\_Y1 1006 - RescuemU Grid G Zea mays genomic, genomic  
DEFINITION survey sequence.  
ACCESSION BH226921  
KEYWORDS GSS, GI:16826390  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 84)  
Walbot, V.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Maize genomic sequences found using engineered RescuemU transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1006135 Column: 32  
Class: transposon-tagged.  
FEATURES  
source  
Location/Qualifiers  
1..84  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - RescuemU Grid G"  
/note="Organ: leaf; Vector: RescuemU (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
RescuemU is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescuemU, go to the web  
site 'www.zmd.iastate.edu' and follow the links for  
'RescuemU'. Grid G was grown at Stanford in 2000. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

Query Match 72.0%; Score 14.4; DB 9; Length 84;  
Best Local Similarity 93.8%; Pred. No. 7.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GAGCAGGGCGCAGCAGC 17  
|||  
Db 69 GACGAGGGCGCAGCAGC 54  
|||

RESULT 10  
DT018411/c 57 bp mRNA linear EST 05-AUG-2005  
LOCUS VV1024A01.586662 CabSau Flower Stage 12 (FlOu0012) Vitis vinifera  
DEFINITION cDNA clone VV1024A01 5, mRNA sequence.  
ACCESSION DT018411  
KEYWORDS EST, GI:71869356  
SOURCE Vitis vinifera  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; Vitaceae; Vitis.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Expressed sequence tags from the grapevine cultivar Cabernet  
Sauvignon  
Unpublished (2003)  
Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcushman@unr.edu  
PCR Primers  
FORWARD: T7 20mer (forward)  
BACKWARD: Sp6 18mer  
Plate: 024 row: A column: 01  
Seq primer: T7 20mer (forward)  
High quality sequence stop: 57.  
FEATURES  
source  
Location/Qualifiers  
1..57  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="VV1024A01"  
/sex="hermaphrodite"  
/dev\_stage="12 - modified E-L system"  
/clone\_lib="CabSau Flower Stage 12 (FlOu0012)"  
/note="Organ: Inflorescence including flowers; Vector:  
pZL; A cDNA library from immature inflorescences at stage  
12 of the modified E-L system. Tissue collected from  
field grown plants. A description of the modified E-L  
system can be found in the paper by B. G. Coombe  
'Adoption of a system for identifying grapevine growth  
stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

Query Match 71.0%; Score 14.2; DB 8; Length 57;  
Best Local Similarity 84.2%; Pred. No. 9.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GAGCAGGGCGCAGCAGC 19  
|||  
Db 41 GAGCAGGGCGCAGCAGC 23  
|||

RESULT 11  
CG601030/c 63 bp mRNA linear GSS 02-OCT-2003  
LOCUS OST271917 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST271917,  
DEFINITION mRNA sequence.  
ACCESSION CG601030  
KEYWORDS GSS, GI:37419251  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 63)  
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Fridolf, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-O., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.  
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
14610273

COMMENT Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.  
Location/Qualifiers  
1. 63  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST271917"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 10; Length 63;  
Best Local Similarity 80.0%; Pred. No. 9.2e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACGAGGCGGACGACGCG 20  
|||||  
44 GGTCCGGGCGGAGNAGCG 25

Db 44 GGTCCGGGCGGAGNAGCG 25

RESULT 12  
AV920979  
LOCUS AV920979 K. Sato unpublished cDNA library, cv. Haruna NiJo  
DEFINITION germination shoots Hordeum vulgare subsp. vulgare cDNA clone  
bag16f09 3', mRNA sequence.  
ACCESSION AV920979  
VERSION AV920979.1 GI:18216758  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticeae; Hordeum.  
1 (bases 1 to 80)  
REFERENCE Sato, K., Saitoh, D. and Takeda, K.  
Barley EST sequencing project in NiG and Okayama Univ  
unpublished (2002)  
CONTACT: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
1. 80  
/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
/cultivar="Haruna NiJo"  
/sub\_species="vulgare"  
/db\_xref="taxon:112509"  
/clone="bag16f09"  
/tissue\_type="shoots"  
/dev\_stage="germination"  
/clone\_lib="K. Sato unpublished cDNA library, cv. Haruna  
NiJo germination shoots"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 1; Length 80;  
Best Local Similarity 84.2%; Pred. No. 9.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGACGCG 20  
|||||  
|||||

Db 48 GACGAGGCGGACGAGCGCG 30

RESULT 13  
LOCUS CM049484  
DEFINITION CM049484 82 bp DNA linear GSS 28-OCT-2004  
104\_288\_10514054\_115\_30199 Sorghum methylation filtered library  
(LibID: 104) Sorghum bicolor genomic clone 10514054, genomic survey  
sequence.  
ACCESSION CM049484  
VERSION CM049484.1 GI:54726214  
KEYWORDS GSS.  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 82)  
REFERENCE Bedell, J. A., Budiman, M. A., Nunberg, A., Citek, R. W., Robbins, D.,  
Jones, J., Flick, B., Rohlfing, T., Fries, J., Bradford, K.,  
McKenamy, J., Smith, M., Holman, H., Roe, B. A., Wiley, G., Korff, I. F.,  
Rabinowicz, P. D., Lakey, N., McCombie, W. R., Jeddeloh, J. A. and  
Martensen, R. A.  
Sorghum genome sequencing by methylation filtration  
Plos Biol. 3 (1), e13 (2005)  
15660154  
CONTACT: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: 288 row: m column: 12  
Seq primer: M13/pUC Reverse  
Class: methylation filtered  
High quality sequence stop: 82.  
Location/Qualifiers  
1. 82  
/organism="Sorghum bicolor"  
/mol\_type="genomic DNA"  
/cultivar="RTx623"  
/db\_xref="taxon:4558"  
/clone="10514054"  
/clone\_lib="Sorghum methylation filtered library (LibID:  
104)"  
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA  
prepared from purified nuclei was randomly sheared,  
end-repaired, size fractionated to enrich for the 0.5 to 5  
kb fraction, ligated into HincII-digested pBCSK(-) vector  
and electroporated into E. coli cells. This is a  
methylation filtered library."

ORIGIN  
Query Match 71.0%; Score 14.2; DB 10; Length 82;  
Best Local Similarity 84.2%; Pred. No. 9.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGACGCG 20  
|||||  
75 GACGAGGCGGACGACGCG 57

RESULT 14  
LOCUS A1430740 83 bp mRNA linear EST 09-MAR-1999  
DEFINITION ths1e05.x1 Soares mouse placenta 4NMP13.5 14.5 Mus musculus cDNA  
clone IMAGE:446048 3', mRNA sequence.  
ACCESSION A1430740  
VERSION A1430740.1 GI:4276576  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds  
(without alignments)  
739.111 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20

Sequence: 1 GAGCAGGCGGAGCAGCGCG 20

Scoring table: IDENTITY\_NUC

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/lna/1\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/lna/5\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/lna/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/lna/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/lna/H\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/lna/PCTUS\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/lna/PP\_COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/lna/RE\_COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/lna/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	26	3	US-09-711-619-5
2	14.2	71.0	30	2	US-07-718-490-2
3	14.2	71.0	50	2	US-07-718-490-1
4	14.2	71.0	65	2	US-08-479-743-5
5	14.2	71.0	65	6	PCT-US94-09705-5
6	14.2	71.0	66	2	US-08-479-743-3
7	14.2	71.0	66	6	PCT-US94-09705-3
8	13.8	69.0	50	3	US-10-131-827-3240
9	13.8	69.0	50	3	US-10-131-827-4792
10	13.8	69.0	60	2	US-08-484-192-151
11	13.6	68.0	30	2	US-08-428-370A-12
12	13.6	68.0	30	2	US-08-600-764-12
13	13.4	67.0	50	3	US-09-907-794A-89
14	13.4	67.0	50	3	US-09-905-125A-89
15	13.4	67.0	50	3	US-09-902-775A-89
16	13.4	67.0	50	3	US-09-906-700-89
17	13.4	67.0	50	3	US-09-903-603A-89
18	13.4	67.0	50	3	US-09-904-920A-89
19	13.4	67.0	50	3	US-09-909-064-89
20	13.4	67.0	50	3	US-09-905-381A-89
21	13.4	67.0	50	3	US-09-906-618-89
22	13.4	67.0	50	3	US-09-906-646-89
23	13.4	67.0	50	3	US-09-904-462-89
24	13.4	67.0	50	3	US-09-902-736A-89

25	13.4	67.0	50	3	US-09-906-722A-89	Sequence 89, Appli
26	13.2	66.0	21	2	US-08-816-105A-3	Sequence 3, Appli
27	13.2	66.0	31	3	US-09-657-453A-6	Sequence 6, Appli
28	13.2	66.0	59	3	US-09-270-767-26314	Sequence 26314, A
29	13.2	66.0	60	2	US-08-484-192-150	Sequence 150, App
30	13.2	66.0	81	3	US-09-621-976-7854	Sequence 7854, App
31	13.2	66.0	84	3	US-09-513-999C-34413	Sequence 34413, A
32	13.2	65.0	37	3	US-09-344-888A-19	Sequence 19, Appli
33	12.6	63.0	23	2	US-08-064-271-8	Sequence 8, Appli
34	12.6	63.0	23	3	US-08-930-589A-8	Sequence 8, Appli
35	12.6	63.0	23	3	US-09-599-781-8	Sequence 8, Appli
36	12.6	63.0	23	3	US-10-027-961A-8	Sequence 8, Appli
37	12.6	63.0	24	3	US-09-182-450-15	Sequence 15, Appli
38	12.6	63.0	25	3	US-09-323-873A-30	Sequence 30, Appli
39	12.6	63.0	25	3	US-09-702-114A-11	Sequence 11, Appli
40	12.6	63.0	25	3	US-09-638-203-19	Sequence 19, Appli
41	12.6	63.0	25	3	US-09-409-938-17	Sequence 17, Appli
42	12.6	63.0	25	3	US-09-680-728-29	Sequence 29, Appli
43	12.6	63.0	25	3	US-10-017-066A-29	Sequence 29, Appli
44	12.6	63.0	25	3	US-09-935-430-669	Sequence 669, App
45	12.6	63.0	25	3	US-10-010-667A-30	Sequence 30, Appli

## ALIGNMENTS

RESULT 1  
US-09-711-619-5/c  
; Sequence 5, Application US/09711619  
; Patent No. 6750380  
; GENERAL INFORMATION:  
; APPLICANT: Johal, Gurmukh S  
; TITLE OF INVENTION: SORGHUM DWARFING GENES AND METHODS OF USE  
; FILE REFERENCE: 5718-100 (035718/205458)  
; CURRENT APPLICATION NUMBER: US/09/711,619  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: 60/165,176  
; PRIOR FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide  
US-09-711-619-5

Query Match 71.0%; Score 14.2; DB 3; Length 26;  
Best Local Similarity 84.2%; Pred. No. 6,7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

cy 2 GAGCAGGCGGAGCAGCGCG 20  
db 24 GAGCAGCGGAGCAGCGCG 6

RESULT 2  
US-07-718-490-2/c  
; Sequence 2, Application US/07718490  
; Patent No. 5340716  
; GENERAL INFORMATION:  
; APPLICANT: Ullman, Edwin F.  
; APPLICANT: Kirakossian, Hrair  
; APPLICANT: Pease, John S.  
; APPLICANT: Daniloff, Yuri  
; APPLICANT: Wagner, Daniel B.  
; TITLE OF INVENTION: Assay Method Utilizing Photoactivated  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:

```
/ ADDRESSER: Syntex (U.S.A.) Inc.
/ STREET: 3401 Hillview Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/718,490
/ FILING DATE: 19910620
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Leitberg, Theodore J.
/ REGISTRATION NUMBER: 28,319
/ REFERENCE/DOCKET NUMBER: 27340/ DO-1557
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 852-1091
/ TELEFAX: (415) 496-3529
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: Internal
/ ORIGINAL SOURCE:
/ ORGANISM: Escherichia coli
/ STRAIN: K12 DNAJ
/ INDIVIDUAL ISOLATE: Synthetic
/ US-07-718-490-2

Query Match          71.0%; Score 14.2; DB 2; Length 30;
Best Local Similarity 84.2%; Pred. No. 6.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GACGAGCGCGACGACGCG 20
      ||| ||| ||| ||| ||| |||
DB      28 GAAGCGCGCGACGATGCG 10

RESULT 3
US-07-718-490-1
/ Sequence 1, Application US/07718490
/ Patent No. 5340716
/ GENERAL INFORMATION:
/ APPLICANT: Ullman, Edwin F.
/ APPLICANT: Kirakosian, Hrair
/ APPLICANT: Pease, John S.
/ APPLICANT: Daniloff, Yuri
/ APPLICANT: Wagner, Daniel B.
/ TITLE OF INVENTION: Assay Method Utilizing Photoactivated
/ TITLE OF INVENTION: Chemiluminescent Label
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Syntex (U.S.A.) Inc.
/ STREET: 3401 Hillview Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
```

```
/ APPLICATION NUMBER: US/07/718,490
/ FILING DATE: 19910620
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Leitberg, Theodore J.
/ REGISTRATION NUMBER: 28,319
/ REFERENCE/DOCKET NUMBER: 27340/ DO-1557
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 852-1091
/ TELEFAX: (415) 496-3529
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)T
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: Internal
/ ORIGINAL SOURCE:
/ ORGANISM: Escherichia coli
/ STRAIN: K12 DNAJ
/ INDIVIDUAL ISOLATE: Synthetic
/ US-07-718-490-1

Query Match          71.0%; Score 14.2; DB 2; Length 50;
Best Local Similarity 84.2%; Pred. No. 6.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GACGAGCGCGACGACGCG 20
      ||| ||| ||| ||| ||| |||
DB      13 GAAGCGCGCGACGATGCG 31

RESULT 4
US-08-479-743-5
/ Sequence 5, Application US/08479743
/ Patent No. 5807675
/ GENERAL INFORMATION:
/ APPLICANT: Davalian, Darlush
/ APPLICANT: Singh, Rajendra
/ APPLICANT: Ullman, Edwin F.
/ TITLE OF INVENTION: Fluorescent Oxygen Channeling Assays
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Syntex (U.S.A.) Inc.
/ STREET: 3401 Hillview Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/479,743
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/117,365
/ FILING DATE: 03-SEP-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Roth, Carol J.
/ REGISTRATION NUMBER: 32,783
/ REFERENCE/DOCKET NUMBER: 27870
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 852-1698
/ TELEFAX: (415) 496-3529
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 65 base pairs
```

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: synthetic  
US-08-479-743-5

Query Match 71.0%; Score 14.2; DB 2; Length 65;  
Best Local Similarity 84.2%; Pred. No. 6.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGGCGAGCAGCGCG 20  
DB 3 GAACGGGGCGAGCATGGCG 21

## RESULT 5

PCT-US94-09705-5  
Sequence 5, Application PC/TUS9409705  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: FLUORESCENT OXYGEN CHANNELLING IMMUNOASSAYS  
NUMBER OF SEQUENCES: 5  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09705  
FILING DATE: 29-AUG-1994  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 65 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: synthetic

Query Match 71.0%; Score 14.2; DB 6; Length 65;  
Best Local Similarity 84.2%; Pred. No. 6.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGGCGAGCAGCGCG 20  
DB 3 GAACGGGGCGAGCATGGCG 21

## RESULT 6

US-08-479-743-3/C  
Sequence 3, Application US/08479743  
Patent No. 5807675  
GENERAL INFORMATION:

APPLICANT: Davalian, Darlush  
APPLICANT: Ullman, Edwin F.  
TITLE OF INVENTION: Fluorescent Oxygen Channeling Assays  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syntex (U.S.A.) Inc.  
STREET: 3401 Hillview Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,743  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117,365  
FILING DATE: 03-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Roth, Carol J.  
REGISTRATION NUMBER: 32,783  
REFERENCE/DOCKET NUMBER: 27870  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 852-1698  
TELEFAX: (415) 496-3529  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 66 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: synthetic

Query Match 71.0%; Score 14.2; DB 2; Length 66;  
Best Local Similarity 84.2%; Pred. No. 6.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGGCGAGCAGCGCG 20  
DB 28 GAACGGGGCGAGCATGGCG 10

## RESULT 7

PCT-US94-09705-3/C  
Sequence 3, Application PC/TUS9409705  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: FLUORESCENT OXYGEN CHANNELLING IMMUNOASSAYS  
NUMBER OF SEQUENCES: 5  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09705  
FILING DATE: 29-AUG-1994  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 66 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: synthetic

Query Match 71.0%; Score 14.2; DB 6; Length 66;  
Best Local Similarity 84.2%; Pred. No. 6.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy**      2 GACGAGGCCGAGCAGCGG 20  
          ||| ||| ||| ||| |||  
**Db**      28 GAAGCGGGCGAGCATGGCG 10

```

RESULT 8
US-10-131-827-3240
: Sequence 3240, Application US/10131827
: Patent No. 6905827
: GENERAL INFORMATION:
: APPLICANT: Wohlgenuth, Jay
: APPLICANT: Fry, Kirk
: APPLICANT: Woodward, Robert
: APPLICANT: Ly, Ngoc
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
: TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
: FILE REFERENCE: 506612000120
: CURRENT APPLICATION NUMBER: US/10/131.827
: CURRENT FILING DATE: 2002-09-06
: PRIOR APPLICATION NUMBER: US 10/006,290
: PRIOR FILING DATE: 2001-10-22
: PRIOR APPLICATION NUMBER: US 60/296,764
: PRIOR FILING DATE: 2001-06-08
: NUMBER OF SEQ ID NOS: 9090
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3240
: LENGTH: 50
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-131-827-3240

```

Query Match	69.0%	Score 13.8;	DB 3;	Length 50;
Best Local Similarity	88.2%	Pred. No. 9.1e+03;		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 GGACGAGGCGGAGCAGC 17  
|||||  
Db 25 GGACGAGGAGCAGGAGC 41

```

RESULT 9
US-10-131-827-4792
; Sequence 4792, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4792
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4792

```

Query Match	69.0%	Score 13.8;	DB 3;	Length 50;
Best Local Similarity	88.2%	Pred. No. 9.1e+03;		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY 1 GGACGAGGGCGAGCAG 17  
|||||  
Db 25 GGACGAGGACGAGGACG 41

```

1      RESULT 10
2      US-08-484-192-151
3      ; Sequence 151: Application US/08484192
4      ; Patent No. 5756281
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: GRIFFIN, LINDA C.
8      ; APPLICANT: ALBRECHT, GLENN
9      ; APPLICANT: LATHAM, JOHN
10     ; APPLICANT: LEUNG, LAWRENCE
11     ; APPLICANT: VERMAAS, ERIC
12     ; APPLICANT: TOOLE, JOHN J.
13     ; TITLE OF INVENTION: APARTERS SPECIFIC FOR BIOMOLECULES AND
14     ; TITLE OF INVENTION: METHODS OF MAKING
15     ; NUMBER OF SEQUENCES: 181
16     ;
17     ; CORRESPONDENCE ADDRESS:
18     ; ADDRESSEE: MORRISON & FOERSTER
19     ; STREET: 755 PAGE MILL ROAD
20     ;
21     ; CITY: PALO ALTO
22     ; STATE: CALIFORNIA
23     ; COUNTRY: USA
24     ; ZIP: 94304
25     ;
26     ; COMPUTER READABLE FORM:
27     ; MEDIUM TYPE: floppy disk
28     ; COMPUTER: IBM PC compatible
29     ; OPERATING SYSTEM: PC-DOS/MS-DOS
30     ; SOFTWARE: Patent Release #1.0, Version #1.25
31     ;
32     ; CURRENT APPLICATION DATA:
33     ; APPLICATION NUMBER: US/08/484,192
34     ; FILING DATE:
35     ;
36     ; CLASSIFICATION: 435
37     ; PRIOR APPLICATION DATA:
38     ; APPLICATION NUMBER: US 07/934,387
39     ; FILING DATE: 21-AUG-1992
40     ; ATTORNEY/AGENT INFORMATION:
41     ; NAME: GRACEY, NANCY J.
42     ; REGISTRATION NUMBER: 28, 216
43     ; REFERENCE/DOCKET NUMBER: 246102002221
44     ; TELECOMMUNICATION INFORMATION:
45     ; TELEPHONE: 415-813-5600
46     ; TELEFAX: 415-494-0792
47     ;
48     ; TELEX: 706141
49     ; INFORMATION FOR SEQ ID NO: 151:
50     ; SEQUENCE CHARACTERISTICS:
51     ; LENGTH: 60 base pairs
52     ; TYPE: nucleic acid
53     ; STRANDEDNESS: single
54     ; TOPOLOGY: linear
55     ;
56     ; US-08-484-192-151

```

Query Match	69.0%	Score 13.8;	DB 2;	Length 60;
Best Local Similarity	88.2%;	Pred. No. 9e+03;		
Matches 15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY            1 GGACGAGGGCCGAGCAGC 17  
               ||| | | | | | | |  
Db            28 GGAAGAGGGCCGAGGACG 44

RESULT 11  
US-08-428-370A-12  
Sequence 12, Application US/08428370A  
Patent No. 5569583  
GENERAL INFORMATION:  
APPLICANT: Greenberg, Steven J.  
APPLICANT: Evans, Mary Jo  
TITLE OF INVENTION: Rapid and Sensitive Detection of  
HERPESVIRUSES  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Ruse, Andrews, Woods & Goodyear  
STREET: 1800 One Mt Plaza

CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for windows 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,370A  
FILING DATE: 25/04/95  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716)856-4000  
TELEFAX: 716-849-0349  
INFORMATION FOR SEQ. ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Herpes simplex virus 2  
FEATURE:  
LOCATION: Polymerase gene sequence bases 2268-2297  
US-08-428-370A-12

Query Match 68.0%; Score 13.6; DB 2; Length 30;  
Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GGACGAGGCGACGACGCGG 20  
DB 1 GGACGAGGCGACGACGCGG 20

RESULT 12  
US-08-600-764-12  
Sequence 12, Application US/08600764  
Patent No. 5846706  
GENERAL INFORMATION:  
APPLICANT: Greenberg, Steven J.  
APPLICANT: Evans, Mary Jo  
TITLE OF INVENTION: Rapid and Sensitive Detection of  
TITLE OF INVENTION: Herpesviruses  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One Mt Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for windows 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/600,764  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/428,370  
FILING DATE: 25/04/95  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud

REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0016  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716)856-4000  
TELEFAX: 716-849-0349  
INFORMATION FOR SEQ. ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Herpes simplex virus 2  
FEATURE:  
LOCATION: Polymerase gene sequence bases 2268-2297  
US-08-600-764-12

Query Match 68.0%; Score 13.6; DB 2; Length 30;  
Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GGACGAGGCGACGACGCGG 20  
DB 1 GGACGAGGCGACGACGCGG 20

RESULT 13  
US-09-907-794A-89  
Sequence 89, Application US/09907794A  
Patent No. 6635468  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,794A  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13

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/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 89
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ US-09-907-794A-89
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Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db       10 GACGAGGCGGAGTAC 24
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RESULT 14
US-09-905-125A-89
/ Sequence 89, Application US/09905125A
/ Patent No. 6664376
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerltisen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
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/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/905,125A
/ CURRENT FILING DATE: 2001-07-12
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
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/ PRIOR APPLICATION NUMBER: PCT/US99/21090
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/ PRIOR FILING DATE: 1999-11-29
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/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 89
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ US-09-905-125A-89
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Query Match      67.0%; Score 13.4; DB 3; Length 50;
Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db       10 GACGAGGCGGAGTAC 24
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US-09-902-775A-89
/ Sequence 89, Application US/09902775A
/ Patent No. 666451
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerltisen, Mary E.
/ APPLICANT: Goddard, A.
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APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,775A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
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PRIOR APPLICATION NUMBER: PCT/US99/28313  
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PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 89  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-902-775A-69

Query Match 67.0%; Score 13.4; DB 3; Length 50;  
Best Local Similarity 93.3%; Pred. No. 1.3e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GACGAGGGGAGAC 16  
|||  
Db 10 GACGAGGGGAGATAC 24

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 : Search time 337.6 seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20

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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	15.8	79.0	25	8	US-10-719-900-385716
3	15.4	77.0	27	9	US-10-502-040-19
4	15.2	76.0	25	10	US-11-036-317-781803
5	14.4	72.0	25	10	US-11-036-317-876911
6	14.4	72.0	25	10	US-11-036-317-812288
7	14.4	72.0	25	10	US-11-036-317-955941
8	14.2	71.0	25	8	US-10-719-900-385715
9	14.2	71.0	25	8	US-10-719-900-776619
10	14.2	71.0	25	10	US-11-036-317-149338
11	14.2	71.0	26	7	US-10-795-931-5
12	14.2	71.0	40	5	US-10-015-536-13
13	14.2	71.0	45	3	US-09-908-153B-26
14	14.2	71.0	45	6	US-10-422-934-62
15	14.2	71.0	60	3	US-09-815-242-1169
16	14.2	71.0	60	3	US-09-815-242-1192
17	14.2	71.0	60	7	US-10-282-122A-3511
18	14.2	71.0	60	7	US-10-282-122A-3511
19	13.8	69.0	25	7	US-10-719-956-297366
20	13.8	69.0	27	9	US-10-502-040-27
21	13.8	69.0	33	9	US-10-965-607-3
22	13.8	69.0	50	6	US-10-131-827-3240
23	13.8	69.0	50	6	US-10-131-827-4792

24	13.6	68.0	25	10	US-11-036-317-248373	Sequence 248373,
25	13.6	68.0	25	10	US-11-036-317-259912	Sequence 259912,
26	13.6	68.0	25	10	US-11-036-317-321489	Sequence 321489,
27	13.6	68.0	25	10	US-11-036-317-781802	Sequence 781802,
28	13.6	68.0	31	7	US-10-375-404-4	Sequence 4, Appl1
29	13.6	68.0	31	7	US-10-375-404-12	Sequence 12, Appl1
30	13.6	68.0	32	7	US-10-375-404-5	Sequence 5, Appl1
31	13.6	68.0	32	7	US-10-375-404-7	Sequence 7, Appl1
32	13.6	68.0	35	7	US-10-375-404-6	Sequence 6, Appl1
33	13.6	68.0	35	7	US-10-375-404-8	Sequence 8, Appl1
34	13.6	68.0	37	3	US-09-894-633A-29	Sequence 29, Appl1
35	13.6	68.0	40	9	US-10-477-173-988	Sequence 989, App
36	13.6	68.0	40	9	US-10-477-173-989	Sequence 989, App
37	13.6	68.0	40	9	US-10-477-173-989	Sequence 989, App
38	13.6	68.0	86	7	US-10-220-481-426	Sequence 426, App
39	13.6	68.0	90	7	US-10-220-481-320	Sequence 320, App
40	13.4	67.0	25	9	US-10-956-157-268664	Sequence 268664,
41	13.4	67.0	25	10	US-11-036-317-876909	Sequence 876909,
42	13.4	67.0	50	3	US-09-909-320-89	Sequence 89, Appl1
43	13.4	67.0	50	3	US-09-909-088B-89	Sequence 89, Appl1
44	13.4	67.0	50	3	US-09-905-221A-89	Sequence 89, Appl1
45	13.4	67.0	50	3	US-09-902-853-89	Sequence 89, Appl1

#### ALIGNMENTS

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RESULT 1
US-09-296-264-3
Sequence 3, Appl1
Publication No. US20030083274A1
GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
TITLE OF INVENTION: NEUROPEPTIDE ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
FILE REFERENCE: 032396-043
CURRENT APPLICATION NUMBER: US/09/296,264
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 20
TYPE: DNA
ORGANISM: Human
US-09-296-264-3

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGACGAGGGCGAGCAGCGCG 20
Db 1 GGACGAGGGCGAGCAGCGCG 20

RESULT 2
US-10-719-900-385716
Sequence 385716, Appl1
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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SEQ ID NO 385716  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-385716

Query Match 79.0%; Score 15.8; DB 8; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGCGCCGACGACGCG 19  
Db 3 GGACGAGCGACGACGATGCG 21

RESULT 3  
US-10-502-040-19  
Sequence 19, Application US/10502040  
Publication No. US2005021466A1  
GENERAL INFORMATION:  
APPLICANT: Liao et al.  
TITLE OF INVENTION: ALANINE 2,3-AMINOMUTASE  
FILE REFERENCE: 63358-09  
CURRENT APPLICATION NUMBER: US/10/502,040  
CURRENT FILING DATE: 2004-07-19  
PRIOR APPLICATION NUMBER: PCT/US03/01635  
PRIOR FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US 60/350,727  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: US 60/375,785  
PRIOR FILING DATE: 2002-04-25  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR primer  
US-10-502-040-19

Query Match 77.0%; Score 15.4; DB 9; Length 27;  
Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACGAGGCGGACGACGCGC 19  
Db 6 ACGAGGCGGACGACGCGC 22

RESULT 4  
US-11-036-317-781803/C  
Sequence 781803, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 781803  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-781803

Query Match 76.0%; Score 15.2; DB 10; Length 25;  
Best Local Similarity 85.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGACGAGCGCCGACGACGCG 20  
Db 24 GCACCGGCGCCGACGACGCGC 5

RESULT 5  
US-11-036-317-876911  
Sequence 876911, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 876911  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-876911

Query Match 72.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 5.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGAGGCGGACGACGCGC 19  
Db 7 CGAGGCGGACGACGCGC 22

RESULT 6  
US-11-036-317-912288  
Sequence 912288, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 912288  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-912288

Query Match 72.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 5.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGAGGCGGACGACGCGC 19  
Db 10 CGAGGCGGACGACGCGC 25

RESULT 7  
US-11-036-317-955941  
Sequence 955941, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan

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; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 955941
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-955941

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 10; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GGAGGCGGCGAGCGGC 19
Db 9 GGAGGCGGCGAGCGGC 24

RESULT 8
US-10-719-900-385715
; Sequence 385715, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 385715
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-385715

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGACGAGGCGGAGCGGC 19
Db 3 GGACGAGGCGGAGCGGC 21

RESULT 9
US-10-719-900-776619
; Sequence 776619, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 776619
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-776619
```

```

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGACGAGGCGGAGCGGC 19
Db 3 GGACGAGGCGGAGCGGC 21

RESULT 10
US-11-036-317-149338/c
; Sequence 149338, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 149338
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-149338

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 10; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGACGAGGCGGAGCGGC 19
Db 24 GGACCACTGGGAGGAGCGGC 6

RESULT 11
US-10-795-931-5/c
; Sequence 5, Application US/10795931
; Publication No. US20040148652A1
; GENERAL INFORMATION:
; APPLICANT: Jomai, Gurmutz S
; APPLICANT: Multani, Dilbag S
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING THE DW3
; TITLE OF INVENTION: P-GLYCOPROTEIN OF SORGHUM AND METHODS OF MODIFYING
; FILE REFERENCE: 035718/275561
; CURRENT APPLICATION NUMBER: US/10/795,931
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 60/165,176
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 09/711,619
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-10-795-931-5

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 7; Length 26;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GACGAGGCGGAGGAGCGGC 20
```

Db 24 GACGAGCGGAGACACGGCG 6

## RESULT 12

US-10-015-536-13/C  
; Sequence 13, Application US/10015536  
; Publication No. US20020165149A1  
; GENERAL INFORMATION:  
; APPLICANT: Kranz, David M.  
; APPLICANT: Starwalt, Scott  
; APPLICANT: Bluestone, Jeffrey A.  
; TITLE OF INVENTION: Mutated Class II Major Histocompatibility Proteins  
; FILE REFERENCE: 103-00  
; CURRENT APPLICATION NUMBER: US/10/015,536  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/254,248  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-015-536-13

## Query Match

Best Local Similarity 71.0%; Score 14.2; DB 5; Length 40;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACGAGCGGAGACACGGCG 20  
Db 39 GACGTGGCGAGTACCGCG 21

## RESULT 13

US-09-908-153B-26  
; Sequence 26, Application US/09908153B  
; Patent No. US20020168714A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbas, Carlos F.  
; APPLICANT: Beerli, Roger  
; APPLICANT: Schodfer, Ulrich  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING  
; TITLE OF INVENTION: SINGLE-CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE  
; FILE REFERENCE: TSRI 725.1  
; CURRENT APPLICATION NUMBER: US/09/908,153B  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 09/619,063  
; PRIOR FILING DATE: 2000-07-18  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 45  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Synthesized  
US-09-908-153B-26

## Query Match

Best Local Similarity 71.0%; Score 14.2; DB 3; Length 45;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGAGGCGGAGACACGGCG 19  
Db 3 GGAGGAGGCGCGCGCCCGCG 21

## RESULT 14

US-10-422-934-62

; Sequence 62, Application US/10422934  
; Publication No. US20030186841A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbas, Carlos F., III  
; APPLICANT: Kadan, Michael  
; APPLICANT: Beerli, Roger  
; TITLE OF INVENTION: LIGAND ACTIVATED TRANSCRIPTIONAL REGULATOR PROTEINS  
; FILE REFERENCE: 22908-1227C  
; CURRENT APPLICATION NUMBER: US/10/422,934  
; CURRENT FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: 09/586,625  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 09/433,042  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 62  
; LENGTH: 45  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
US-10-422-934-62

## Query Match

Best Local Similarity 71.0%; Score 14.2; DB 6; Length 45;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGAGGCGGAGACACGGCG 19  
Db 3 GGAGGAGGCGCGCGCCCGCG 21

## RESULT 15

US-09-815-242-1169/C  
; Sequence 1169, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zykkind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J. T.  
; APPLICANT: Yamamoto, Robert T.  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1169  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa

US-09-815-242-1169

Query Match 71.0%; Score 14.2; DB 3; Length 60;  
 Best Local Similarity 84.2%; Pred. No. 5.5e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGAGGGCGACACGGC 19  
 |||||  
 Db 47 GGACCGAGGGCGACACGGC 29

Search completed: December 25, 2005, 04:14:20  
 Job time : 337.6 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 / Search time 135.3 seconds  
(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20  
Sequence: 1 gacgagcgagcgagcgagcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 416828 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications NA New:

1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.8	74.0	25	US-11-121-849-468072	Sequence 468072, A
2	14.4	72.0	25	US-11-121-849-154619	Sequence 154619, A
3	13.6	68.0	25	US-11-121-849-52835	Sequence 52835, A
4	13.6	68.0	25	US-11-121-849-52836	Sequence 52836, A
5	13.6	68.0	25	US-11-121-849-52837	Sequence 52837, A
6	13.6	68.0	25	US-11-121-849-52838	Sequence 52838, A
7	13.6	68.0	25	US-11-121-849-52823	Sequence 52823, A
8	13.6	68.0	25	US-11-121-849-53224	Sequence 53224, A
9	13.6	68.0	25	US-11-121-849-364778	Sequence 364778, A
10	13.6	68.0	25	US-11-121-849-365185	Sequence 365185, A
11	13.6	68.0	32	US-10-939-294A-16208	Sequence 16208, A
12	13.6	68.0	32	US-10-939-294A-16756	Sequence 16756, A
13	13.6	68.0	32	US-10-939-294A-16816	Sequence 16816, A
14	12.8	64.0	21	US-10-770-726-16681	Sequence 16681, A
C 15	12.8	64.0	25	US-11-121-849-322231	Sequence 322231, A
16	12.8	64.0	25	US-11-121-849-529557	Sequence 529557, A
17	12.6	63.0	25	US-11-121-849-14063	Sequence 14063, A
18	12.6	63.0	25	US-11-121-849-50575	Sequence 50575, A
19	12.6	63.0	25	US-11-121-849-357017	Sequence 357017, A
20	12.6	63.0	25	US-11-121-849-357018	Sequence 357018, A
21	12.6	63.0	25	US-11-121-849-661347	Sequence 661347, A
22	12.6	63.0	32	US-10-939-294A-17643	Sequence 17643, A
23	12.6	63.0	32	US-10-939-294A-19935	Sequence 19935, A

24	12.6	63.0	38	US-11-092-988-45	Sequence 45, Appl
25	12.4	62.0	21	US-11-112-882-53	Sequence 53, Appl
26	12.4	62.0	25	US-11-121-849-22698	Sequence 22698, A
27	12.4	62.0	25	US-11-121-849-469681	Sequence 469681, A
C 28	12.4	62.0	32	US-10-939-294A-16788	Sequence 16788, A
C 29	12.4	62.0	32	US-10-939-294A-16792	Sequence 16792, A
C 30	12.4	62.0	32	US-10-939-294A-17186	Sequence 17186, A
C 31	12.4	62.0	32	US-10-939-294A-18059	Sequence 18059, A
C 32	12.4	62.0	32	US-10-939-294A-18119	Sequence 18119, A
C 33	12.2	61.0	25	US-11-121-849-31702	Sequence 31702, A
34	12.2	61.0	25	US-11-121-849-32295	Sequence 32295, A
C 35	12.2	61.0	25	US-11-121-849-51406	Sequence 51406, A
C 36	12.2	61.0	25	US-11-121-849-490705	Sequence 490705, A
C 37	12.2	61.0	25	US-11-121-849-632887	Sequence 632887, A
C 38	12.2	61.0	25	US-11-121-849-640971	Sequence 640971, A
39	12.2	61.0	25	US-11-121-849-640972	Sequence 640972, A
40	12.2	61.0	28	US-11-046-645-145	Sequence 145, App
41	12.2	61.0	28	US-11-046-644-145	Sequence 145, App
C 42	12.2	61.0	58	US-11-013-247A-44	Sequence 44, Appl
C 43	12.2	60.0	25	US-11-121-849-138726	Sequence 138726, A
44	12	60.0	32	US-10-939-294A-15268	Sequence 15268, A
C 45	12	60.0	32	US-10-939-294A-15327	Sequence 15327, A

#### ALIGNMENTS

```

RESULT 1
US-11-121-849-468072/c
; Sequence 468072, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121, 849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567, 949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 468072
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-468072

Query Match      74.0%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy      2 GACGAGCGGCGAGCGGC 19
Db      23 GACCTGGCGGCGCTCGGC 6

RESULT 2
US-11-121-849-154619
; Sequence 154619, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121, 849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567, 949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 154619

```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-154619
```

```
Query Match          72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      4 CGAGGCGGCGGCGGCGG 19
        ||||| ||||| |||||
Db       5 CGAGGCGGCGGCGGCGG 20
```

RESULT 3

```
US-11-121-849-52835
; Sequence 52835, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 52835

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-52835

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      1 GGAGGAGGCGGCGGCGGCGG 20
        ||||| ||||| |||||
Db       6 GGACTACTGCGGAGCACCGCG 25
```

RESULT 4

US-11-121-849-52836

Sequence 52836, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 52836

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-52836

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      1 GGAGGAGGCGGCGGCGGCGG 20
        ||||| ||||| |||||
Db       5 GGACTACTGCGGAGCACCGCG 24
```

```
RESULT 5
US-11-121-849-52837
; Sequence 52837, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 52837

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-52837

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      1 GGAGGAGGCGGCGGCGGCGG 20
        ||||| ||||| |||||
Db       3 GGACTACTGCGGAGCACCGCG 22
```

RESULT 6

US-11-121-849-52838

Sequence 52838, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 52838

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-52838

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      1 GGAGGAGGCGGCGGCGGCGG 20
        ||||| ||||| |||||
Db       1 GGACTACTGCGGAGCACCGCG 20
```

RESULT 7

US-11-121-849-53223

Sequence 53223, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 53223  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-53223

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGCGCGCG 20  
DB 5 GGACTACTGCGAGCAGCCGCG 24

RESULT 8  
US-11-121-849-53224  
Sequence 53224, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121.849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 53224  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-53224

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGCGCGCG 20  
DB 1 GGACTACTGCGAGCAGCCGCG 20

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGCGCGCG 20  
DB 1 GGACTACTGCGAGCAGCCGCG 20

RESULT 9  
US-11-121-849-364778  
Sequence 364778, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121.849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 364778  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-364778

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGCGCGCG 20  
DB 2 GGACCGGCGGCGGCGCGCG 21

RESULT 10  
US-11-121-849-365185  
Sequence 365185, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121.849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 365185  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-365185

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGCGCGCG 20  
DB 2 GGACCGGCGGCGGCGCGCG 21

RESULT 11  
US-10-939-294A-16208  
Sequence 16208, Application US/10939294A  
Publication No. US20050266417A1  
GENERAL INFORMATION:  
APPLICANT: Barney, Francis  
APPLICANT: Turner, Daniel  
APPLICANT: Pingle, Maneesh  
APPLICANT: Pincas, Hanna  
TITLE OF INVENTION: Methods for identifying target nucleic acid molecules  
FILE REFERENCE: 19603/4121 (CRF D-2995-02)  
CURRENT APPLICATION NUMBER: US/10/939.294A  
CURRENT FILING DATE: 2004-09-10  
PRIOR APPLICATION NUMBER: US 60/502/731  
PRIOR FILING DATE: 2003-09-12  
NUMBER OF SEQ ID NOS: 38895  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 16208  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-16208

Query Match 68.0%; Score 13.6; DB 6; Length 32;  
Best Local Similarity 80.0%; Pred. No. 4.9e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGCGGCGCGCG 20  
DB 10 GGACGAGGCGGCGGCGCGCG 29

RESULT 12  
US-10-939-294A-16756  
Sequence 16756, Application US/10939294A  
Publication No. US20050266417A1

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RESULT 14
US-10-770-726-16681
; Sequence 16681, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

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Search completed: December 25, 2005, 04:37:02  
Job time : 135.3 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds  
(without alignments)  
1953.383 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20  
Sequence: 1 ttcttcagggaatccg9999 20

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_scs:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	BD211662	BD211662 Antisense
2	15.4	77.0	25	AX609775	AX609775 Sequence
3	14.2	71.0	25	CQ428968	CQ428968 Sequence
4	14.2	71.0	52	TCUMIRO3	AP154453 Toxostoma
5	13.8	69.0	25	AX609773	AX609773 Sequence
6	13.8	69.0	25	AX612836	AX612836 Sequence
7	13.8	69.0	53	TCIMIRO3	AP154452 Toxostoma
8	13.8	69.0	72	AX604622	AP154452 Toxostoma
9	13.8	69.0	86	AJ840678	AJ840678 Arabidops
10	13.6	68.0	37	AX698174	AX698174 Sequence
11	13.6	68.0	50	AX160046	AX160046 Sequence
12	13.6	68.0	51	AX160045	AX160045 Sequence
13	13.6	68.0	54	TCIMIRO3	AP154447 Toxostoma
14	13.6	68.0	65	CQ559452	CQ559452 Sequence
15	13.6	68.0	72	AX655469	AX655469 Sequence
16	13.6	68.0	73	AX520567	AX520567 Sequence
17	13.6	68.0	97	AL772837	AL772837 Arabidops
18	13.6	68.0	100	AX993510	AX993510 Sequence

19	13.4	67.0	21	6	AR020977	AR020977 Sequence
20	13.4	67.0	21	6	AR020978	AR020978 Sequence
21	13.4	67.0	21	6	AR043392	AR043392 Sequence
22	13.4	67.0	21	6	AR043393	AR043393 Sequence
23	13.4	67.0	21	6	AR062307	AR062307 Sequence
24	13.4	67.0	21	6	AR062308	AR062308 Sequence
25	13.4	67.0	21	6	BD078760	BD078760 Recombine
26	13.4	67.0	21	6	BD078761	BD078761 Recombine
27	13.4	67.0	21	6	BD085587	BD085587 Recombine
28	13.4	67.0	21	6	BD085588	BD085588 Recombine
29	13.4	67.0	21	6	AR183766	AR183766 Sequence
30	13.4	67.0	21	6	AR183767	AR183767 Sequence
31	13.4	67.0	21	6	AR221165	AR221165 Sequence
32	13.4	67.0	21	6	AR221166	AR221166 Sequence
33	13.4	67.0	21	6	AR230592	AR230592 Sequence
34	13.4	67.0	21	6	AR230593	AR230593 Sequence
35	13.4	67.0	21	6	AR234066	AR234066 Sequence
36	13.4	67.0	21	6	AR234067	AR234067 Sequence
37	13.4	67.0	21	6	AR237676	AR237676 Sequence
38	13.4	67.0	21	6	AR237677	AR237677 Sequence
39	13.4	67.0	21	6	AR353186	AR353186 Sequence
40	13.4	67.0	21	6	AR353187	AR353187 Sequence
41	13.4	67.0	21	6	AR368149	AR368149 Sequence
42	13.4	67.0	21	6	AR368150	AR368150 Sequence
43	13.4	67.0	80	6	AX656204	AX656204 Sequence
44	13.4	67.0	100	6	AX99486	AX99486 Sequence
45	13.2	66.0	25	6	CQ862079	CQ862079 Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS BD211662 20 bp DNA linear PAR 17-JUL-2003  
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION BD211662.1 GI:33021432  
VERSION JP 2002512793-A/5.

KEYWORDS SOURCE  
Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.  
TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

JOURNAL Patent: JP 2002512793-A 5 08-MAY-2002;  
GENENSENSE TECHNOLOGIES INC

COMMENT  
OS Homo sapiens (human)  
PN JP 2002512793-A/5  
PD 08-MAY-2002

PR 23-APR-1998 JP 2000545999  
PI JIM A WRIGHT, AIPING H YOUNG, YOON S LEE

PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC  
Antisense oligonucleotide sequence of neuropilin and method of

CC same for controlling cell proliferation  
using the

PH key Location/Qualifiers  
FT source 1..20

FT Location/Qualifiers  
1..20 /organism='Homo sapiens (human)'.  
Location/Qualifiers

FEATURES  
source  
1..20 /organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'

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Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGG 20  
Db 1 TTTTCAGGGAATCCGGG 20

RESULT 2  
AX609775  
LOCUS AX609775 25 bp DNA linear PAT 17-FEB-2003  
DEFINITION Sequence 800 from Patent WO02072882.  
ACCESSION AX609775  
VERSION AX609775.1 GI:28405204  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Cullen.P. and Seedorf,U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 800 19-SEP-2002;  
OGHAM GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 77.0%; Score 15.4; DB 6; Length 25;  
Best Local Similarity 94.1%; Pred. No. 9.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGG 17  
Db 2 TTTTCAGGGAATCTCG 18

RESULT 3  
LOCUS CQ428968 25 bp DNA linear PAT 28-JAN-2004  
DEFINITION Sequence 14002 from Patent WO0151628.  
ACCESSION CQ428968  
VERSION CQ428968.1 GI:41381197  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.  
TITLE Novel genes, compositions, kits, and methods for identification,  
assessment, prevention, and therapy of breast cancer  
JOURNAL Patent: WO 0151628-A 14002 19-JUL-2001;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGG 19  
Db 19 TTTTCAGGGAATCCGGTG 1

RESULT 4  
TCUMIT03/C 52 bp DNA linear VRT 23-SEP-1999  
LOCUS TCUMIT03  
DEFINITION Toxostoma curvirostre isolate C87H6TX tRNA-Glu gene, partial  
sequence; mitochondrial gene for mitochondrial product.  
ACCESSION AF154453  
VERSION AF154453.1 GI:5918791  
KEYWORDS  
SEGMENT 3 of 6  
SOURCE mitochondrion Toxostoma curvirostre  
ORGANISM Toxostoma curvirostre  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Passeriformes; Mimidae; Toxostoma.  
REFERENCE 1  
AUTHORS Zink,R.M., Dittmann,D.L., Klicka,J. and Blackwell-Rago,R.C.  
TITLE Evolutionary patterns of morphometrics, allozymes and mitochondrial  
DNA in thrashers (Toxostoma)  
JOURNAL The Auk (1999) In press  
2 (bases 1 to 52)  
Zink,R.M., Dittmann,D.L., Klicka,J. and Blackwell-Rago,R.C.  
REFERENCE Direct Submission  
AUTHORS Submitted (26-MAY-1999) Bell Museum, University of Minnesota, 100  
TITLE Ecology Bldg, 1987 Upper Buford Circle, St Paul, MN 55108, USA  
JOURNAL  
FEATURES Location/Qualifiers  
source 1..52  
/organism="Toxostoma curvirostre"  
/organelle="mitochondrion"  
/mol\_type="genomic DNA"  
/isolate="C87H6TX"  
/specimen\_voucher="RMZ 2951, ISU Museum of Zoology"  
/db\_xref="taxon:99878"  
/sex="male"  
/country="USA:Texas", 10 miles SSE of Charlotte"  
/note="Isolated May 26, 1992"  
<1..>52  
/product="tRNA-Glu"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 5; Length 52;  
Best Local Similarity 84.2%; Pred. No. 3.7e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCGGG 20  
Db 32 TTTTCAGGGAATCTCGAG 14

RESULT 5  
AX609773 25 bp DNA linear PAT 17-FEB-2003  
LOCUS AX609773  
DEFINITION Sequence 798 from Patent WO02072882.  
ACCESSION AX609773  
VERSION AX609773.1 GI:28405202  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Cullen.P. and Seedorf,U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 798 19-SEP-2002;  
OGHAM GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 69.0%; Score 13.8; DB 6; Length 25;

Best Local Similarity 88.2%; Pred. No. 6.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGG 17  
|||||  
2 TTTTCAGGGAATCTCG 18

RESULT 6  
LOCUS AK612836 25 bp DNA linear PAT 17-FEB-2003

DEFINITION Sequence 3861 from Patent WO02072882.

ACCESSION AK612836

VERSION AK612836.1 GI:28408265

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS Cullen, P. and Seedorf, U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 3861 19-SEP-2002;  
OGHAM GmbH (DE)

FEATURES  
SOURCE location/Qualifiers

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/organism="Homo sapiens"  
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ORIGIN

Query Match 59.0%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 6.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGG 17  
|||||  
7 TTTTCAGGGAATCTCG 23

RESULT 7  
LOCUS TCIMT03 53 bp DNA linear VRT 23-SEP-1999

DEFINITION Toxostoma cinereum isolate GRTH4BN tRNA-Glu gene, partial sequence;  
mitochondrial gene for mitochondrial product.

ACCESSION AF154459

VERSION AF154459.1 GI:5918797

KEYWORDS

SEGMENT

SOURCE

ORGANISM

3 of 6  
mitochondrion Toxostoma cinereum  
Toxostoma cinereum  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Passeriformes; Mimidae; Toxostoma.

REFERENCE  
AUTHORS Zink, R.M., Dittman, D.L., Klicka, J. and Blackwell-Rago, R.C.  
TITLE Evolutionary patterns of morphometrics, allozymes and mitochondrial DNA in thrashers (Toxostoma)  
JOURNAL The Auk (1999) in press  
2 (bases 1 to 53)  
2 (bases 1 to 53)  
Zink, R.M., Dittman, D.L., Klicka, J. and Blackwell-Rago, R.C.  
Direct Submission  
Submitted (26-MAY-1999) Bell Museum, University of Minnesota, 100  
Ecology Bldg, 1987 Upper Buford Circle, St Paul, MN 55108, USA

FEATURES  
SOURCE location/Qualifiers  
1..53  
/organism="Toxostoma cinereum"  
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/mol\_type="genomic DNA"  
/isolate="GRTH4BN"  
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/specimen\_voucher="RMZ 2165, American Museum, New York"  
/db\_xref="taxon:99877"

/sex="female"  
/country="Mexico:Baja California, 3 km. west of Camalu"  
/note="isolated November 10, 1983"  
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/product="tRNA-Glu"

ORIGIN

Query Match 69.0%; Score 13.8; DB 5; Length 53;  
Best Local Similarity 88.2%; Pred. No. 6.1e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCGG 18  
|||||  
33 TTTTCAGGGAATCTCG 17

RESULT 8  
LOCUS AY604622

DEFINITION AY604622 72 bp mRNA linear MAM 09-JUN-2004  
Sus scrofa clone 8401-10 T-cell receptor delta chain CDR3 region  
(TCRD) mRNA, partial cds.

ACCESSION AY604622

VERSION AY604622.1 GI:48249542

KEYWORDS

SOURCE

ORGANISM

Sus scrofa (pig)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE

AUTHORS Holtheier, W., Geisel, W., Bernert, K., Butler, J.E., Sinkora, M.,  
1 (bases 1 to 72)  
Rehakova, Z., Sinkora, J. and Caspar, W.F. delta repertoire: Dominant  
prenatal development of the porcine TCR delta repertoire: Dominant  
expression of an invariant T cell receptor Vdelta3-Vdelta3 chain  
Eur. J. Immunol. (2004) in press  
2 (bases 1 to 72)  
Holtheier, W., Geisel, W., Bernert, K., Butler, J.E., Sinkora, M.,  
Rehakova, Z., Sinkora, J. and Caspar, W.F.

JOURNAL Direct Submission  
Submitted (22-APR-2004) Medizinische Klinik II, Department of  
Gastroenterology, Johann Wolfgang Goethe-Universität,  
Theodor-Stern-Kai 7, Frankfurt am Main 60590, Germany

FEATURES  
SOURCE location/Qualifiers

1..72  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
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/clone="8401-10"  
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CDS

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/db\_xref="GI:48249543"  
/translation="ADARVYFCAFMWSWTDKILFGKG"

ORIGIN

Query Match 69.0%; Score 13.8; DB 4; Length 72;  
Best Local Similarity 88.2%; Pred. No. 5.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTTTCAGGGAATCCGG 19  
|||||  
27 TTTTCAGGGAATCTCG 43

RESULT 9  
LOCUS AJ840678

LOCUS AJ840678 86 bp DNA linear PLN 22-SEP-2004  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 605E05  
 ACCESSION AJ840678  
 VERSION AJ840678.1 GI:52544884  
 KEYWORDS right border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana (chale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
 REFERENCE PUBMED 12446565  
 AUTHORS Balzerque, S.  
 TITLE Direct Submision  
 JOURNAL Submitted (21-SEP-2004) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaetan Cremieux, 91057 Evry cedex, FRANCE  
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'genoplante' (<http://www.genoplante.com> and <http://genoplante.info.inbioigen.fr>).  
 FEATURES  
 source  
 1..86  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
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 /clone="605E05"  
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 /ecotype="Massilewska"  
 1..86  
 /note="T-DNA flanking sequence  
 right border"

ORIGIN  
 Query Match 69.0%; Score 13.8; DB 15; Length 86;  
 Best Local Similarity 88.2%; Pred. No. 5.8e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTTCAGGGAATCCGG 17  
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 19 TTTTCAGGGAATCAG 35

Db 19 TTTTCAGGGAATCAG 35

RESULT 10  
 AX698174 37 bp DNA linear PAT 02-APR-2003  
 LOCUS AX698174  
 DEFINITION Sequence 23 from Patent WO03010332.  
 ACCESSION AX698174  
 VERSION AX698174.1 GI:29499183  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 synthetic construct  
 other sequences; artificial sequences.

REFERENCE  
 AUTHORS Vollenhofer-Schrumpf, S., Schinkinger, M. and Fraenzl, G.  
 TITLE Test-kit for detecting enterohemorrhagic \_E. coli strains (ehec)  
 JOURNAL Patent: WO 03010332-A 23 06-FEB-2003;  
 Sy-Lab GmbH (AT)

FEATURES  
 source  
 Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Random oligonucleotide"

ORIGIN  
 Query Match 68.0%; Score 13.6; DB 6; Length 37;  
 Best Local Similarity 80.0%; Pred. No. 8.1e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTTCAGGGAATCCGGGGG 20  
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 9 TTTTCCGGGTAGTCCGGGGG 28

Db 9 TTTTCCGGGTAGTCCGGGGG 28

RESULT 11  
 AX160046 50 bp DNA linear PAT 22-JUN-2001  
 LOCUS AX160046  
 DEFINITION Sequence 3374 from Patent WO0140521.  
 ACCESSION AX160046  
 VERSION AX160046.1 GI:14541377  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Shimkets, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
 JOURNAL Patent: WO 0140521-A 3374 07-JUN-2001;  
 Curagen Corporation (US)  
 FEATURES  
 source  
 1..50  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 25..26  
 /note="Nucleotide deleted between bases 25 and 26  
 Accession number cg43253001"  
 26  
 /note="2 of 2 allelic variants (3373 is other entry)"

ORIGIN  
 Query Match 68.0%; Score 13.6; DB 6; Length 50;  
 Best Local Similarity 80.0%; Pred. No. 7.8e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTTCAGGGAATCCGGGGG 20  
 |||||  
 4 TGTCTCGGGGAAGCCGGGGG 23

Db 4 TGTCTCGGGGAAGCCGGGGG 23

RESULT 12  
 AX160045 51 bp DNA linear PAT 22-JUN-2001  
 LOCUS AX160045  
 DEFINITION Sequence 3373 from Patent WO0140521.  
 ACCESSION AX160045  
 VERSION AX160045.1 GI:14541376  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Shimkets, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
 JOURNAL Patent: WO 0140521-A 3373 07-JUN-2001;



FEATURES	Curation Corporation (US)
source	Location/Qualifiers
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	/mol_type="unassigned DNA"
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	26
	/note="1 of 2 allelic variants (3374 is other entry)
	Accession number CG43253001"
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Best Local Similarity	80.0%; Pred. No. 7.8e+04;
Matches	16; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
OY	
1	TTTTTCAGGGAATCCGGGGG 20
4	TGTCGCGGAGAACCGGGGG 23
RESULT 13	
LOCUS	54 bp DNA linear VRT 23-SEP-1999
DEFINITION	Toxostoma ocellatum isolate OCTH2MX cRNA-Glu gene, partial
VERSION	AF154447
ACCESSION	AF154447.1 GI:5918785
KEYWORDS	
SEGMENT	
SOURCE	
ORGANISM	3 of 6
	mitochondrion Toxostoma ocellatum
	Toxostoma ocellatum
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Archosauaria; Aves; Neognathae; Passeriformes; Mimidae; Toxostoma.
	1 (bases 1 to 54)
REFERENCE	Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C.
AUTHORS	Evolutionary patterns of morphometrics, allozymes and mitochondrial
TITLE	DNA in thashers (Toxostoma)
JOURNAL	The Auk (1999) In press
REFERENCE	2 (bases 1 to 54)
AUTHORS	Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C.
TITLE	Direct Submission
JOURNAL	Submitted (26-May-1999) Bell Museum, University of Minnesota, 100
	Ecology Bldg, 1967 Upper Buford Circle, St Paul, MN 55108, USA
FEATURES	Location/Qualifiers
source	1..54
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	/organelle="mitochondrion"
	/mol_type="genomic DNA"
	/isolate="OCTH2MX"
	/specimen_voucher="RMZ 2190, American Museum, New York"
	/specimen_voucher="B16570, LSU Museum of Zoology"
	/db_xref="Taxon:99881"
	/sex="male"
	/country="Mexico:Oaxaca, 5 km SE of Matatlan"
	/note="Isolated November 18, 1993"
	<1..>54
	/product="cRNA-Glu"
ORIGIN	
Query Match	68.0%; Score 13.6; DB 5; Length 54;
Best Local Similarity	80.0%; Pred. No. 7.7e+04;
Matches	16; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
OY	
1	TTTTTCAGGGAATCCGGGGG 20
34	TTTTTCAGGGAATCCGGGGG 15
RESULT 14	
LOCUS	65 bp DNA linear PAT 30-JAN-2004
DEFINITION	CO559452
ACCESSION	Sequence 29087 from Patent WOO210449.
	CO559452

```

VERSION      CQ559452.1  GI:41525879
KEYWORDS
SOURCE
ORGANISM     Mus musculus (house mouse)
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurgnathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Shoshan,A., Wasserman,A., Mirtz,E., Mirtz,L. and Faigler,S.
TITLE        Oligonucleotide library for detecting rna transcripts and splice
              variants that populate a transcriptome
JOURNAL      Patent: WO 0210449-A 29087 07-FEB-2002;
              Compugen Inc. (US)

FEATURES
SOURCE
              Location/Qualifiers
                1..65
                  /organism="Mus musculus"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:10090"

ORIGIN
Query Match      68.0%; Score 13.6; DB 6; Length 65;
Best Local Similarity 80.0%; Pred. No. 7.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      1 TTTTCAGGGGAAATCCGGGG 20
          ||| ||||| ||||| ||| |||
Db      39 TTGTTCCGGGAAATCTCGTGG 58

RESULT 15
AX655469      72 bp      DNA      linear      PAT 22-MAR-2003
LOCUS         AX655469
DEFINITION    Sequence 5339 from Patent WO03000898.
ACCESSION     AX655469
VERSION       AX655469.1  GI:29158283
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
              Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatopsida; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS       Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
              Katagiri,F., Quan,S., Tao,Y., Whitman,S., Xie,Z., Zhu,T. and Zou,G.
TITLE         Plant genes involved in defense against pathogens
JOURNAL      Patent: WO 03000898-A 5339 03-JAN-2003;
              Syngenta Participations AG (CH)

FEATURES
SOURCE
              Location/Qualifiers
                1..72
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                  /mol_type="unassigned DNA"
                  /db_xref="taxon:4530"

ORIGIN
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Best Local Similarity 72.2%; Pred. No. 7.5e+04;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy      2 TTTTCAGGGGAAATCCGGGG 19
          ||||| ||||| ||||| |||
Db      38 TTTTCCGGGAAATCCCGGK 55

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Job time : 584 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
777.677 Million cell updates/sec

Title: US-09-296-264-5

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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneeqn1990s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001s:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002as:\*  
7: geneeqn2002bs:\*  
8: geneeqn2003as:\*  
9: geneeqn2003bs:\*  
10: geneeqn2003cs:\*  
11: geneeqn2003ds:\*  
12: geneeqn2004as:\*  
13: geneeqn2004bs:\*  
14: geneeqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AA231435 Human neu
2	20	100.0	20	4	ADA74687 GTI3605 a
3	14.2	71.0	25	4	AAU21532 Human bre
4	14.2	71.0	51	10	ACF79352 Upstream
5	14.2	71.0	57	10	ADD94398 Mouse HUI
6	14.2	71.0	57	10	ADD94399 Mouse HUI
7	14	70.0	57	10	ADD94400 Mouse HUI
8	13.8	69.0	21	10	ADG84972 FAM/TMRA
9	13.8	69.0	24	10	ADF72668 E. coli v
10	13.8	69.0	57	6	ABK36270 HIV DNA e
11	13.8	69.0	57	10	ADD94401 Mouse HUI
12	13.8	69.0	80	12	ADM95446 Rat anti
13	13.6	68.0	33	12	ADM6724 primer 3
14	13.6	68.0	37	8	ABX94733 Negative
15	13.6	68.0	50	4	AA176433 Human sll
16	13.6	68.0	51	4	AA176432 Human sll
17	13.6	68.0	55	10	ADK12084 Breast ca
18	13.6	68.0	65	6	ABN56339 Mouse spl
19	13.6	68.0	68	14	ACL59655 Human col

20	13.6	68.0	72	8	ADA72014	Ada72014 Rice gene
21	13.6	68.0	88	12	ACH84195	Ach84195 Human gen
22	13.6	68.0	91	2	AAT22379	Aat22379 Human gen
23	13.6	68.0	100	8	ACD73703	Act73703 E. coli K
24	13.4	67.0	21	2	AAQ86161	Aaq86161 Sindbis p
25	13.4	67.0	21	2	AAQ86162	Aaq86162 Sindbis p
26	13.4	67.0	21	2	AAT35060	Aat35060 Sindbis v
27	13.4	67.0	21	2	AAT35061	Aat35061 Sindbis v
28	13.4	67.0	21	2	AAT30796	Aat30796 Sindbis g
29	13.4	67.0	21	2	AAT30795	Aat30795 Sindbis g
30	13.4	67.0	21	2	AAK59247	Aak59247 primer 73
31	13.4	67.0	21	2	AAK59246	Aak59246 primer 73
32	13.4	67.0	21	2	AAV42372	AAv42372 PCR prime
33	13.4	67.0	21	2	AAV42373	AAv42373 PCR prime
34	13.4	67.0	21	2	AAV60134	AAv60134 PCR prime
35	13.4	67.0	21	2	AAV60133	AAv60133 PCR prime
36	13.4	67.0	21	2	AAV70693	AAv70693 PCR prime
37	13.4	67.0	21	2	AAV70692	AAv70692 PCR prime
38	13.4	67.0	21	2	AAK58488	Aak58488 primer 73
39	13.4	67.0	21	2	AAK58489	Aak58489 primer 73
40	13.4	67.0	21	3	AAZ92901	Aaz92901 Sindbis v
41	13.4	67.0	21	3	AAZ92900	Aaz92900 Sindbis v
42	13.4	67.0	21	3	AAZ92773	Aaz92773 Sindbis v
43	13.4	67.0	21	3	AAZ92774	Aaz92774 Sindbis v
44	13.4	67.0	21	6	AAI38780	AAi38780 Alphaviru
45	13.4	67.0	21	6	AAI38781	AAi38781 Alphaviru

## ALIGNMENTS

RESULT 1	AA231435	standard; DNA; 20 BP.
ID	AA231435	
AC	AA231435;	
XX	07-FEB-2000	(first entry)
DT		
XX		
DE		Human neuropilin mRNA specific antisense oligo GTI3605.
XX		
KW		Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;
XX		papilloma; diabetic retinopathy; antisense; se.
OS		Synthetic.
XX		
OS		Homo sapiens.
XX		
PN		W0955855-A2.
XX		
PD		04-NOV-1999.
XX		
PF		23-APR-1999; 99WO-CA000324.
XX		
PR		23-APR-1998; 98US-0082791P.
XX		
XX		(GENE-) GENESENSE TECHNOLOGIES INC.
XX		
PI		Wright JA, Young AH, Lee YS;
XX		
DR		WPI; 2000-023357/02.
XX		
PT		Antisense oligonucleotides that inhibit neuropilin expression, useful for
XX		treating cancer.
PS		Claim 4; Page 16; 57pp; English.
XX		
CC		Sequences AA231431-460 represent antisense oligonucleotides which inhibit
CC		human neuropilin expression. The antisense oligonucleotides can be used
CC		to inhibit the growth or metastasis of a mammalian tumor and inhibit
CC		neovascularisation. The oligonucleotides may be used to treat various
CC		forms of cancers or tumors, such as sarcomas, melanomas, adenomas,
CC		carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of
CC		the mouth, throat, larynx and lung, genitourinary cancers such as

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
CC cancer, head and neck cancers, and nervous system cancers, as well as  
CC benign lesions such as papillomas. The methods may be used to treat  
CC neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration  
XX  
SQ Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 20  
1 TTTTCAGGGAATCCGGGG 20  
DB 1 TTTTCAGGGAATCCGGGG 20

RESULT 2  
ADA74687  
ID ADA74687 standard; DNA; 20 BP.  
XX  
AC ADA74687;

DT 20-NOV-2003 (first entry)  
DE GT13605 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
KM cytosolic; growth; tumor metastasis; angiogenesis; gene therapy;  
KW GT13605; antisense; human; ss.  
XX  
OS Homo sapiens.

XX  
PN US2003083274-A1.  
XX  
PD 01-MAY-2003.

XX  
PF 22-APR-1999; 99US-00296264.  
XX  
PR 23-APR-1998; 98US-0082791P.

XX (WRIG/) WRIGHT J A.  
PA (YOUNG/) YOUNG A H.  
PA (LEEY/) LEE Y S.

XX PI Wright JA, Young AH, Lee YS;  
XX  
DR WPI; 2003-576622/54.

PT New antisense oligonucleotide that inhibits neuropilin expression, useful  
PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
XX mammalian tumor.  
XX

PS Claim 1; Page 5; 27pp; English.

CC The invention relates to a novel antisense oligonucleotide that inhibits  
CC the expression of neuropilin, also known as VEGF165R (vascular  
CC endothelial growth factor receptor). The oligonucleotide of the invention  
CC demonstrates cytostatic activity and may be useful for inhibiting the  
CC growth or metastasis of a mammalian tumor and to inhibit angiogenesis in  
CC mammals. Furthermore, the oligonucleotide may be utilized during gene  
CC therapy. The current sequence is that of the GT13605 antisense  
CC oligonucleotide of the invention which is targeted to human neuropilin  
CC mRNA.  
CC  
SQ Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 20

DB 1 TTTTCAGGGAATCCGGGG 20

RESULT 3  
AAL21532/c  
ID AAL21532 standard; cDNA; 25 BP.  
XX  
AC AAL21532;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 13989.

XX Human; breast cancer; cell marker; cytosolic; ss.  
XX

OS Homo sapiens.

PN WO200151628-A2.

PD 19-JUL-2001.

PF 10-JAN-2001; 2001WO-US000798.

PR 14-JAN-2000; 2000US-0176077P.

PR 14-MAR-2000; 2000US-0189167P.

PR 24-MAR-2000; 2000US-0192099P.

PR 29-MAR-2000; 2000US-0193480P.

PR 15-MAY-2000; 2000US-0205230P.

PR 09-JUN-2000; 2000US-0211315P.

PR 25-JUL-2000; 2000US-0220534P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX  
PI Lillie J, Xu Y, Wang Y, Steinmann K;

DR WPI; 2001-451856/48.

PT New peptide useful as a marker for the diagnosis of breast cancer.

PS Claim 1; Page 2494; 3695pp; English.

CC The invention relates to human breast cancer expressed polynucleotides  
CC (AAL07544-AAL26789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterizing, treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity  
XX

SQ Sequence 25 BP; 6 A; 7 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.9e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 19  
1 TTTTCAGGGAATCCGGGG 19  
DB 19 TTTTCAGGGAATCCGGGG 1

RESULT 4  
ACF79352/c  
ID ACF79352 standard; DNA; 51 BP.

XX  
AC ACF79352;

DT 18-DEC-2003 (first entry)

DE Upstream primer for construction of pMPDLM-12alpha-E3L.

XX

KW Z-alpha; DLM-1; mouse; E3L; Z-DNA; virucide; vaccine; PCR; primer; ss.  
XX Mus sp.  
OS  
XX WO2003066807-A2.  
PN  
XX  
XX 14-AUG-2003.  
PD  
XX  
PF 19-DEC-2002; 2002WO-US041107.  
XX  
XX 20-DEC-2001; 2001US-0343028P.  
PR 16-DEC-2002; 2002US-00321785.  
XX  
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA (UYAR-) UNIV ARIZONA.  
XX  
XX Jacobs BL, Rich A;  
PI  
XX WPI; 2003-679540/64.  
DR  
XX  
XX Detecting or identifying an inhibitor of binding of a Z-DNA binding  
PT ligand to Z-DNA by combining an agent to be tested, Z-DNA and a  
PT composition comprising a Z-DNA binding ligand or Z-DNA binding variant.  
XX  
XX Example 2; Page 44; 105pp; English.  
PS  
XX The present sequence is an upstream primer used in the construction of  
CC plasmid pMFDLM-1alpha-E3L in which nucleotides 61-261 of the vaccinia  
CC virus E3L gene (coding for amino acids 1-67) were replaced by nucleotides  
CC 116-316 from the Z-alpha domain of the mouse DLM-1 gene. Vaccinia virus  
CC E3L and DLM-1 are Z-DNA binding ligands. Domain swapping was performed in  
CC order to identify E3L residues responsible for vaccinia virus  
CC pathogenicity. The invention relates to methods of identifying inhibitors  
CC of binding of a Z-DNA binding ligand to Z-DNA, methods of inhibiting the  
CC pathogenicity of an infectious agent, and antiviral therapies. The  
CC inhibitors are used to treat a poxvirus infection caused by variola  
CC virus, vaccinia virus, orf virus, mousepox virus, monkeypox virus,  
CC eczema virus, yaba-like disease virus, cowpox virus, myxoma virus,  
CC rabbit fibroma virus or lumpy skin disease virus (claimed).  
XX  
SQ Sequence 51 BP; 14 A; 14 C; 13 G; 10 T; 0 U; 0 Other;  
Query Match 71.0%; Score 14.2; DB 10; Length 51;  
Best Local Similarity 84.2%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TTTTCAGGGAATCCGGGG 20  
DB 31 TTTTCAGGGAATCCGGGG 13  
RESULT 5  
ADD94398/C  
ID ADD94398 standard; DNA; 57 BP.  
XX  
XX ADD94398;  
AC  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Mouse HUIV26 antibody mutagenic PCR primer SegID283.  
DE  
XX grafted antibody; complementarity determining region; CDR; light CDR;  
KW heavy CDR; cryptic collagen epitope; solid tumour;  
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
KW collagen agonist; collagen antagonist; cancer metastasis;  
KW anti-cryptic collagen; PCR; primer; ss; mouse; murine; HUIV26; mutagenic.  
XX  
XX Synthetic.  
OS Mus musculus.  
XX WO2003046204-A2.  
PN  
XX 05-JUN-2003.  
PD

XX 26-NOV-2002; 2002WO-US038147.  
PF  
XX 26-NOV-2001; 2001US-00995529.  
PR  
XX 06-DEC-2001; 2001US-00011250.  
PR  
XX  
XX (CELL-) CELL MATRIX INC.  
PA  
XX  
XX Waking JD, Huse WD, Tang Y, Broek D, Brooks PC;  
PI  
XX WPI; 2003-513649/48.  
DR  
XX  
XX New cryptic collagen antibody with one or more complementarity  
PT determining regions; useful for diagnosing and treating disorders  
PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
XX  
XX Example 2; SEQ ID NO 283; 232pp; English.  
PS  
XX This invention relates to a novel grafted antibody or its functional  
CC fragment comprising one or more complementarity determining regions  
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
CC acid (aa) substitution where the antibody has specific binding activity  
CC for a cryptic collagen epitope. The growth of all solid tumours requires  
CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
CC to limiting tumour growth. The invention may allow development of  
CC therapeutics with a cytostatic activity as a collagen agonist or  
CC antagonist. The invention is useful for diagnosing and treating disorders  
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
CC present sequence is that of a mutagenic PCR primer which was used to  
CC amplify a region of the sequence encoding the mouse HUIV26 antibody  
CC during the exemplification of the invention.  
XX  
SQ Sequence 57 BP; 13 A; 12 C; 18 G; 11 T; 0 U; 3 Other;  
Query Match 71.0%; Score 14.2; DB 10; Length 57;  
Best Local Similarity 84.2%; Pred. No. 4.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TTTTCAGGGAATCCGGGG 19  
DB 33 TTTTCAGGGAATCCGGGG 15  
RESULT 6  
ADD94399/C  
ID ADD94399 standard; DNA; 57 BP.  
XX  
XX ADD94399;  
AC  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Mouse HUIV26 antibody mutagenic PCR primer SegID284.  
DE  
XX grafted antibody; complementarity determining region; CDR; light CDR;  
KW heavy CDR; cryptic collagen epitope; solid tumour;  
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
KW collagen agonist; collagen antagonist; cancer metastasis;  
KW anti-cryptic collagen; PCR; primer; ss; mouse; murine; HUIV26; mutagenic.  
XX  
XX Synthetic.  
OS Mus musculus.  
XX WO2003046204-A2.  
PN  
XX 05-JUN-2003.  
PD  
XX 26-NOV-2002; 2002WO-US038147.  
PF  
XX 26-NOV-2001; 2001US-00995529.  
PR 06-DEC-2001; 2001US-00011250.  
PR  
XX  
XX (CELL-) CELL MATRIX INC.  
PA  
XX

PI Wackling JD, Huse WD, Tang Y, Broek D, Brooks PC;  
XX  
DR WPI; 2003-513649/48.  
XX  
PT New cryptic collagen antibody with one or more complementarity  
PT determining regions, useful for diagnosing and treating disorders  
PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
XX  
PS Example 2; SEQ ID NO 284; 232pp; English.  
XX  
CC This invention relates to a novel grafted antibody or its functional  
CC fragment comprising one or more complementarity determining regions  
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
CC acid (aa) substitution where the antibody has specific binding activity  
CC for a cryptic collagen epitope. The growth of all solid tumours requires  
CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
CC to limiting tumour growth. The invention may allow development of  
CC therapeutics with a cytostatic activity as a collagen agonist or  
CC antagonist. The invention is useful for diagnosing and treating disorders  
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
CC present sequence is that of a mutagenic PCR primer which was used to  
CC amplify a region of the sequence encoding the mouse HUIV26 antibody  
CC during the exemplification of the invention.  
CC  
SQ Sequence 57 BP; 13 A; 14 C; 17 G; 10 T; 0 U; 3 Other;  
XX  
Query Match 71.0%; Score 14.2; DB 10; Length 57;  
Best Local Similarity 84.2%; Pred. No. 4.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 1 TTTTTCAGGGATCCGGGG 19  
| | | | | | | | | | | | | | | | | | | | | |  
DB 33 TCTACAGGGATCCGGGG 15  
| | | | | | | | | | | | | | | | | | | | | |  
XX  
RESULT 7  
ADD94400/C  
ID ADD94400 standard; DNA; 57 BP.  
XX  
AC ADD94400;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Mouse HUIV26 antibody mutagenic PCR primer SeqID285.  
XX  
KW grafted antibody; complementarity determining region; CDR; light CDR;  
KW heavy CDR; cryptic collagen epitope; solid tumour;  
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;  
KW collagen agonist; collagen antagonist; cancer metastasis;  
KW anti-cryptic collagen; PCR; primer; ss; mouse; murine; HUIV26; mutagenic.  
XX  
OS Synthetic.  
OS Mus musculus.  
XX  
PN WO2003046204-A2.  
XX  
PD 05-JUN-2003.  
XX  
PF 26-NOV-2002; 2002WO-US038147.  
XX  
PR 26-NOV-2001; 2001US-00995529.  
XX  
PR 06-DEC-2001; 2001US-00011250.  
XX  
PA (CELL-) CELL MATRIX INC.  
XX  
PI Wackling JD, Huse WD, Tang Y, Broek D, Brooks PC;  
XX  
DR WPI; 2003-513649/48.  
XX  
PT New cryptic collagen antibody with one or more complementarity  
PT determining regions, useful for diagnosing and treating disorders  
PT associated with angiogenesis, tumor growth and/or cancer metastasis.  
XX

PS Example 2; SEQ ID NO 285; 232pp; English.  
XX  
CC This invention relates to a novel grafted antibody or its functional  
CC fragment comprising one or more complementarity determining regions  
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino  
CC acid (aa) substitution where the antibody has specific binding activity  
CC for a cryptic collagen epitope. The growth of all solid tumours requires  
CC new blood vessel growth, angiogenesis, inhibition of which is an approach  
CC to limiting tumour growth. The invention may allow development of  
CC therapeutics with a cytostatic activity as a collagen agonist or  
CC antagonist. The invention is useful for diagnosing and treating disorders  
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The  
CC present sequence is that of a mutagenic PCR primer which was used to  
CC amplify a region of the sequence encoding the mouse HUIV26 antibody  
CC during the exemplification of the invention.  
XX  
SQ Sequence 57 BP; 11 A; 15 C; 17 G; 11 T; 0 U; 3 Other;  
XX  
Query Match 70.0%; Score 14; DB 10; Length 57;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 6 CAGGGAATCCGGGG 19  
| | | | | | | | | | | | | | | | | | | | | |  
DB 28 CAGGGAATCCGGGG 15  
| | | | | | | | | | | | | | | | | | | | | |  
XX  
RESULT 8  
ADG84972  
ID ADG84972 standard; DNA; 21 BP.  
XX  
AC ADG84972;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE FAM/TAMRA labelled probe #SEQ ID 25.  
XX  
KW Cytostatic; gene therapy; cancer; TDRD1; Tudor Domain Protein 1; probe;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003091690-A2.  
XX  
PD 06-NOV-2003.  
XX  
PF 17-APR-2003; 2003WO-US011933.  
XX  
PR 26-APR-2002; 2002US-0375879P.  
XX  
PA (LUDWIG INST CANCER RES.  
XX  
PI De Smet C, Boon-Falleur T, Lortiot A;  
XX  
DR WPI; 2003-865624/80.  
XX  
PD  
XX  
PF Diagnosing cancer in a subject by obtaining a non-testis biological  
PT sample from the subject and determining the expression in the sample of  
PT one or more cancer-associated nucleic acid molecules.  
XX  
PS Example 5; SEQ ID NO 25; 94pp; English.  
XX  
CC The invention relates to a method for diagnosing cancer in a subject,  
CC comprising obtaining a non-testis biological sample from a subject and  
CC determining the expression in the sample of one or more cancer-associated  
CC nucleic acid molecules comprising a sequence having 833-8370 bp. Also  
CC disclosed is a method for selecting a course of treatment of a subject  
CC having or suspected of having cancer, and a kit for diagnosis of cancer  
CC in a subject. The sample comprises tissue or cells. The tissue comprises  
CC lung, bladder, epidermoid, breast, esophageal, renal, prostate, brain,  
CC spleen, blood, bone marrow, epidermis, cutaneous, neuronal, colorectal or  
CC thyroid. The cancer is cutaneous melanomas, sarcomas, lung, bladder,  
CC epidermoid, breast or esophageal carcinomas, renal, prostate, brain,

CC uterine or thyroid tumours, neuroblastomas, colorectal carcinomas,  
 CC mesotheliomas, uveal melanomas or myelomas. The method is useful in  
 CC diagnosing or treating cancer. The current sequence represents a probe  
 CC used in an example from the invention for the detection of the Tudor  
 CC Domain Protein 1 gene (TDRD1).

SQ Sequence 21 BP; 4 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 10; Length 21;

Best Local Similarity 88.2%; Pred. No. 6e+03; Mismatches 2; Indels 0; Gaps 0;

OY 3 TTTTCAGGGAATCCGGG 19  
 |||||  
 DB 3 TTTTCAGGGAATCCGGT 19

# RESULT 9

ADP72668/C  
 ID ADP72668 standard; DNA; 24 BP.

AC ADP72668;

DT 12-FEB-2004 (first entry)

DE E. coli VT1B forward PCR primer SEQ ID NO:1.

KW ss; primer; PCR; contamination; pathogenic microbe; food poisoning.

OS Escherichia coli.

PN JP200325099-A.

PD 12-AUG-2003.

PF 04-FEB-2002; 2002JP-00027106.

PR 04-FEB-2002; 2002JP-00027106.

PA (NITTL ) NITTO DENKO CORP.

DR WPI; 2003-868855/81.

XX Detecting target DNA useful for determining contamination of the

PT foodstuff, by introducing test sample on absorptive base material

PT containing labeled RNA probe and measuring signal from labeled RNA probe.

PS Example 1; SEQ ID NO 1; 11pp; Japanese.

CC The invention relates to a novel method for detecting target DNA using a

CC labelled RNA probe. The method of the invention is useful for detecting

CC target DNA present in the sample, for determining contamination of

CC foodstuffs by pathogenic microbes, food poisoning, diagnosing condition

CC of disease and genotyping of an organism. The present sequence is used in

CC the exemplification of the invention.

SQ Sequence 24 BP; 12 A; 5 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 10; Length 24;

Best Local Similarity 88.2%; Pred. No. 6.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTTTCAGGGAATCCGG 17  
 |||||  
 DB 17 TTTTTCAGGGAATTCGG 1

# RESULT 10

ABK36270/C

ID ABK36270 standard; DNA; 57 BP.

AC ABK36270;

XX

DT 08-MAY-2002 (first entry)

XX HIV DNA encoding GAG segment 33.

DE

KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;

KW viral infection; human immunodeficiency virus; melanoma;

KW bacterial infection; Salmonella; Legionella; parasitic infection;

KW Trypanosoma; Toxoplasma; Giardia; de.

OS Human immunodeficiency virus 1.

PN WO200190197-A1.

PD 29-NOV-2001.

PF 25-MAY-2001; 2001WO-AU00622.

PR 26-MAY-2000; 2000AU-00007761.

PA (AUSU ) UNIV AUSTRALIAN NAT.

PI Thomson SA, Ramshaw IA;

DR WPI; 2002-147575/19.

DR P-RSD; AUA04431.

XX New synthetic polypeptides having several different segments of at least

PT one parent polypeptide linked together differently compared to the

PT linkage in the parent polypeptide, for inducing immune response against a

PT pathogen or cancer.

XX Example 1; Fig 12; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising

XX several different segments of at least one parent polypeptide linked

XX together in a different relationship relative to their linkage in the

XX parent polypeptide to impede, abrogate or otherwise alter at least one

XX function associated with the parent polypeptide and for inducing an

XX immune response against a pathogen or cancer. Also included are a

XX synthetic polynucleotide encoding and a computer system for designing the

XX synthetic polynucleotides. The synthetic polypeptides and polynucleotides

XX are referred to as a Savine. The synthetic polypeptide is useful for

XX modulating immune responses preferably directed against a pathogen or a

XX cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head

XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,

XX oesophagus, brain, testicle, uterus), as potentiating agents.

XX Compositions comprising the polypeptide may be used in the treatment or

XX prophylaxis against viral (such as infections caused by HIV (human

XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis

XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial

XX (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,

XX Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic

XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,

XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence

XX encodes a peptide derived from a parent protein used to construct a

XX Savine of the invention

SQ Sequence 57 BP; 13 A; 22 C; 6 G; 13 T; 0 U; 3 Other;

Query Match 69.0%; Score 13.8; DB 6; Length 57;

Best Local Similarity 78.9%; Pred. No. 6.6e+03;

Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTTTCAGGGAATCCGGGG 20  
 |||||  
 DB 28 TTTTCAGGGAAGCTTAGG 10

# RESULT 11

ADD94401/C

ID ADD94401 standard; DNA; 57 BP.

XX

AC	ADD944401,	
AD	29-JAN-2004 (first entry)	
DE	Mouse HUIV26 antibody mutagenic PCR primer SegID286.	
XX		
KW	granted antibody; complementarity determining region; CDR; light CDR;	
KW	heavy CDR; cryptic collagen epitope; solid tumour;	
KW	new blood vessel growth; angiogenesis; tumour growth; cytosstatic;	
KW	collagen agonist; collagen antagonist; cancer metastasis;	
XX	anti-cryptic collagen; PCR; primer; ss; mouse; murine; HUIV26; mutagenic.	
OS	Synthetic.	
OS	Mus musculus.	
PN	WO2003046204-A2.	
PN		
PD	05-JUN-2003.	
XX		
XX	26-NOV-2002; 2002WO-US038147.	
PF		
PR	26-NOV-2001; 2001US-00995529.	
PR	06-DEC-2001; 2001US-00011250.	
XX		
PA	(CELL-) CELL MATRIX INC.	
XX		
P1	Wacking JD, Huse WD, Tang Y, Broek D, Brooks PC;	
DR	WPI; 2003-513649/48.	
XX		
PT	New cryptic collagen antibody with one or more complementarity	
PT	determining regions, useful for diagnosing and treating disorders	
XX	associated with angiogenesis, tumor growth and/or cancer metastasis.	
XX		
PS	Example 2; SEQ ID NO 286; 232pp; English.	
CC		
CC	This invention relates to a novel grafted antibody or its functional	
CC	fragment comprising one or more complementarity determining regions	
CC	(CDRs) of a defined light CDR and a heavy CDR with at least one amino	
CC	acid (aa) substitution where the antibody has specific binding activity	
CC	for a cryptic collagen epitope. The growth of all solid tumours requires	
CC	new blood vessel growth, angiogenesis, inhibition of which is an approach	
CC	to limiting tumor growth. The invention may allow development of	
CC	therapeutics with a cytostatic activity as a collagen agonist or	
CC	antagonist. The invention is useful for diagnosing and treating disorders	
CC	associated with angiogenesis, tumor growth and/or cancer metastasis. The	
CC	present sequence is that of a mutagenic PCR primer which was used to	
CC	amplify a region of the sequence encoding the mouse HUIV26 antibody	
CC	during the exemplification of the invention.	
XX		
SQ	Sequence 57 BP; 13 A; 15 C; 16 G; 10 T; 0 U; 3 Other;	
	Query Match	69.0%; Score 13.8; DB 10; Length 57;
	Best Local Similarity	78.9%; Pred. No. 6, 6e+03;
	Matches 15; Conservative	0; Mismatches 4; Indels 0; Gaps 0
QY	1 TTTTTCAGGGAATCCGGG 19	
DB	33 TCTNNKAGGGAATCCGGG 15	
RESULT 12		
ID	ADM95446/C	
AC	ADM95446 standard; DNA; 80 BP.	
XX		
XX	ADM95446;	
DT	01-JUN-2004 (first entry)	
XX		
DE	Rat antisense oligonucleotide #339.	
XX		
KW	Rat; antisense oligonucleotide; ss; antisense RNA production; oncogenes;	
KW	tumour suppressor; cell cycle regulator; ion channel protein;	

KM	transport protein; intracellular signal transduction;
KM	transcription factor; DNA-binding protein; stress response gene;
KM	cell-cell communication protein; growth factor; chemokine; interleukin;
KM	apoptosis related gene; growth factor; chemokine; interleukin;
KW	interferon; hormone; neurotransmitter; cell surface antigen;
KX	cell adhesion molecule.
OS	Rattus sp.
XX	
PN	US2004072191-A1.
PD	15-APR-2004.
XX	
PF	07-MAR-2003; 2003US-00384245.
PR	07-MAR-2002; 2002US-0362823P.
PA	(CHEN)/ CHENCHIK A.
P1	Chenchik A;
DR	WPI; 2004-373913/35.
XX	
PT	New standardizing control for RNA samples to be tested on non-control
PT	gene sequences on nucleic acid arrays, useful for producing a population
PT	of distinct antisense RNA molecules from an initial population of
PT	distinct mRNA molecules.
XX	
PS	Disclosure; SEQ ID NO 339; 282zp; English.
XX	
CC	The invention relates to a standardising control for RNA samples to be
CC	tested on non-control gene sequences on nucleic acid arrays, comprising a
CC	pool of unique tagged synthetic antisense RNA molecules of a known
CC	concentration, where any two sequences are unique if their sequences
CC	differ. The non-control gene sequences on the nucleic acid array comprise
CC	oncogenes, genes encoding tumour suppressors, cell cycle regulators, ion
CC	channel proteins, transport proteins, intracellular signal transduction
CC	modulator and effector factors, transcription factors, DNA-binding
CC	proteins, receptors or cell-cell communication proteins, stress response
CC	genes, apoptosis related genes, DNA synthesis/recombination/repair genes
CC	and DNA-binding proteins. The genes encoding receptors comprise receptors
CC	for growth factors, chemokines, interleukins, interferons, hormones,
CC	neurotransmitters, cell surface antigens or cell adhesion molecules. The
CC	genes encoding cell-cell communication proteins comprise growth factors,
CC	cytokines, chemokines, interleukins, interferons or hormones. The
CC	standardising control for RNA samples to be tested on non-control gene
CC	sequences on nucleic acid arrays is useful for producing a population of
CC	distinct antisense RNA molecules from an initial population of distinct
CC	mRNA molecules. This sequence represents an antisense oligonucleotide of
CC	the invention.
XX	
SQ	Sequence 80 BP; 17 A; 29 C; 10 G; 24 T; 0 U; 0 Other;
Query Match	59.0%; Score 13.8; DB 12; Length 80;
Best Local Similarity	88.2%; Pred. No. 6.8e+03;
Matches 15; Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
OY	3 TTTCAGGGAATCGGGC 19       
Db	50 TTTCAGGGAATCGGGC 34
RESULT 13	
ID	ADM66724 standard; DNA; 33 BP.
AC	ADM66724;
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Primer 3 used to generate B. caldolyticus mutant TLP neutral protease.
KW	thermolysin-like protease; TLP; SI' site; gluten degradation; wheat;



KM baking industry; beer clarification; brewing; dehairing; skin dewooling;  
 KM leather; protein hydrolyzate production; artificial sweetener; aspartame;  
 KM PCR; primer; ss; neutral; mutant.  
 XX  
 XX Bacillus caldolyticus.  
 OS Synthetic.  
 XX  
 XX WO2004011619-A2.  
 PN  
 XX  
 PD 05-FEB-2004.  
 XX  
 XX 28-JUL-2003; 2003WO-US023726.  
 PF  
 XX  
 XX 26-JUL-2002; 2002US-0398656P.  
 PR  
 XX  
 XX (STRA-) STRATAGEME.  
 PA  
 XX  
 XX Clark DD, Bramean JC;  
 PI  
 XX  
 DR WPI; 2004-143847/14.  
 XX  
 XX  
 PT New thermolysin-like protease with substrate specificity for a basic or  
 PT an acidic amino acid, useful in biological and biomedical research,  
 PT identifying therapeutic agents and diagnostic markers, or producing  
 PT artificial sweeteners.  
 XX  
 XX Example 2; SEQ ID NO 16; 82pp; English.  
 PS  
 XX  
 XX The invention relates to a novel thermolysin-like protease (TLP)  
 CC comprising an S1' site and modified to have a substrate specificity for a  
 CC basic or an acidic amino acid. The thermolysin-like protease of the  
 CC invention may be useful in proteolysis applications, biological and  
 CC biomedical research, identifying therapeutic agents and diagnostic  
 CC markers, characterizing cells and organisms that have undergone genetic  
 CC modifications, identifying unknown illnesses, characterizing polypeptides  
 CC or identifying biological samples. The thermolysin-like protease may also  
 CC be useful in industrial processes, such as the degradation of gluten from  
 CC wheat within the baking industry, clarification of beer within the  
 CC brewing industry, dehairing or dewooling of skins within the leather  
 CC industry, preparation of protein hydrolyzates or production of artificial  
 CC sweeteners like aspartame. The current sequence is that of a PCR primer  
 CC of the invention which was used to generate Bacillus caldolyticus mutant  
 CC TLP neutral protease.  
 XX  
 XX  
 SQ Sequence 33 BP; 6 A; 9 C; 10 G; 8 T; 0 U; 0 Other;  
 Query Match 68.0%; Score 13.6; DB 12; Length 33;  
 Best Local Similarity 80.0%; Pred. No. 7.9e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 TTTTTCAGGGAATCCGGGG 20  
 |||||  
 Db 7 TTTTTCGCGAATCCGGCGG 26  
 |||||  
 RESULT 14  
 ABX94733  
 ID ABX94733 standard; DNA; 37 BP.  
 XX  
 XX  
 AC ABX94733;  
 XX  
 XX 07-JUL-2003 (first entry)  
 DT  
 XX  
 DE Negative control probe RAN 3.  
 XX  
 XX Probe; detection; EHEC; enterohaemorrhagic Escherichia coli; SLT1; SLT2;  
 KM rfbE; eaeA; KCMJ9; food testing; contamination; se.  
 XX  
 OS Unidentified.  
 XX  
 XX 30-NOV-1999; 99US-0168138P.  
 PR 29-NOV-2000; 2000US-00726173.  
 PN  
 XX  
 PD 06-FEB-2003.

XX  
 XX 26-JUL-2002; 2002WO-AT000222.  
 PF  
 XX  
 XX 26-JUL-2001; 2001AT-00001172.  
 PR  
 XX  
 XX (SYVE-) SY-LAB VERTRIEBS GMBH.  
 PA  
 XX  
 XX Vollenhofer-Schrumpf S, Schlinkinger M, Fraenzl G;  
 PI  
 XX  
 XX WPI; 2003-248085/24.  
 DR  
 XX  
 XX  
 PT Test kit for detecting enterohaemorrhagic Escherichia coli, useful for  
 PT testing foods, comprises primers, capture and detection probes for  
 PT specific genes.  
 XX  
 XX Claim 19; Page 35; 35pp; German.  
 PS  
 XX  
 XX This invention describes a novel test kit for detecting  
 CC enterohaemorrhagic Escherichia coli strains (EHEC). The kit comprises  
 CC primers for amplification of at least part of the SLT1, SLT2, rfbE and  
 CC eaeA genes and a control gene in a single reaction. It also includes  
 CC capture probes and detection probes for hybridisation to the amplicons at  
 CC room temperature. All capture probes are immobilised on the same solid  
 CC surface and detection probes are labeled with a visually detectable  
 CC label. The kit is used to test foods for contamination by EHEC. The kit  
 CC provides rapid, simple and reliable detection of EHEC in a single  
 CC reaction. No specialised apparatus is required (contrast use of  
 CC microarrays) and the method can be performed in routine laboratories. The  
 CC combination of capture probe and directly labeled probe provides high  
 CC specificity (typically 1-10 colony-forming units/25 g of food, after an  
 CC enrichment stage of only 8 hours) and purification of amplicons and  
 CC separation of unbound label are not required. This sequence represents a  
 CC probe used to detect an EHEC E. coli gene used in the product of the  
 CC invention  
 XX  
 XX  
 SQ Sequence 37 BP; 2 A; 9 C; 12 G; 14 T; 0 U; 0 Other;  
 Query Match 68.0%; Score 13.6; DB 8; Length 37;  
 Best Local Similarity 80.0%; Pred. No. 8e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 TTTTTCAGGGAATCCGGGG 20  
 |||||  
 Db 9 TTTTCCCGTATGTCGGGGG 28  
 |||||  
 RESULT 15  
 AAI76433  
 ID AAI76433 standard; DNA; 50 BP.  
 XX  
 XX  
 AC AAI76433;  
 XX  
 XX 09-NOV-2001 (first entry)  
 DT  
 XX  
 DE Human silent SNP containing nucleic acid SEQ.3374.  
 XX  
 XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
 KM protein therapy; vaccine; probe; diagnostic assay; detection;  
 KM quantitation; restorative therapy; polymorphic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200140521-A2.  
 FN  
 XX  
 XX 07-JUN-2001.  
 PD  
 XX  
 XX 30-NOV-2000; 2000WO-US032758.  
 PF  
 XX  
 XX 30-NOV-1999; 99US-0168138P.  
 PR 29-NOV-2000; 2000US-00726173.  
 PN  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and therapy.

PS Claim 1; Page 1083; 2653pp; English.

PS Claim 1; Page 1083; 2653pp; English.

CC AA173060-0 AA173867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53314 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

SQ Sequence 50 BP; 10 A; 12 C; 19 G; 9 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 4; Length 50;

Best Local Similarity 80.0%; Pred. No. 8.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

QY 1 TTTTTCAGGGAATCCGGGG 20

Db 4 TGTCTCGGGAGCCCGGGG 23

0  
1  
2  
3  
4  
5  
6  
7  
8  
9

```
Search completed: December 24, 2005, 12:28:56
Job time : 174.4 secs
```

Job time : 174.4 sec

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OM nucleic - nucleic search, using bw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds  
(without alignments)  
595.256 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20  
Sequence: 1 ttttcagggaatccggggg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	76.0	89	6	CB046782 NISC_gf06
2	14.8	74.0	71	1	AJ665651 AJ665651
3	14.8	74.0	79	1	AI925202 wmg9h04.x
4	14.8	74.0	96	8	F26680 HSPD14248.H
5	14.2	71.0	51	11	CR010521 Reverse
6	14.2	71.0	61	10	CG646119 OST391595
7	14.2	71.0	77	10	CG553405 OST165917
8	14.2	71.0	87	10	CG653617 OST19275
9	14	70.0	88	10	CG581950 OST222704
10	14	70.0	96	8	CX287425 C01009007
11	13.8	69.0	49	1	A1756242 EBSRta41
12	13.8	69.0	53	11	CR235685 Reverse
13	13.8	69.0	55	10	C2169440 P020C06.G
14	13.8	69.0	64	8	H41671 yoc6f01.81
15	13.8	69.0	66	9	B2353185 SALK.1198
16	13.8	69.0	73	10	CG648700 OST402480
17	13.8	69.0	73	10	CG658614 OST434889
18	13.8	69.0	90	10	CG650838 OST409692
19	13.6	68.0	33	10	AL945989 Arabidops
20	13.6	68.0	43	9	AZ346730 IM0082A11
21	13.6	68.0	67	1	A1799398 tws6a01.x
22	13.6	68.0	70	1	A1356377 qz21d04.x

23	13.6	68.0	75	10	BX890679 Arabidops
24	13.6	68.0	79	6	CD712552 VIB019C09
25	13.6	68.0	84	10	CZ907257 401106C0
26	13.6	68.0	85	1	AA854921 aJ78h10.s
27	13.6	68.0	88	5	C01948 HUMGS000395
28	13.6	68.0	89	5	B0585916 E012532-0
29	13.6	68.0	89	7	CV306463 Cj08f11.b
30	13.6	68.0	89	9	CC480457 CH240.307
31	13.6	68.0	90	1	AM102784 xD38a06.X
32	13.6	68.0	97	9	CC591487 CH240.391
33	13.6	68.0	100	2	BG672884 DRNAOH08
34	13.4	67.0	61	10	CG667953 OST462938
35	13.4	67.0	63	8	T68724 YC29d01.81
36	13.4	67.0	64	10	CG587635 OST3737428
37	13.4	67.0	65	10	CG588816 OST240242
38	13.4	67.0	67	10	CG587718 OST237588
39	13.4	67.0	69	10	CZ490302 F07553-5P
40	13.4	67.0	73	7	CR428430 CR428430
41	13.4	67.0	79	1	AA140294 mr83c12.r
42	13.4	67.0	82	10	CG574583 OST207590
43	13.2	66.0	50	1	AU107883 AU107883
44	13.2	66.0	58	10	CL423647 0150726-0
45	13.2	66.0	59	11	CR003993 Reverse s

#### ALIGNMENTS

RESULT 1  
CB046782  
LOCUS  
DEFINITION NISC\_gf06g08.x1 NCI CGAP\_Kid12 Homo sapiens CDNA clone  
IMAGE:3253047.3, mRNA sequence.  
ACCESSION CB046782  
VERSION CB046782.1 GI:27785069  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 89)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TUMOR Tumor  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
CDNA Library Preparation: CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)  
Plate: LLMW7960 row: M column: 16  
Seq primer: -21M13 forward primer (ABI).  
Location/Qualifiers  
1..89  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/feature="IMAGE:3253047"  
/clone\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Kid12"  
/note="Organ: kidney; Vector: pTZ19-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Plasmid DNA from the normalized library NCI CGAP Kids was  
prepared, and 98 circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subretractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library

ORIGIN (cloneIds 132912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bernaldo.

Query Match 76.0%; Score 15.2; DB 6; Length 89;  
Best Local Similarity 85.0%; Pred. No. 7.5e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGGAATCCGGGG 20  
|||||  
Db 27 TTTTTCAGGGAATCCGGGG 46

RESULT 2  
AJ665651 71 bp mRNA linear EST 28-JUN-2004  
LOCUS AJ665651 CSEORAN09 Sus scrofa cDNA clone C0000031\_P13, mRNA  
DEFINITION sequence.  
AJ665651  
VERSION AJ665651.1 GI:49350102  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 71)  
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII(+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.argenomics.org.

FEATURES  
source 1..71  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0000031\_P13"  
/issue\_type="placenta"  
/note="Vector: pBluescriptII(+) R. Site 1: EcoRI, Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

## ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 71;  
Best Local Similarity 88.9%; Pred. No. 1.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGGAATCCGGGG 18  
|||||  
Db 71 TTTTTCAGGGAATCCGGGG 54

RESULT 3  
AI925202 79 bp mRNA linear EST 07-MAR-2000  
LOCUS AI925202 wmg99H04.X1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2444119 3'  
DEFINITION similar to SW:BAT2\_HUMAN P48634 LARGE PROLINE-RICH PROTEIN BAT2 ;,  
mRNA sequence.  
AI925202  
ACCESSION AI925202.1 GI:5661166  
VERSION

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1 (bases 1 to 79)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at:  
www-bio.llnl.gov/bbrp/image/image.html

FEATURES  
source Trace considered overall poor quality  
Insert Length: 768 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
location/Qualifiers  
1..79  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2444119"  
/issue\_type="moderately-differentiated endometrial adenocarcinoma 3 pooled tumors"  
/ad\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Ut2"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

## ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 79;  
Best Local Similarity 88.9%; Pred. No. 1.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTTTCAGGGAATCCGGGG 20  
|||||  
Db 10 TTTTCAGGGAATCCGGGG 27

## ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 79;  
Best Local Similarity 88.9%; Pred. No. 1.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTTTCAGGGAATCCGGGG 20  
|||||  
Db 10 TTTTCAGGGAATCCGGGG 27

RESULT 4  
F26680 96 bp mRNA linear EST 13-MAY-1999  
LOCUS HSPD14248 HM3 Homo sapiens cDNA clone s4000058G04, mRNA sequence.  
DEFINITION F26680  
VERSION F26680.1 GI:4812306  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 96)  
Lanitranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.  
Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization  
Genome Res. 6 (1), 35-42 (1996)  
8681137  
Contact: Valle G.  
CIRIBI Biotechnology Centre

University of Padua  
Via Trieste 75, 35121 Padua, Italy  
ABI Chromatograms and other information are available on WWW at  
<http://9rup.bio.unipd.it>.  
Location/Qualifiers

## FEATURES

source

1..96  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="s400058G04"  
/sex="female"  
/cisse\_type="pectoral muscle (after mastectomy)"  
/clone\_lib="HM3"  
/note="Vector: pCDNA1 (Invitrogen); Site 1: BstXI;  
Site 2: NotI; The library was constructed by G.  
Lanfanchi. This library is not subcloned nor normalized.  
The first strand cDNA was primed with a biotinylated  
oligo-dT-NotI primer  
(5'-biotin-AACCGGCTCGAGCGCGCTTTTCTTTTCTTTT-3'). The  
ds cDNA was sonicated and size-selected in the range  
350-550 bp. The 3' specific fragments were selected by  
streptavidin coated magnetic beads, ligated to  
non-palindromic BstXI adapters, NotI digested and  
directionally cloned into BstXI-NotI cut pCDNA1 vector."

## ORIGIN

Query Match 74.0%; Score 14.8; DB 8; Length 96;  
Best Local Similarity 88.9%; Pred. No. 1.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCGGG 19  
|||||  
Db 79 TTTTCAGGGAATCCGGG 96

## RESULT 5

CR010521/c

LOCUS

CR010521 51 bp DNA linear GSS 05-JUL-2004  
Reverse strand read from insert in 5'HPRT insertion targeting and  
chromosome engineering clone MHPN125K14, genomic survey sequence.

ACCESSION

CR010521

VERSION

CR010521.1

KEYWORDS

GSS; genome survey sequence; MICR.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurionathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 51)

Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,

Jonkers,J., Smith,J., Plum,R.W., Taylor,R.G., Nienhijma,I., Yu,Y.,

Rogers,J. and Bradley,A.

Direct Submission

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>

JOURNAL

FEATURES

source

1..51  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN125K14"  
/clone\_lib="MHPN"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 11; Length 51;  
Best Local Similarity 84.2%; Pred. No. 2.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGGG 19  
|||||  
Db 20 TTTTCAGGGAATCCGGG 2

## RESULT 6

CG646119

LOCUS

CG646119 61 bp mRNA linear GSS 02-OCT-2003  
OST391595 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST391595,  
mRNA sequence.

ACCESSION

CG646119

VERSION

CG646119.1

KEYWORDS

GSS; genome survey sequence

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurionathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 61)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

Piggott,J., Beltranderio,H., Buxton,E.C., Edwards,J., Finch,R.A.,

Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jang,C.,

Key,B.W., Jr., Kipp,P., Konhauff,B., Ma,Z.-Q., Markesich,D.,

Payne,R., Porter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,

Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,

Zhu,Q., Person,C. and Sands,A.T.

Mx1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

14610273

COMMENT

Contact: Zambrowicz BP

Omnibank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: [materials@lexgen.com](mailto:materials@lexgen.com)Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene trap.

Location/Qualifiers

1..61  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST391595"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

FEATURES

source

Query Match 71.0%; Score 14.2; DB 10; Length 61;  
Best Local Similarity 80.0%; Pred. No. 2.4e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

## ORIGIN

Qy 1 TTTTCAGGGAATCCGGG 20  
|||||  
Db 1 TTTTCAGGGAATCCGGG 20

## RESULT 7

CG553405/c

LOCUS

CG553405 77 bp mRNA linear GSS 01-OCT-2003  
OST165917 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST165917,  
mRNA sequence.

ACCESSION

CG553405

VERSION

CG553405.1

KEYWORDS

GSS; genome survey sequence

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurionathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 77)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

Piggott,J., Beltranderio,H., Buxton,E.C., Edwards,J., Finch,R.A.,

Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jang,C.,

Key,B.W., Jr., Kipp,P., Konhauff,B., Ma,Z.-Q., Markesich,D.,

Payne,R., Porter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,

Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,

TITLE  
Zhu,Q., Person,C. and Sands,A.T.  
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
PUBMED  
14610273  
COMMENT  
Contact: Zambrowicz BP  
Omnibank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Classes: Gene Trap.

FEATURES  
source  
1..77  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST165917"  
/cell\_type="embryonic stem cell"  
/clone\_1fb="Mus musculus 129Sv/Ev"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 10; Length 77;  
Best Local Similarity 80.0%; Pred. No. 2.4e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGGAATCCGGGG 20  
|||||  
49 TGTTCAGGAGANTCTCGGG 30

RESULT 8  
CG653617 87 bp mRNA linear GSS 02-OCT-2003  
LOCUS OST19275 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST19275,  
DEFINITION mRNA sequence.  
ACCESSION CG653617  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 87)  
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
Piggott,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-O., Markesich,D.,  
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
Zhu,Q., Person,C. and Sands,A.T.  
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
PUBMED  
14610273  
COMMENT  
Contact: Zambrowicz BP  
Omnibank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Classes: Gene Trap.

FEATURES  
source  
1..87  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST19275"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 10; Length 87;  
Best Local Similarity 84.2%; Pred. No. 2.5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGGAATCCGGG 19  
|||||  
23 TTTTTCAGGGAATCCGGG 41

RESULT 9  
CG581950 88 bp mRNA linear GSS 02-OCT-2003  
LOCUS OST222704 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST222704,  
DEFINITION mRNA sequence.  
ACCESSION CG581950  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 88)  
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
Piggott,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-O., Markesich,D.,  
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
Zhu,Q., Person,C. and Sands,A.T.  
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
PUBMED  
14610273  
COMMENT  
Contact: Zambrowicz BP  
Omnibank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Classes: Gene Trap.

FEATURES  
source  
1..88  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST222704"  
/cell\_type="embryonic stem cell"  
/clone\_1fb="Mus musculus 129Sv/Ev"

ORIGIN  
Query Match 70.0%; Score 14; DB 10; Length 88;  
Best Local Similarity 93.3%; Pred. No. 3.1e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTTTCAGGGAATCCGGG 18  
|||||  
48 TTTTCAGGGAATCCGGG 62

RESULT 10  
CX287425 96 bp mRNA linear EST 06-MAY-2005  
LOCUS CX287425  
DEFINITION C01009D07SK Veg1 Citrus clementina cDNA clone C01009D07, mRNA  
sequence.  
ACCESSION CX287425  
VERSION CX287425.1 GI:63056124

**KEYWORDS**  
**SOURCE** EST.  
**ORGANISM** Citrus clementina

**REFERENCE**  
**AUTHORS** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Sapindales; Rutaceae; Citrus.  
 1 (bases 1 to 96)  
 Forment, J., Gadea, J., Huerta, L., Abizanda, L., Agustí, J., Alamar, S., Aloe, E., Andres, F., Arribas, R., Beltrán, J.P., Berbel, A., Blazquez, M.A., Brumos, J., Canas, L.A., Cercos, M., Colmenero-Flores, J.M., Conesa, A., Estabes, B., Gandia, M., Garcia-Martinez, J.L., Gimeno, J., Gisbert, A., Gomez, G., Gonzalez-Candelas, L., Granell, A., Guerri, J., Lafuente, M.T., Madueno, F., Marcos, J.F., Marques, M.C., Martinez, F., Martinez-Godoy, M.A., Miralles, S., Moreno, P., Navarro, L., Pallas, V., Perez-Amador, M.A., Perez-Valle, J., Pons, C., Rodrigo, I., Rodriguez, P.L., Royo, C., Serrano, R., Soler, G., Tadeo, F., Talon, M., Terol, J., Trenor, M., Vaello, L., Vicente, O., Vidal, Ch., Zacarias, L. and Conejero, V.  
 Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies  
 Plant Mol. Biol. 57 (3), 375-391 (2005)  
 15830128

**COMMENT**  
 Contact: Forment J  
 Genomics Laboratory  
 Instituto de Biologia Molecular y Celular de Plantas (Universidad Politecnica de Valencia - Consejo Superior de Investigaciones Cientificas)  
 Avenida de los Naranjos s/n, 46022 Valencia, Spain  
 Email: jforment@bmcp.upv.es.  
 Location/Qualifiers

**FEATURES**  
 source  
 1..96  
 /organism="Citrus clementina"  
 /mol\_type="mRNA"  
 /cultivar="Clemenules"  
 /db\_xref="taxon:85681"  
 /clone="C0109007"  
 /sex="hermaphrodite"  
 /dev\_stage="adult trees"  
 /lab\_host="Escherichia coli"  
 /clone\_lib="Veg1"  
 /note="Organ: leaves, shoots and internodes; Vector: lambda-zap II; cDNA library made from a mixture of equal amounts of poly-A+ RNA from vegetative developing shoots of plants treated with G43 or with paclobutrazol, and leaves and internodes of untreated plants"

**ORIGIN**  
 Query Match 70.0%; Score 14; DB 8; Length 96;  
 Beet Local Similarity 100.0%; Pred. No. 3.2e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
 2 TTTTCAGGGAATCC 15  
 |||||  
 14 TTTTCAGGGAATCC 27

**DB**  
 14 TTTTCAGGGAATCC 27

**RESULT 11**  
 A1756242 49 bp mRNA linear EST 18-JAN-2000  
 LOCUS E185441.1.v1 Eimeria S5-2 Sporozoite stage Eimeria tenella cDNA  
 DEFINITION 5' similar to SW-U2AG\_HUMAN Q01081 SPLICING FACTOR U2AF 35 KD  
 SUBUNIT; mRNA sequence.  
 A1756242  
 A1756242 GI:5149965

**ACCESSION**  
 A1756242  
 A1756242 GI:5149965

**VERSION**  
 A1756242.1 GI:5149965

**KEYWORDS**  
 EST.

**SOURCE**  
 Eimeria tenella

**ORGANISM**  
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae; Eimeria.

**REFERENCE**  
 1 (bases 1 to 49)  
 Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Stepec, M., Theising, B.,

**TITLE**  
**JOURNAL** Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurr, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R., Wilson, R. and Sibley, D.  
 WashU-Merck Eimeria tenella project  
 Unpublished (1999)  
**COMMENT**  
 Contact: David Sibley, Ph.D.  
 Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 Contact David Sibley (rooseborcim.wustl.edu) for further information relating to organism, libraries, or clone availability.  
 Possible reversed clone: Similarly on wrong strand  
 Seq primer: -40RP from Glbco  
 High quality sequence stop: 1.  
 Location/Qualifiers

**FEATURES**  
 source  
 1..49  
 /organism="Eimeria tenella"  
 /mol\_type="mRNA"  
 /strain="LS18"  
 /db\_xref="taxon:5802"  
 /dev\_stage="Sporozoite"  
 /lab\_host="SOIR E. coli"  
 /clone\_lib="Eimeria S5-2 Sporozoite stage"  
 /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Sporozoites were obtained from in vitro sporulated and excysted oocysts of E. tenella grown in chickens. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size-selected on Sephacryl S500. cDNAs were digested with EcoRI/XhoI and cloned into lambda Zap II (Stratagene). Clones were converted to phagemids by mass excision using Exaseist helper phage and SOUR cells (Stratagene). Insert sizes range from 1.2-2.9 kb."

**ORIGIN**  
 Query Match 69.0%; Score 13.8; DB 1; Length 49;  
 Beet Local Similarity 88.2%; Pred. No. 3.8e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY**  
 3 TTTTCAGGGAATCCGCG 19  
 |||||  
 15 TTTTCAGGGAATCCGCG 31

**DB**  
 15 TTTTCAGGGAATCCGCG 31

**RESULT 12**  
 CR235685 53 bp DNA linear GSS 06-JUN-2004  
 LOCUS CR235685/c  
 DEFINITION Reverse strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN203d10, genomic survey sequence.  
 CR235685  
 CR235685 GI:50014534

**ACCESSION**  
 CR235685.1 GI:50014534

**KEYWORDS**  
 GSS; genome survey sequence; MICR.

**SOURCE**  
 Mus musculus  
 Mus musculus (house mouse)

**ORGANISM**  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

**REFERENCE**  
 1 (bases 1 to 53)  
 Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.  
 Direct Submission  
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICR

**TITLE**  
**JOURNAL**

**FEATURES**  
 source  
 1..53  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"

ORIGIN

Query Match 69.0%; Score 13.8; DB 11; Length 53;  
Best Local Similarity 88.2%; Pred. No. 3.8e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTCAGGGAAATCCGGCG 19  
|||||  
18 TTTCAGGGAAATCCGGCG 2

Db

RESULT 13  
CZ169440  
LOCUS CZ169440 55 bp mRNA linear GSS 22-MAR-2005  
DEFINITION P020C06 GGTTC Gene Trap Library GV08C05 Mus musculus cDNA clone  
ACCESSION P020C06, mRNA sequence.  
CZ169440  
VERSION CZ169440.2 GI:61684171  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 55)  
Hansen, J., Flores, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,  
Arnold, H.H., Schuttgen, F., Wurst, W., Von Melchner, H., and Ruiz, P.  
A large-scale, gene-driven mutagenesis approach for the functional  
analysis of the mouse genome  
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
12904583  
JOURNAL PUMED  
PUBMED On Mar 22, 2005 this sequence version replaced gi:58224038.  
COMMENT Contact: GGTTC  
German Genetrap Consortium (GGTC)  
Email: info@genetrap.de  
FliPROSbetageo gene trap. Sequence tag generated by 5'RACE.  
Additional sequence information can be found at:  
'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=P020C06'. ES cell line harboring insertion mutation of  
target gene is available at:  
'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'  
1' Inhouse Sequence Identifier: 20257  
Class: Gene Trap.  
Location/Qualifiers  
1. .55  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Sv"  
/db\_xref="taxon:10090"  
/clone="P020C06"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
/clone\_lib="GGTTC Gene Trap Library GV08C05"  
/note="Vector: FliPROSbetageo"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 55;  
Best Local Similarity 88.2%; Pred. No. 3.8e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTTCAGGGAAATCCGGCG 20  
|||||  
22 TTTCAGGGAAATCCGGCG 38

Db

RESULT 14  
H41671 64 bp mRNA linear EST 31-JUL-1995  
LOCUS H41671  
DEFINITION Y006F01.s1 Soares adult brain N2bSHB55Y Homo sapiens cDNA clone

IMAGE:177145 3' similar to SP:RS9\_RAT P29314 40S RIBOSOMAL PROTEIN  
; mRNA sequence.  
H41671  
VERSION H41671.1 GI:9177723  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 64)  
Hillier, L., Clark, N., Dubague, T., Ellstrom, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlffing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterson, R., Williamson, A., Wohldmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1652  
Insert quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LNL.  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Insert length: 1652 Std Error: 0.00  
Seq primer: Promega -21m13  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .64  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3839341"  
/db\_xref="taxon:9606"  
/clone="IMAGE:177145"  
/sex="Male"  
/dev\_stage="55-Year old"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares adult brain N2bSHB55Y"  
/note="Organ: Brain; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer (5'  
TGTTACCAATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'),  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 53. Library constructed by Bento  
Soares and M.Fatima Bonaldo. The adult brain RNA was  
provided by Dr. Donald H. Gilden. Tissue was acquired  
17-18 hours after death which occurred in consequence of a  
ruptured aortic aneurysm. RNA was prepared from a pool of  
tissues representing the following areas of the brain:  
frontal, parietal, temporal and occipital cortex from the  
left and right hemispheres, subcortical white matter,  
basal ganglia, thalamus, cerebellum, midbrain, pons and  
medulla."

ORIGIN

Query Match 69.0%; Score 13.8; DB 8; Length 64;  
Best Local Similarity 88.2%; Pred. No. 3.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTTCAGGGAAATCCGGCG 20  
|||||  
6 TTTCAGGGAAATCCAGGG 22

Db



RESULT 15  
B2353185/c

LOCUS B2353185 66 bp DNA linear GSS 14-NOV-2002  
 DEFINITION SALK\_119899.28.80.x Arabidopsis thaliana TDNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_119899.28.80.x, genomic  
 survey sequence.

ACCESSION B2353185  
 VERSION B2353185  
 KEYWORDS GI:24944047

SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 66)  
 Alonso, J.M., Leisbe, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 Shin, P., Zimmerman, J., and Ecker, J.R.  
 A Sequence-indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 CONTACT: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu

TITLE Arabidopsis thaliana TDNA insertion lines  
 JOURNAL Arabidopsis thaliana TDNA insertion lines  
 COMMENT This is single pass sequence recovered from the left border of  
 TDNA. This sequence lies within an annotated exon of At2g28150.  
 Class: TDNA tagged.

FEATURES  
 source Location/Qualifiers

1..66  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_119899.28.80.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 66;  
 Best Local Similarity 88.2%; Pred.No. 3.9e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTTCAGGCAATCCG 17  
 |||||  
 Db 38 TTTTCAGGCAATCCG 22

Search completed: December 24, 2005, 18:28:29  
 Job time : 1582 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds  
(without alignments)  
739.111 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20  
Sequence: 1 ttttcagggaatccggg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	74.0	25	3	US-09-396-196G-54618
2	13.6	68.0	25	3	US-09-396-196G-86875
3	13.6	68.0	73	3	US-09-270-767-25527
4	13.4	67.0	21	2	US-08-741-881-9
5	13.4	67.0	21	2	US-08-741-881-10
6	13.4	67.0	21	2	US-08-739-158-9
7	13.4	67.0	21	2	US-08-739-158-10
8	13.4	67.0	21	2	US-08-739-167-9
9	13.4	67.0	21	2	US-08-739-167-10
10	13.4	67.0	21	3	US-08-404-796-9
11	13.4	67.0	21	3	US-08-404-796-10
12	13.4	67.0	21	3	US-08-931-869-9
13	13.4	67.0	21	3	US-08-931-869-10
14	13.4	67.0	21	3	US-09-350-399-9
15	13.4	67.0	21	3	US-09-350-399-10
16	13.4	67.0	21	3	US-09-236-140A-9
17	13.4	67.0	21	3	US-09-236-140A-10
18	13.4	67.0	21	3	US-09-415-784-17
19	13.4	67.0	21	3	US-09-415-784-18
20	13.4	67.0	21	3	US-09-415-785A-17
21	13.4	67.0	21	3	US-09-415-785A-18
22	13.4	67.0	21	3	US-08-944-465-17
23	13.4	67.0	21	3	US-08-944-465-18
24	13.4	67.0	21	3	US-09-415-868-17

c	25	13.4	67.0	21	3	US-09-415-868-18	Sequence 18, Appl
c	26	13.4	67.0	21	3	US-09-415-900-17	Sequence 17, Appl
c	27	13.4	67.0	21	3	US-09-415-900-18	Sequence 18, Appl
c	28	13.4	67.0	21	3	US-09-507-362-17	Sequence 17, Appl
c	29	13.4	67.0	21	3	US-09-507-362-18	Sequence 18, Appl
c	30	13.2	66.0	25	3	US-09-396-196G-49693	Sequence 49693, A
c	31	13.2	66.0	36	2	US-08-486-969-47	Sequence 47, Appl
c	32	13.2	66.0	36	3	US-09-403-752A-14	Sequence 14, Appl
c	33	13.2	66.0	36	3	US-09-622-951-21	Sequence 21, Appl
c	34	13.2	66.0	36	3	US-09-551-151A-14	Sequence 14, Appl
c	35	13.2	66.0	50	3	US-10-131-827-7280	Sequence 7280, Ap
c	36	13	65.0	25	3	US-09-396-196G-54629	Sequence 54629, A
c	37	13	65.0	47	3	US-09-422-978-3512	Sequence 3512, Ap
c	38	12.8	64.0	22	3	US-09-462-606-47	Sequence 47, Appl
c	39	12.8	64.0	25	3	US-09-661-596A-70	Sequence 70, Appl
c	40	12.8	64.0	25	3	US-09-396-196G-48432	Sequence 48432, A
c	41	12.8	64.0	25	3	US-10-288-823-70	Sequence 70, Appl
c	42	12.8	64.0	50	3	US-10-131-827-1528	Sequence 1528, Ap
c	43	12.8	64.0	81	3	US-09-270-767-2645	Sequence 2645, Ap
c	44	12.8	64.0	81	3	US-09-270-767-17927	Sequence 17927, A
c	45	12.6	63.0	23	3	US-09-303-040-40	Sequence 40, Appl

## ALIGNMENTS

RESULT 1  
US-09-396-196G-54618/c  
Sequence 54618, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 54618  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-54618  
Query Match 74.0%; Score 14.8; DB 3; Length 25;  
Best Local Similarity 88.9%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 18 TTTTCAGGGAATCCGGG 18  
18 TTTTCAGGGAATCGGG 1  
RESULT 2  
US-09-396-196G-86875  
Sequence 86875, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 86875  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-86875

Query Match 68.0%; Score 13.6; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGGGG 20  
Db 1 TTTTCAGGGAATCCATGG 20

RESULT 3  
US-09-270-767-25527/c

Sequence 25527, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 25527  
LENGTH: 73  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-25527

Query Match 68.0%; Score 13.6; DB 3; Length 73;  
Best Local Similarity 80.0%; Pred. No. 1.9e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGGGG 20  
Db 39 TGTTCAGGGAATCCGGTGG 20

RESULT 4  
US-08-741-881-9

Sequence 9, Application US/08741881  
Patent No. 5789245  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/741,881  
FILING DATE: 30-OCT-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-741-881-9

Query Match 67.0%; Score 13.4; DB 2; Length 21;  
Best Local Similarity 93.3%; Pred. No. 2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCG 16  
Db 3 TTTTCAGGGAATCCG 17

RESULT 5  
US-08-741-881-10/c

Sequence 10, Application US/08741881  
Patent No. 5789245  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/741,881  
FILING DATE: 30-OCT-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-741-881-10

Query Match 67.0%; Score 13.4; DB 2; Length 21;  
Best Local Similarity 93.3%; Pred. No. 2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTTTCAGGGAATCCG 16  
|||||  
Db 19 TTTTCAGGGAATCCG 5

## RESULT 6

US-08-739-158-9  
Sequence 9, Application US/08739158  
Patent No. 5814482  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/739,158  
FILING DATE: 30-OCT-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-739-158-9  
Query Match 67.0%; Score 13.4; DB 2; Length 21;  
Best Local Similarity 93.3%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 2 TTTTCAGGGAATCCG 16  
|||||  
Db 3 TTTTCAGGGAATCCG 17

## RESULT 7

US-08-739-158-10/c  
Sequence 10, Application US/08739158  
Patent No. 5814482  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/739,158

FILING DATE: 30-OCT-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: McMaisters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-739-158-10

## Query Match

67.0%; Score 13.4; DB 2; Length 21;

Best Local Similarity 93.3%; Pred. No. 2e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTTTCAGGGAATCCG 16

|||||

Db 19 TTTTCAGGGAATCCG 5

## RESULT 8

US-08-739-167-9  
Sequence 9, Application US/08739167  
Patent No. 5843723  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/739,167  
FILING DATE: 30-OCT-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-739-167-9

Query Match 67.0%; Score 13.4; DB 2; Length 21;  
Best Local Similarity 93.3%; Pred. No. 2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCG 16  
|||||  
Db 3 TTTTCAGGGAATCCG 17

RESULT 9  
US-08-739-167-10/c  
Sequence 10, Application US/08739167  
Patent No. 5843723

GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/739,167  
FILING DATE: 30-OCT-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaesters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-739-167-10

Query Match 67.0%; Score 13.4; DB 2; Length 21;  
Best Local Similarity 93.3%; Pred. No. 2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCG 16  
|||||  
Db 19 TTTTCAGGGAATCCG 5

RESULT 10  
US-08-404-796-9  
Sequence 9, Application US/08404796

Patent No. 6015686

GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/404,796  
FILING DATE: 15-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaesters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-404-796-9

Query Match 67.0%; Score 13.4; DB 3; Length 21;  
Best Local Similarity 93.3%; Pred. No. 2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCG 16  
|||||  
Db 3 TTTTCAGGGAATCCG 17

RESULT 11  
US-08-404-796-10/c  
Sequence 10, Application US/08404796  
Patent No. 6015686

GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/404,796  
FILING DATE: 15-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-404-796-10

Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 3; Length 21;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCG 16  
Db 19 TTTTCAGGGAATCCG 5

RESULT 12  
US-08-931-869-9  
Sequence 9, Application US/08931869  
Patent No. 6015694  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,869  
FILING DATE: 16-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/404,796  
FILING DATE: 15-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-931-869-9

Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 3; Length 21;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCG 16  
Db 3 TTTTCAGGGAATCCG 17

RESULT 13  
US-08-931-869-10/c  
Sequence 10, Application US/08931869  
Patent No. 6015694  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,869  
FILING DATE: 16-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/404,796  
FILING DATE: 15-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-931-869-10

Query Match  
Best Local Similarity 93.3%; Score 13.4; DB 3; Length 21;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCG 16  
Db 19 TTTTCAGGGAATCCG 5

RESULT 14  
US-09-350-399-9  
Sequence 9, Application US/09350399  
Patent No. 6342372  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
Jolly, Douglas J.  
Driver, David A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESS: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,399  
FILING DATE: 08-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-350-399-9  
Query Match 67.0%; Score 13.4; DB 3; Length 21;  
Best Local Similarity 93.3%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 TTTTCAGGGGAAATCCG 16  
Db 3 TTTTCAGGGGAAATCCG 17  
RESULT 15  
US-09-350-399-10/c  
Sequence 10, Application US/09350399  
Patent No. 6342372  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
Jolly, Douglas J.  
Driver, David A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESS: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,399  
FILING DATE: 08-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-350-399-10  
Query Match 67.0%; Score 13.4; DB 3; Length 21;  
Best Local Similarity 93.3%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 TTTTCAGGGGAAATCCG 16  
Db 19 TTTTCAGGGGAAATCCG 5

Search completed: December 24, 2005, 18:36:28  
Job time : 49.1 secs



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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20

Sequence: 1 ttttcagggaatccggggg 20

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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA Main:  
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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	15.8	79.0	25	9	US-10-956-157-293978
3	15.8	79.0	25	10	US-11-036-317-44538
4	14.8	79.0	25	9	US-10-809-189-54618
5	14.4	72.0	25	10	US-11-036-317-425139
6	14.4	72.0	25	10	US-11-036-317-608322
7	14.2	71.0	25	7	US-10-719-956-341263
8	14.2	71.0	51	6	US-10-321-785-20
9	14.2	71.0	57	3	US-09-995-529-283
10	14.2	71.0	57	3	US-09-995-529-284
11	14.2	71.0	57	3	US-09-995-529-283
12	14.2	71.0	57	3	US-09-995-529-284
13	14.2	71.0	57	3	US-09-995-529-283
14	14.2	71.0	57	3	US-09-995-529-284
15	14.2	71.0	57	3	US-09-995-529-283
16	14.2	71.0	57	3	US-09-995-529-284
17	13.8	69.0	25	8	US-10-719-900-795020
18	13.8	69.0	25	8	US-10-719-900-795020
19	13.8	69.0	25	8	US-10-719-900-795020
20	13.8	69.0	25	8	US-10-719-900-795020
21	13.8	69.0	25	8	US-10-719-900-795020
22	13.8	69.0	25	8	US-10-719-900-795020
23	13.8	69.0	25	8	US-10-719-900-795020

c 24	13.6	68.0	25	7	US-10-719-956-25043	Sequence 25043, A
c 25	13.6	68.0	25	7	US-10-719-956-321181	Sequence 321181, A
c 26	13.6	68.0	25	7	US-10-719-956-681900	Sequence 681900, A
c 27	13.6	68.0	25	7	US-10-719-956-680268	Sequence 680268, A
c 28	13.6	68.0	25	8	US-10-719-900-259080	Sequence 259080, A
c 29	13.6	68.0	25	8	US-10-719-900-980929	Sequence 980929, A
c 30	13.6	68.0	25	8	US-10-719-900-981979	Sequence 981979, A
c 31	13.6	68.0	25	9	US-10-809-189-68875	Sequence 68875, A
c 32	13.6	68.0	25	10	US-11-036-317-759092	Sequence 759092, A
c 33	13.6	68.0	45	9	US-10-973-783-204	Sequence 204, App
c 34	13.6	68.0	65	3	US-09-908-975-29087	Sequence 29087, A
c 35	13.6	68.0	88	6	US-10-029-386-17390	Sequence 17390, A
c 36	13.4	67.0	21	3	US-09-507-362-17	Sequence 17, App1
c 37	13.4	67.0	21	3	US-09-507-362-18	Sequence 18, App1
c 38	13.4	67.0	21	6	US-10-346-880-9	Sequence 9, App1
c 39	13.4	67.0	21	6	US-10-346-880-10	Sequence 10, App1
c 40	13.4	67.0	21	6	US-10-391-441-17	Sequence 17, App1
c 41	13.4	67.0	21	6	US-10-391-441-18	Sequence 18, App1
c 42	13.4	67.0	21	7	US-10-150-407-9	Sequence 9, App1
c 43	13.4	67.0	25	5	US-10-150-407-10	Sequence 10, App1
c 44	13.4	67.0	25	5	US-10-215-112-2573	Sequence 2573, App
c 45	13.4	67.0	25	7	US-10-719-956-585686	Sequence 585686, A

#### ALIGNMENTS

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RESULT 1
US-09-296-264-5
; Sequence 5, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: NEUROPILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
; US-09-296-264-5

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTTTCAGGGAATCCGGGGG 20
Db 1 TTTTCAGGGAATCCGGGGG 20

RESULT 2
US-10-956-157-293978
; Sequence 293978, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (Am 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 31805
; SOFTWARE: PatentIn version 3.2
```

SEQ ID NO 293978  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Probe Sequence  
US-10-956-157-293978

Query Match 79.0%; Score 15.8; DB 9; Length 25;  
Best Local Similarity 89.5%; Pred. No. 5.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGG 19  
|||||  
DB 7 TTTTTCAGGGAATCCAGG 25

RESULT 3  
US-11-036-317-44538/c  
Sequence 44538, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 44538  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-44538

Query Match 79.0%; Score 15.8; DB 10; Length 25;  
Best Local Similarity 89.5%; Pred. No. 5.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGG 19  
|||||  
DB 22 TTTTCAGGGAATCCGGT 4

RESULT 4  
US-10-809-189-54618/c  
Sequence 54618, Application US/10809189  
Publication No. US20050048531A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 54618  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-809-189-54618

Query Match 74.0%; Score 14.8; DB 9; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGG 18  
|||||  
DB 18 TTTTCAGGGAATCGG 1

RESULT 5  
US-11-036-317-425139/c  
Sequence 425139, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 425139  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-425139

Query Match 72.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 2.8e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCG 16  
|||||  
DB 16 TTTTCAGGGAATCCG 1

RESULT 6  
US-11-036-317-608322/c  
Sequence 608322, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 608322  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-608322

Query Match 72.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 2.8e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCG 16  
|||||  
DB 16 TTTTCAGGGAATCCG 1

RESULT 7  
US-10-719-956-341263/c  
Sequence 341263, Application US/10719956  
Publication No. US20040146910A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat

```
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 341263
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-341263

Query Match      71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 TTTTCAGGGAATCCGGGG 20
        |||||
Db      22 TTTTCAGGACTCATGGG 4

RESULT 8
US-10-321-785-20/c
; Sequence 20, Application US/10321785
; Publication No. US20030211964A1
; GENERAL INFORMATION:
; APPLICANT: Bertam J. Jacobs
; TITLE OF INVENTION: METHOD OF INHIBITING PATHOGENICITY OF
; FILE REFERENCE: 0050 2037-001
; CURRENT APPLICATION NUMBER: US/10/321,785
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/343,028
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer used to amplify Z-DLM nucleic acid molecule
US-10-321-785-20

Query Match      71.0%; Score 14.2; DB 6; Length 51;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 TTTTCAGGGAATCCGGGG 20
        |||||
Db      31 TTTTCAGGAGCCCGGGG 13

RESULT 9
US-09-995-529-283/c
; Sequence 283, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 57
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: 38, 39
; OTHER INFORMATION: n = A,T,C or G
US-09-995-529-283

Query Match      71.0%; Score 14.2; DB 3; Length 57;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 TTTTCAGGGAATCCGGG 19
        |||||
Db      33 TCTACAGGGAATCCGGG 15

RESULT 10
US-09-995-529-284/c
; Sequence 284, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: 35, 36
; OTHER INFORMATION: n = A,T,C or G
US-09-995-529-284

Query Match      71.0%; Score 14.2; DB 3; Length 57;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 TTTTCAGGGAATCCGGG 19
        |||||
Db      33 TCTACAGGGAATCCGGG 15

RESULT 11
US-09-995-529-283/c
; Sequence 283, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
```

NAME/KEY: misc feature  
LOCATION: 38, 39  
OTHER INFORMATION: n = A,T,C or G  
US-09-995-529-283

Query Match 71.0%; Score 14.2; DB 3; Length 57;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGG 19  
DB 33 TCTACAGGGAATCCGGG 15

RESULT 12  
US-09-995-529-284/C  
Sequence 284, Application US/09995529  
Publication No. US20040091482A9  
GENERAL INFORMATION:  
APPLICANT: Watkins, Jeffrey D.  
APPLICANT: Huse, William D.  
APPLICANT: Tang, Ying  
TITLE OF INVENTION: Humanized Collagen Antibodies and  
FILE REFERENCE: P-IX 4976  
CURRENT APPLICATION NUMBER: US/09/995,529  
CURRENT FILING DATE: 2001-11-26  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 284  
LENGTH: 57  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer  
NAME/KEY: misc\_feature  
LOCATION: 35, 36  
OTHER INFORMATION: n = A,T,C or G  
US-09-995-529-284

Query Match 71.0%; Score 14.2; DB 3; Length 57;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGG 19  
DB 33 TCTACAGGGAATCCGGG 15

RESULT 13  
US-11-036-317-490296/C  
Sequence 490296, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 490296  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-490296

Query Match 70.0%; Score 14; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCC 15  
DB 21 TTTTCAGGGAATCC 8

RESULT 14  
US-11-036-317-832220/C  
Sequence 832220, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Blume, John  
APPLICANT: Williams, Alan  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 832220  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-832220

Query Match 70.0%; Score 14; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCC 15  
DB 21 TTTTCAGGGAATCC 8

RESULT 15  
US-09-995-529-285/C  
Sequence 285, Application US/09995529  
Publication No. US20030099655A1  
GENERAL INFORMATION:  
APPLICANT: Watkins, Jeffrey D.  
APPLICANT: Huse, William D.  
APPLICANT: Tang, Ying  
TITLE OF INVENTION: Humanized Collagen Antibodies and  
FILE REFERENCE: P-IX 4976  
CURRENT APPLICATION NUMBER: US/09/995,529  
CURRENT FILING DATE: 2001-11-26  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 285  
LENGTH: 57  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer  
NAME/KEY: misc\_feature  
LOCATION: 32, 33  
OTHER INFORMATION: n = A,T,C or G  
US-09-995-529-285

Query Match 70.0%; Score 14; DB 3; Length 57;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGGAATCCGGG 19  
DB 28 CAGGGAATCCGGG 15

Search completed: December 25, 2005, 04:14:21  
Job time : 338.6 secs



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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 seconds  
(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20  
Sequence: 1 ttttcagggaatccgsgg95 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:

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10: /cgn2\_6/ptodata/2/pubpna/US60\_NEM\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.8	69.0	25	US-11-121-849-240361	Sequence 240361, A
C 2	13.6	68.0	25	US-11-121-849-22867	Sequence 22867, A
C 3	13.2	66.0	25	US-11-121-849-181142	Sequence 181142, A
C 4	13.2	66.0	25	US-11-121-849-338152	Sequence 338152, A
C 5	13.2	66.0	25	US-11-121-849-497393	Sequence 497393, A
C 6	13.2	66.0	25	US-11-121-849-600267	Sequence 600267, A
C 7	13.2	66.0	25	US-11-121-849-600268	Sequence 600268, A
C 8	13.2	66.0	32	US-10-864-079-8	Sequence 8, Appl1
C 9	13.2	66.0	36	US-10-893-584-14	Sequence 14, Appl1
C 10	13	65.0	23	US-10-750-185-15044	Sequence 15044, A
C 11	13	65.0	25	US-11-121-849-183597	Sequence 183597, A
C 12	12.8	64.0	25	US-11-121-849-90190	Sequence 90190, A
C 13	12.8	64.0	25	US-11-121-849-90416	Sequence 90416, A
C 14	12.8	64.0	25	US-11-121-849-249360	Sequence 249360, A
C 15	12.8	64.0	25	US-11-121-849-466854	Sequence 466854, A
C 16	12.8	64.0	25	US-11-121-849-552041	Sequence 552041, A
C 17	12.8	64.0	25	US-11-121-849-552700	Sequence 552700, A
C 18	12.8	64.0	25	US-11-121-849-539135	Sequence 539135, A
C 19	12.6	63.0	25	US-11-121-849-24779	Sequence 24779, A
C 20	12.6	63.0	25	US-11-121-849-32312	Sequence 32312, A
C 21	12.6	63.0	25	US-11-121-849-33918	Sequence 33918, A
C 22	12.6	63.0	25	US-11-121-849-124009	Sequence 124009, A
C 23	12.6	63.0	25	US-11-121-849-148217	Sequence 148217, A

24	12.6	63.0	25	US-11-121-849-194169	Sequence 194169, A
25	12.6	63.0	25	US-11-121-849-296434	Sequence 296434, A
C 26	12.6	63.0	25	US-11-121-849-307950	Sequence 307950, A
C 27	12.6	63.0	25	US-11-121-849-310010	Sequence 310010, A
C 28	12.6	63.0	25	US-11-121-849-310627	Sequence 310627, A
C 29	12.6	63.0	25	US-11-121-849-398509	Sequence 398509, A
C 30	12.6	63.0	25	US-11-121-849-399245	Sequence 399245, A
C 31	12.6	63.0	25	US-11-121-849-399246	Sequence 399246, A
C 32	12.6	63.0	25	US-11-121-849-449121	Sequence 449121, A
C 33	12.6	63.0	25	US-11-121-849-579858	Sequence 579858, A
C 34	12.6	63.0	72	US-10-469-561-12	Sequence 12, Appl1
C 35	12.4	62.0	25	US-11-121-849-95142	Sequence 89342, A
C 36	12.4	62.0	25	US-11-121-849-95144	Sequence 95144, A
C 37	12.4	62.0	25	US-11-121-849-95145	Sequence 95145, A
C 38	12.4	62.0	25	US-11-121-849-162004	Sequence 162004, A
C 39	12.4	62.0	25	US-11-121-849-192387	Sequence 392387, A
C 40	12.4	62.0	25	US-11-121-849-420287	Sequence 420287, A
C 41	12.4	62.0	25	US-11-121-849-420253	Sequence 420253, A
C 42	12.4	62.0	25	US-11-121-849-581733	Sequence 581733, A
C 43	12.4	62.0	25	US-11-121-849-661763	Sequence 661763, A
C 44	12.2	61.0	25	US-11-121-849-24805	Sequence 24805, A
C 45	12.2	61.0	25	US-11-121-849-25366	Sequence 25366, A

#### ALIGNMENTS

```
RESULT 1
US-11-121-849-240361/c
; Sequence 240361, Application US//11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 240361
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-121-849-240361

Query Match      69.0% Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTTTTCAGGATCCCG 17
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Db       25 TTTTTCAGGATCCCG 9

RESULT 2
US-11-121-849-22867
; Sequence 22867, Application US//11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 22867
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PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 600268  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-600268

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TTTTCAGGGAATCCGGG 18  
Db 2 TTTTCATGAAATCCAGG 19

RESULT 8  
US-10-864-079-8/c  
Sequence 8, Application US/10864079  
Publication No. US20050277607A1  
GENERAL INFORMATION:  
APPLICANT: DINMAN, JONATHAN D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING  
FILE REFERENCE: 4010.3005US  
CURRENT APPLICATION NUMBER: US/10/864,079  
CURRENT FILING DATE: 2004-06-09  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 8  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-864-079-8

Query Match 66.0%; Score 13.2; DB 6; Length 32;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TTTTCAGGGAATCCGGG 19  
Db 18 TTGTAGGGGATCCGGG 1

RESULT 9  
US-10-893-584-14  
Sequence 14, Application US/10893584  
Publication No. US20050272048A1  
GENERAL INFORMATION:  
APPLICANT: Borgford, Thor  
APPLICANT: Braun, Curtis  
APPLICANT: Purac, Adam  
APPLICANT: Stoll, Dominik  
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,  
FILE REFERENCE: 10447-025  
CURRENT APPLICATION NUMBER: US/10/893,584  
CURRENT FILING DATE: 2004-07-19  
PRIOR APPLICATION NUMBER: US 09/551,151  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: US 09/403,752  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 10/089,058  
PRIOR FILING DATE: 2000-10-04  
NUMBER OF SEQ ID NOS: 274  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 36

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: P.falciparum-B linker regions of pAP-225  
US-10-893-584-14

Query Match 66.0%; Score 13.2; DB 6; Length 36;  
Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TTTTCAGGGAATCCGGG 19  
Db 8 TTTTCGGGGAATCCGAGG 25

RESULT 10  
US-10-750-185-15044/c  
Sequence 15044, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:  
APPLICANT: MMT GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: PANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15044  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Forward Primer  
US-10-750-185-15044

Query Match 65.0%; Score 13; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTTCAGGGAAT 13  
Db 16 TTTTCAGGGAAT 4

RESULT 11  
US-11-121-849-383597  
Sequence 383597, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 383597  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-383597

Query Match 65.0%; Score 13; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCAGGAATCCG 16  
|||||  
DB 7 TTCAGGAATCCG 19

RESULT 12  
US-11-121-849-90190/c  
; Sequence 90190, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 90190  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-90190

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 8.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTTCAGGAATCCG 17  
|||||  
DB 21 TTTTCAGGAATCCG 6

RESULT 13  
US-11-121-849-90416  
; Sequence 90416, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 90416  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-90416

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 8.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCAGGAATCCGGGG 20  
|||||  
DB 5 TCAGGAATCCGGGG 20

RESULT 14  
US-11-121-849-249360/c  
; Sequence 249360, Application US/11121849  
; Publication No. US20050272080A1

; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 249360  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-249360

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 8.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCAGGAATCCGGGG 20  
|||||  
DB 16 TCAGGAATCCGTAG 1

RESULT 15  
US-11-121-849-466854  
; Sequence 466854, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 466854  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-466854

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 8.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTTCAGGAATCCG 17  
|||||  
DB 7 TATTCAGGAATCCG 22

Search completed: December 25, 2005, 04:37:02  
Job time : 135.3 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 : Search time 582 Seconds  
(without alignments)  
1953.383 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20  
Sequence: 1 gggtagtcagcgcgagcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_in: \*  
3: gb\_env: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pr: \*  
9: gb\_ro: \*  
10: gb\_sts: \*  
11: gb\_sy: \*  
12: gb\_un: \*  
13: gb\_vl: \*  
14: gb\_htg: \*  
15: gb\_pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match length	DB ID	Description
1	20	100.0	20	6	BD211663
2	20	100.0	20	6	BD211668
3	15.2	76.0	100	6	AX990338
4	14.8	74.0	100	6	CQ000292
5	14.2	71.0	51	6	AX158137
6	14.2	71.0	57	6	BD080430
7	14.2	71.0	65	6	COS55988
8	14.2	71.0	75	1	ECCTRNAV
9	14.2	71.0	95	6	AX088789
10	14.2	71.0	97	6	AX088790
11	13.6	68.0	27	6	CQ973172
12	13.6	68.0	38	6	CQ973152
13	13.6	68.0	63	6	E27556
14	13.6	68.0	76	1	ECOTRNAPHE
15	13.6	68.0	88	6	BD033603
16	13.6	68.0	88	6	AX898070
17	13.4	67.0	42	6	ARI04424
18	13.4	67.0	42	6	BD062184

19	13.4	67.0	63	6	ARI27588	ARI27588 Sequence
20	13.4	67.0	63	6	I75257	I75257 Sequence 6
21	13.4	67.0	73	6	I13478	I13478 Sequence 12
22	13.2	66.0	28	6	I67871	I67871 Sequence 7
23	13.2	66.0	33	6	BD234609	BD234609 Thymidine
24	13.2	66.0	33	6	AR230205	AR230205 Sequence
25	13.2	66.0	51	6	AX199369	AX199369 Sequence
26	13.2	66.0	51	6	AX199370	AX199370 Sequence
27	13.2	66.0	60	6	CQ540119	CQ540119 Sequence
28	13.2	66.0	60	6	CQ553070	CQ553070 Sequence
29	13.2	66.0	65	6	CQ532735	CQ532735 Sequence
30	13.2	66.0	65	6	CQ559822	CQ559822 Sequence
31	13.2	66.0	75	6	BD054182	BD054182 Sequence
32	13.2	66.0	75	6	AX918649	AX918649 Sequence
33	13.2	66.0	97	6	BD037478	BD037478 Sequence
34	13.2	66.0	97	6	AX901945	AX901945 Sequence
35	13.2	66.0	100	6	CQ824802	CQ824802 Sequence
36	12.8	64.0	21	6	ARI48748	ARI48748 Sequence
37	12.8	64.0	40	6	AR279477	AR279477 Sequence
38	12.8	64.0	40	6	AX025223	AX025223 Sequence
39	12.8	64.0	48	6	AR031652	AR031652 Sequence
40	12.8	64.0	48	6	I90270	I90270 Sequence 11
41	12.8	64.0	60	6	BD247649	BD247649 A method
42	12.8	64.0	60	6	CQ755289	CQ755289 Sequence
43	12.8	64.0	60	6	AR345118	AR345118 Sequence
44	12.8	64.0	65	6	CQ556456	CQ556456 Sequence
45	12.8	64.0	74	6	AX662284	AX662284 Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS BD211663 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION BD211663.1 GI:33021433  
VERSION JP 2002512793-A/6.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

REFERENCE  
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.

TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

JOURNAL Patent: JP 2002512793-A 6 08-MAY-2002;

COMMENT GENENSENSE TECHNOLOGIES INC

OS Homo sapiens (human)

PN JP 2002512793-A/6

PD 08-MAY-2002

PF 23-APR-1999 JP 2000545999

PR 23-APR-1998 US 60/082791

PI JIM A WRIGHT, AIPING H YOUNG, YOON S LEE

PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC

CC Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

CC name for controlling cell proliferation

FH key

FT source

1.20 Location/Qualifiers

1.20 /organism="Homo sapiens (human)"

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTACTTCAGCGCGGAGCG 20  
|||||  
1 GGGTACTTCAGCGCGGAGCG 20

Db 1 GGGTACTTCAGCGCGGAGCG 20

RESULT 2  
BD211688/c 20 bp DNA linear PAT 17-JUL-2003  
LOCUS Antisense oligonucleotide sequence of neuropilin and method of  
DEFINITION using the same for controlling cell proliferation.  
ACCESSION BD211688  
VERSION BD211688.1 GI:33021458  
KEYWORDS JP 2002512793-A/31.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
1 (bases 1 to 20)  
Wright, V.A., Young, A.H. and Lee, Y.S.  
Antisense oligonucleotide sequence of neuropilin and method of  
using the same for controlling cell proliferation  
Patent: JP 2002512793-A 31 08-MAY-2002;  
JOURNAL GENESENSE TECHNOLOGIES INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002512793-A/31  
PD 08-MAY-2002  
PP 23-APR-1999 JP 2000545999  
PR 23-APR-1998 US 60/082791  
PI JIM A WRIGHT, AIPING H YOUNG, YOON S LEE  
PC C12N15/09, A61K31/711, A61K48/00, A61P35/00, C12N15/00 CC  
Antisense oligonucleotide sequence of neuropilin and method of  
using the  
CC same for controlling cell proliferation  
Location/Qualifiers  
FT source 1..20  
/organism="Homo sapiens (human)".

FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTACTTCAGCGCGGAGCG 20  
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20 GGGTACTTCAGCGCGGAGCG 1

Db 20 GGGTACTTCAGCGCGGAGCG 1

RESULT 3  
AX990338/c 100 bp DNA linear PAT 16-JAN-2004  
LOCUS Sequence 1801 from Patent EP1260592.  
DEFINITION AX990338  
ACCESSION AX990338  
VERSION AX990338.1 GI:40996684  
KEYWORDS  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Escherichia.  
1  
Donner, H., Drescher, B., Huber, A. and Weber, J.  
Biochip Patent: EP 1260592-A 1801 27-NOV-2002;  
JOURNAL MWG - Biotech AG (DE)  
Location/Qualifiers  
FEATURES  
source 1..100

ORIGIN  
Query Match 76.0%; Score 15.2; DB 6; Length 100;  
Best Local Similarity 85.0%; Pred. No. 1.3e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTACTTCAGCGCGGAGCG 20  
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44 GGGTCTTCGCCGCGGAGCG 25

Db 44 GGGTCTTCGCCGCGGAGCG 25

RESULT 4  
CQ000292 100 bp DNA linear PAT 16-JAN-2004  
LOCUS Sequence 11754 from Patent EP1260592.  
DEFINITION CQ000292  
ACCESSION CQ000292  
VERSION CQ000292.1 GI:41006930  
KEYWORDS  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Escherichia.  
1  
Donner, H., Drescher, B., Huber, A. and Weber, J.  
Biochip Patent: EP 1260592-A 11754 27-NOV-2002;  
JOURNAL MWG - Biotech AG (DE)  
Location/Qualifiers  
FEATURES  
source 1..100  
/organism="Escherichia coli"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:562"  
/note="ygaA ygaA U00096 complement(2828798\_2830387)"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 100;  
Best Local Similarity 68.9%; Pred. No. 2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGTAGTTCTGCGGAGCG 19  
|||||  
8 GGTAGTTCTGCGGAGCG 25

Db 8 GGTAGTTCTGCGGAGCG 25

RESULT 5  
AX158137/c 51 bp DNA linear PAT 22-JUN-2001  
LOCUS Sequence 1465 from Patent WO0140521.  
DEFINITION AX158137  
ACCESSION AX158137  
VERSION AX158137.1 GI:14539468  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
1  
Shinkets, R.A. and Leach, M.  
Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
Patent: WO 0140521-A 1465 07-JUN-2001;  
JOURNAL Curagen Corporation (US)  
Location/Qualifiers  
FEATURES  
source 1..51  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="1 of 2 allelic variants (1466 is other entry)"

ORIGIN Accession number cg29363109"

Query Match 71.0%; Score 14.2; DB 6; Length 51;  
Best Local Similarity 84.2%; Pred. No. 4.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 GGGTAGTTCAGCGCGGAGCG 19  
28 GGGTGTGACGCGCGGAGCG 10

RESULT 6  
LOCUS BD080430 57 bp DNA linear PAT 27-AUG-2002  
DEFINITION Biomolecule containing rubber-elastic peptide.  
ACCESSION BD080430  
VERSION BD080430.1 GI:22626033  
KEYWORDS JP 2001514263-A/1.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 57)  
AUTHORS Reiersen,H., Rees,A. and Korsnes,L.  
TITLE Biomolecule containing rubber-elastic peptide  
JOURNAL Patent: JP 2001514263-A 1 11-SEP-2001;  
DYNAL AS

COMMENT OS Artificial Sequence  
PN JP 2001514263-A/1  
PD 11-SEP-2001  
PF 28-AUG-1998 JP 2000508699  
PR 29-AUG-1997 GB 9718463 4  
PI HERALD REIERSEN,ANTHONY REES,LARS KORSNES  
PC C07K14/00,A61K38/00,C07K14/78,C07K16/44,C07K19/00,C12N15/09,  
PC G01N33/53//  
PC A61K39/395,A61K37/02,C12N15/00  
CC Description of Artificial Sequence:Scfv linker sequence FH  
Key Location/Qualifiers  
FT source 1..57  
Location/Qualifiers  
1..57  
/organism='Artificial Sequence'.  
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/db\_xref='taxon:32630'

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Query Match 71.0%; Score 14.2; DB 6; Length 57;  
Best Local Similarity 84.2%; Pred. No. 4.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2 GGGTAGTTCAGCGCGGAGCG 20  
16 GCGGTTCAGCGCGGCGCG 34

RESULT 7  
LOCUS CQ555988/c 65 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 25623 from Patent WO0210449.  
ACCESSION CQ555988  
VERSION CQ555988  
KEYWORDS GI:41522415  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
MUSKRYCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcriptome  
JOURNAL Patent: WO 0210449-A 25623 07-FEB-2002;

FEATURES CompuGen Inc. (US)  
source Location/Qualifiers  
1..65  
/organism="Mus musculus"  
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ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 65;  
Best Local Similarity 84.2%; Pred. No. 4.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2 GGGTAGTTCAGCGCGGAGCG 20  
65 GGGTAGTTCCTGTGGAGCG 47

RESULT 8  
LOCUS ECCTRNAV 75 bp DNA linear BCT 11-JUN-2003  
DEFINITION E.coli gene for chimeric transfer RNA-Val.  
ACCESSION X70451  
VERSION X70451.1 GI:312130  
KEYWORDS chimeric; transfer RNA-Val.  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
REFERENCE 1 (bases 1 to 75)  
AUTHORS Meinzel,T., Mechulam,Y., Lazemec,C., Blanquet,S. and Fayat,G.  
TITLE Critical role of the acceptor stem of tRNAs(Val) in their  
JOURNAL aminoacylation by Escherichia coli methionyl-tRNA synthetase  
PUBMED 5. Mol. Biol. 229 (1), 26-36 (1993)  
8421312

FEATURES  
source Location/Qualifiers  
1..75  
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/product="tRNA-Val"

ORIGIN

Query Match 71.0%; Score 14.2; DB 1; Length 75;  
Best Local Similarity 80.0%; Pred. No. 4.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 GGGTAGTTCAGCGCGGAGCG 20  
5 GGGTAGCTCAGCGGAGAG 24

RESULT 9  
LOCUS AX088789/c 95 bp DNA linear PAT 17-MAR-2001  
DEFINITION Sequence 115 from Patent WO0114416.  
ACCESSION AX088789  
VERSION AX088789.1 GI:13397585  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Nepper,M.P., McClements,W.L., Jansen,K.U., Schultz,L.D., Chen,L.  
and Wang,X.M.  
TITLE Synthetic human papillomavirus genes  
JOURNAL Patent: WO 0114416-A 115 01-MAR-2001;  
Merck & Co., Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..95  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN /note="Codon-Optimized HPV6 E2 fragment"

Query Match 71.0%; Score 14.2; DB 6; Length 95;  
Best Local Similarity 84.2%; Pred. No. 4.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGTAAGTCAGCGCGGAGCG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 92 GATCGTTCAGCGCGGTAGCG 74

RESULT 10  
LOCUS AX088790 96 bp DNA linear PAT 17-MAR-2001  
DEFINITION Sequence 116 from Patent WO0114416.  
ACCESSION AX088790  
VERSION AX088790.1 GI:13397586  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Neeper,M.P., McClements,W.L., Jansen,K.U., Schultz,L.D., Chen,L.  
and Wang,X.M.  
TITLE Synthetic human papillomavirus genes  
JOURNAL Patent: WO 0114416-A 116 01-MAR-2001;  
Merck & Co., Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/note="Codon-Optimized HPV6 E2 fragment"

ORIGIN

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Best Local Similarity 84.2%; Pred. No. 4.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGTAAGTCAGCGCGGAGCG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 73 GATCGTTCAGCGCGGTAGCG 91

RESULT 11  
LOCUS CQ973172 27 bp DNA linear PAT 20-JAN-2005  
DEFINITION Sequence 26 from Patent WO2004111225.  
ACCESSION CQ973172  
VERSION CQ973172.1 GI:57997919  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Wu,Q.  
TITLE Novel modified corin molecules having substitute activation  
JOURNAL Patent: WO 2004111225-A 26 23-DEC-2004;  
Schering Aktiengesellschaft (DE)  
FEATURES  
source Location/Qualifiers  
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/note="Forward Primer EntPCRIA"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 27;  
Best Local Similarity 80.0%; Pred. No. 8.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGTAAGTCAGCGCGGAGCG 20  
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Db 25 GCCTAGTCCAGGCTGGAACG 6

RESULT 12  
LOCUS CQ973152 38 bp DNA linear PAT 20-JAN-2005  
DEFINITION Sequence 6 from Patent WO2004111225.  
ACCESSION CQ973152  
VERSION CQ973152.1 GI:57997907  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Wu,Q.  
TITLE Novel modified corin molecules having substitute activation  
JOURNAL Patent: WO 2004111225-A 6 23-DEC-2004;  
Schering Aktiengesellschaft (DE)  
FEATURES  
source Location/Qualifiers  
1..38  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Reverse Primer Cor/Twb"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 38;  
Best Local Similarity 80.0%; Pred. No. 8.5e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGTAAGTCAGCGCGGAGCG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 10 GCCTAGTCCAGGCTGGAACG 29

RESULT 13  
LOCUS E27556 63 bp DNA linear PAT 18-JUN-2001  
DEFINITION Isolation and cloning of nucleic acid molecule by using hairpin  
ACCESSION E27556  
VERSION E27556.1 GI:13018221  
KEYWORDS JP 1999206381-A/4.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 63)  
AUTHORS Jun,F. and Koji,S.  
TITLE Isolation and cloning of nucleic acid molecule by using hairpin  
JOURNAL Patent: JP 1999206381-A 4 03-AUG-1999;  
Aisin COSMOS R&D CO LTD  
COMMENT OS Unidentified  
PN JP 1999206381-A/4  
PD 03-AUG-1999  
PF 29-JAN-1998 JP 1998016987  
PR JUN FUJIWARA,KOJI SHIGEMORI  
PI C12N15/09,C12Q1/68,C12N15/00  
PC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
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1..63  
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ORIGIN

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Oy	1 GGGTAGTTCAGCGCGGAGCG	20				
Db	30 GGGCAGGTCAAGCGCGGCCGC	49				
RESULT 14						
ECOTRNAPHE			76 bp	tRNA	linear	BCT 15-APR-1994
LOCUS	E. coli transfer RNA-Phe.					
DEFINITION	M24882					
ACCESSION	M24882.1 GI:290481					
VERSION	transfer RNA-Phe.					
KEYWORDS	Escherichia coli					
SOURCE	Escherichia coli					
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.					
REFERENCE	1 (bases 1 to 76)					
AUTHORS	Kitchingman,G.R. and Fournier,M.J.					
TITLE	Modification-deficient transfer ribonucleic acids from relaxed control Escherichia coli: structures of the major undermodified phenylalanine and leucine transfer RNAs produced during leucine starvation					
JOURNAL	Biochemistry	16 (10),	2213-2220	(1977)		
PUBMED	324516					
COMMENT	Original source text: Escherichia coli tRNA.					
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source	1..76					
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cRNA	1..76					
	/product="tRNA-Phe"					
ORIGIN	/note="codon recognized: UUC"					
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Best Local Similarity	75.0%;	Pred. No. 8.3e+04;				
Matches	15;	Conservative	2;	Mismatches	3;	Indels
Oy	1 GGGTAGTTCAGCGCGGAGCG	20				
Db	5 GGATGACTCAAGDCGGADAG	24				
RESULT 15						
BD033603/c						
LOCUS	BD033603		88 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Sequence tag and encoded human protein.					
ACCESSION	BD033603					
VERSION	BD033603.1 GI:22575345					
KEYWORDS	JP 2001269182-A/9849.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiinae; Homo.					
	1 (bases 1 to 88)					
	Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.					
	Sequence tag and encoded human protein					
	Patent: JP 2001269182-A 9849 02-OCT-2001;					
REFERENCE	GENSET					
AUTHORS	OS Homo sapiens (human)					
TITLE	PN JP 2001269182-A/9849					
JOURNAL	PD 02-OCT-2001					
	PF 24-FEB-2000 JP 2000118773					
	PR 26-FEB-1999 US 60/122487					
	PI JEAN BAUTIST DUMAS MILNE EDWARDS, RIMERIC DUCLAIR,JEAN YVES					
	PI JEAN DANV					

	PC	C12N15/.09,C07K14/.435,C07K16/.18,C12N1/.15,C12N1/.19,C12N1/.21,	PC
	C12N5/.10,		
	PC	C12P21/.02,C12P21/.08,C12Q1/58//G06F17/30,C12N15/.00,C12N5/.00,	PC
	G06F15/.40		
	CC		
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ORIGIN			
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Best Local Similarity	80.0%;	Pred. No. 8.2e+04;	Length 88;
Matches 16; Conservative	0;	Mismatches 4;	Indels 0;
		Gaps	0;
Oy	1 GGGTAGTTCAGGCCGAGCGC 20		
Dd	85 GGGAAGTTCAAGGCGGACGC 66		

Search completed: December 24, 2005, 14:06:09  
Job time : 584 secs

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GenCore version 5.1.6  
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Title: US-09-296-264-6

Perfect score: 20

Sequence: 1 gggtagtcagcgcgagcg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001s.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002s.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003s.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004s.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AA231436 Human neu
2	20	100.0	20	3	ADA74668 GTT3606 a
3	20	100.0	20	3	ADA74713 Forward p
4	18	90.0	30	4	AAAF8316 Human neu
5	18	90.0	30	8	ACC80171 Human neu
6	15.2	76.0	100	8	ACD70531 E. coli K
7	14.8	74.0	100	8	ACD80478 E. coli K
8	14.4	72.0	20	13	ADU78696 Antisense
9	14.4	72.0	20	13	ADU78697 Antisense
10	14.2	71.0	51	4	AA174524 Human sll
11	14.2	71.0	65	6	ABNS2875 Mouse spl
12	14.2	71.0	95	4	AA75497 Codon-opt
13	14.2	71.0	96	4	AA75498 Codon-opt
14	14	70.0	74	6	ABSS2685 Elongator
15	13.8	69.0	66	9	ADA14180 C3 nucleic
16	13.6	68.0	27	14	ADW42868 Modified
17	13.6	68.0	30	6	ABK53798 DMS:accep
18	13.6	68.0	38	14	ADW42848 Human cor
19	13.6	68.0	60	14	ADV11266 Nitrous a

C	20	13.6	68.0	60	14	ADV11268 Nitrous a
C	21	13.6	68.0	60	14	ADV11262 Nitrous a
C	22	13.6	68.0	63	2	AA209153 Hairpin t
C	23	13.6	68.0	74	6	ABSS2700 Mutant el
C	24	13.6	68.0	76	6	ABK87519 Human imm
C	25	13.6	68.0	76	6	ABK87514 Human imm
C	26	13.6	68.0	76	6	ABK87515 Human imm
C	27	13.6	68.0	76	6	ABK87517 Human imm
C	28	13.6	68.0	76	6	ABK87516 Human imm
C	29	13.6	68.0	76	6	ABK87518 Human imm
C	30	13.6	68.0	88	3	AA209858 Human sec
C	31	13.4	67.0	42	12	AD180492 Human mut
C	32	13.4	67.0	63	2	AAV00294 Bacillus
C	33	13.4	67.0	63	5	AA73212 Oligonuc1
C	34	13.2	66.0	25	13	ADW80828 RACE PCR
C	35	13.2	66.0	28	2	AA739026 Circular
C	36	13.2	66.0	28	2	AA739026 Circular
C	37	13.2	66.0	31	13	AD18022 Target se
C	38	13.2	66.0	33	2	AA705187 Peronospo
C	39	13.2	66.0	33	2	AA705187 Mutant HS
C	40	13.2	66.0	33	2	AA757634 Codons 16
C	41	13.2	66.0	33	8	AA757634 Codons 16
C	42	13.2	66.0	37	3	AA704777 Thymidine
C	43	13.2	66.0	41	8	AA282822 Human bet
C	44	13.2	66.0	51	4	AA233802 Glycosyl-
C	45	13.2	66.0	51	4	AAH89519 Human cod
C	45	13.2	66.0	51	4	AAH89518 Human cod

## ALIGNMENTS

RESULT 1	AA231436	standard; DNA, 20 BP.
ID	AA231436	standard; DNA, 20 BP.
XX	AA231436	
AC	AA231436	
XX		
DT	07-FEB-2000	(first entry)
XX		
DE	Human neuropilin mRNA specific antisense oligo GTT3606.	
XX		
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer; papilloma; diabetic retinopathy; antisense; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	W09955855-A2.	
XX		
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA000324.
XX		
PR	23-APR-1998;	98US-0082791P.
XX		
XX	(GENE-) GENESENSE TECHNOLOGIES INC.	
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI; 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for treating cancer.	
PT		
PS	Claim 4; Page 16; 57BP; English.	
XX		
CC	Sequences AA231431-460 represent antisense oligonucleotides which inhibit human neuropilin expression. The antisense oligonucleotides can be used to inhibit the growth or metastasis of a mammalian tumor and inhibit neovascularisation. The oligonucleotides may be used to treat various forms of cancers or tumors, such as sarcomas, melanomas, adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of the mouth, throat, larynx and lung, genitourinary cancers such as	

```
CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred.No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTAGTTCAGCGCGGAGCG 20
1 GGGTAGTTCAGCGCGGAGCG 20
Db 1 GGGTAGTTCAGCGCGGAGCG 20

RESULT 2
ADA74688
ID ADA74688 standard; DNA; 20 BP.
AC ADA74688;
XX
XX 20-NOV-2003 (first entry)
XX
DE GT13606 antisense oligonucleotide targeted to human neuropilin mRNA.
XX
XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;
XX cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;
XX GT13606; antisense; human; ss.
XX
OS Homo sapiens.
XX
PN US2003083274-A1.
XX
PD 01-MAY-2003.
XX
PF 22-APR-1999; 99US-00296264.
XX
PR 23-APR-1998; 98US-0082791P.
XX
XX (WRIG/) WRIGHT J A.
XX (YOUN/) YOUNG A H.
XX (LEEY/) LEE Y S.
XX
PI Wright JA, Young AH, Lee YS;
XX
XX WPI; 2003-576622/54.
XX
XX New antisense oligonucleotide that inhibits neuropilin expression, useful
XX PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a
XX PT mammalian tumor.
XX
XX Claim 1; Page 5; 27pp; English.
XX
XX The invention relates to a novel antisense oligonucleotide that inhibits
XX CC the expression of neuropilin, also known as VEGF165R (vascular
XX CC endothelial growth factor receptor). The oligonucleotide of the invention
XX CC demonstrates cytostatic activity and may be useful for inhibiting the
XX CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
XX CC mammals. Furthermore, the oligonucleotide may be utilised during gene
XX CC therapy. The current sequence is that of the GT13606 antisense
XX CC oligonucleotide of the invention which is targeted to human neuropilin
XX CC mRNA.
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred.No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTAGTTCAGCGCGGAGCG 20
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```
Db 1 GGGTAGTTCAGCGCGGAGCG 20

RESULT 3
ADA74713/C
ID ADA74713 standard; DNA; 20 BP.
XX
XX ADA74713;
XX
XX 20-NOV-2003 (first entry)
XX
XX Forward PCR primer used during development of antisense oligonucleotides.
XX DE neuropilin; VEGF165R; vascular endothelial growth factor receptor;
XX CC cytosolic; growth; tumour metastasis; angiogenesis; gene therapy; ss;
XX CC primer; PCR.
XX
XX Unidentified.
XX
XX US2003083274-A1.
XX
XX 01-MAY-2003.
XX
XX 22-APR-1999; 99US-00296264.
XX
XX 23-APR-1998; 98US-0082791P.
XX
XX (WRIG/) WRIGHT J A.
XX (YOUN/) YOUNG A H.
XX (LEEY/) LEE Y S.
XX
XX Wright JA, Young AH, Lee YS;
XX
XX WPI; 2003-576622/54.
XX
XX New antisense oligonucleotide that inhibits neuropilin expression, useful
XX PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a
XX PT mammalian tumor.
XX
XX Example 2; Page 12; 27pp; English.
XX
XX The invention relates to a novel antisense oligonucleotide that inhibits
XX CC the expression of neuropilin, also known as VEGF165R (vascular
XX CC endothelial growth factor receptor). The oligonucleotide of the invention
XX CC demonstrates cytostatic activity and may be useful for inhibiting the
XX CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
XX CC mammals. Furthermore, the oligonucleotide may be utilised during gene
XX CC therapy. The current sequence is that of the forward PCR primer of the
XX CC invention which was used during development of the antisense
XX CC oligonucleotides.
XX
SQ Sequence 20 BP; 3 A; 11 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred.No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 20 GGGTAGTTCAGCGCGGAGCG 1

RESULT 4
AAF83316/C
ID AAF83316 standard; DNA; 30 BP.
XX
XX AAF83316;
XX
XX 09-JUL-2001 (first entry)
XX
XX Human neuropilin-1 (NP-1) DNA amplifying sense primer BUL-259.
XX
DE
```

KM Receptor protein; vascular endothelial growth factor receptor-2; NP-1;  
 KM VEGFR-2; neuropilin-1; co-receptor; human; angiogenic; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200131346-A2.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 26-OCT-2000; 2000WO-US029579.  
 XX  
 PR 28-OCT-1999; 99US-0162367P.  
 XX  
 PA (PROC ) PROCTER & GAMBLE CO.  
 XX  
 PI Rosenbaum JS, Whitaker GB, Limberg BJ;  
 XX  
 DR WPI; 2001-308686/32.  
 XX  
 XX Determining compounds which bind to a complex comprising vascular  
 PT endothelial growth factor receptor-2 and Neuropilin-1 to provide superior  
 PT pro- and anti-angiogenic agents.  
 XX  
 PS Example 1; Fig 3; 82pp; English.  
 XX  
 CC The invention relates to determining whether a compound is capable of  
 CC binding to a receptor protein complex comprising a vascular endothelial  
 CC growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1  
 CC (NP-1) receptor protein. One method comprises introducing a sample  
 CC comprising the compound to the receptor protein and allowing the compound  
 CC to bind to the complex. Signaling through VEGFR-2 is enhanced in the  
 CC presence of the NP-1 co-receptor. The methods of the invention can be  
 CC used for identifying novel pro- and anti-angiogenic compounds. Sequences  
 CC AAF83314-16 represents PCR primers used for isolating human NP-1 DNA  
 XX  
 SQ Sequence 30 BP; 5 A; 11 C; 8 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 90.0%; Score 18; DB 4; Length 30;  
 Best Local Similarity 100.0%; Pred.No. 41;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GTAGTTACGCGCGAGCG 20  
 Db 30 GTAGTTACGCGCGAGCG 13  
 XX  
 RESULT 5  
 ACC80171/C  
 ID ACC80171 standard; DNA; 30 BP.  
 XX  
 AC ACC80171;  
 XX  
 DT 04-AUG-2003 (first entry)  
 XX  
 DE Human neuropilin-1 gene PCR primer #4.  
 XX  
 KM Cytostatic; Neuropilin-1 receptor; NP-1 receptor; angiogenesis; cancer;  
 KM Vascular Endothelial Growth Factor Receptor-2; VEGFR-2; PlGF; VEGF;  
 KM Placental Growth Factor; Vascular Endothelial Growth Factor;  
 KM anti-angiogenic; human; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003029275-A2.  
 XX  
 PD 10-APR-2003.  
 XX  
 PF 02-OCT-2002; 2002WO-US031386.  
 XX  
 PR 03-OCT-2001; 2001US-0326712P.  
 XX  
 PA (REGG-) REGENERON PHARM INC.  
 PA (PROC ) PROCTER & GAMBLE CO.  
 PA

XX  
 PI Rosenbaum JS, Jones DR, Whitaker GB;  
 XX  
 DR WPI; 2003-371982/35.  
 XX  
 PT New anti-angiogenic peptides that are capable of binding to NP-1 or  
 PT vascular endothelial growth factor receptor (VEGFR)-2/NP-1 complex,  
 PT useful for treating diseases characterized by abnormal angiogenesis, such  
 PT as cancer.  
 XX  
 PS Disclosure; Page 21; 115pp; English.  
 XX  
 CC The present invention relates to peptides that are capable of binding to  
 CC Neuropilin-1 (NP-1) receptor or the Vascular Endothelial Growth Factor  
 CC Receptor (VEGFR)-2/NP-1 complex. The peptides are derived from a  
 CC combination of peptides from Exon 6 of Placental Growth Factor (PlGF),  
 CC coupled at the carboxyl terminus to either Exon 8 of Vascular Endothelial  
 CC Growth Factor (VEGF) isoform 165 (VEGF165, also referred to as p68) or  
 CC Exon 7 of PlGF (referred to as p67). The peptides and compositions are  
 CC useful for treating diseases characterized by abnormal angiogenesis, such  
 CC as cancer. The present peptide is a PCR primer, which was used to  
 CC illustrate the invention  
 XX  
 SQ Sequence 30 BP; 5 A; 11 C; 8 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 90.0%; Score 18; DB 8; Length 30;  
 Best Local Similarity 100.0%; Pred.No. 41;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GTAGTTACGCGCGAGCG 20  
 Db 30 GTAGTTACGCGCGAGCG 13  
 XX  
 RESULT 6  
 ACD70531/C  
 ID ACD70531 standard; DNA; 100 BP.  
 XX  
 AC ACD70531;  
 XX  
 DT 18-SEP-2003 (first entry)  
 XX  
 DE E. coli K12 MG1655 biochip probe SEQ ID 1801.  
 XX  
 KM Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 PN EP1260592-A1.  
 XX  
 PD 27-NOV-2002.  
 XX  
 PF 17-MAY-2001; 2001EP-00112179.  
 XX  
 PR 17-MAY-2001; 2001EP-00112179.  
 XX  
 PA (MMGB-) MMGB-BIOTECH AG.  
 XX  
 PI Donner H, Drescher B, Huber A, Weber J;  
 XX  
 DR WPI; 2003-241155/24.  
 XX  
 PT Biochip containing probes complementary with open reading frames in  
 PT Escherichia coli K12, useful for detecting gene expression and expression  
 PT patterns.  
 XX  
 PS Claim 3; Page 290; 2004pp; German.  
 XX  
 CC This invention describes a novel biochip comprising probe spots, each  
 CC containing many identical probes. The probes are nucleotide sequences of  
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
 CC least one includes a segment of at least 20 bases identical with, or  
 CC complementary to, a segment of an open reading frame (orf) of Escherichia

CC coli K12. The biochip is used for specific detection of gene expression  
CC in K12 and for determining the gene expression pattern, e.g. for  
CC diagnostic determination of which E. coli strains are present in the gut,  
CC and to determine the effects of e.g. growth media on gene expression. The  
CC biochip provides as comprehensive as possible detection of the K12  
CC genome, with simultaneous analysis of many different genes with a single  
CC device, and comparison of gene expression between K12 and its mutants or  
CC other E. coli strains in a single experiment. Apart from qualitative and  
CC quantitative information about gene expression, it also allows  
CC measurements of population densities for the various strains. The use of  
CC synthetic oligonucleotides for preparation of probes allows free  
CC variation in probe length and ensures high purity (and thus selectivity,  
CC reactivity and reproducibility); also synthetic probes are generally  
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to  
CC ACD81540 represent oligonucleotide probes used with the biochip described  
CC in the invention

SQ Sequence 100 BP; 17 A; 28 C; 26 G; 29 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 8; Length 100;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTACTCAGCGCGGAGCG 20  
|||||  
44 GGGTCGTCGCGCGGAGCG 25

Db

RESULT 7  
ACD80478  
ID ACD80478 standard; DNA; 100 BP.

XX ACD80478;

XX 19-SEP-2003 (first entry)

XX

DE E. coli K12 MG1655 biochip probe SEQ ID 11754.

XX

KM Biochip; gene expression; gnc; diagnostic; detection; probe; ss.

XX

OS Escherichia coli.

XX

PN EP1260592-A1.

XX

PD 27-NOV-2002.

XX

PF 17-MAY-2001; 2001EP-00112179.

XX

PR 17-MAY-2001; 2001EP-00112179.

XX

PA (MMGB-) MMG-BIOTECH AG.

XX

PI Donner H, Drescher B, Huber A, Weber J;

XX

DR WPI; 2003-241155/24.

XX

PT Biochip containing probes complementary with open reading frames in  
PT Escherichia coli K12, useful for detecting gene expression and expression  
PT patterns.

XX

PS Claim 3; Page 1831; 2004pp; German.

XX

XX This invention describes a novel biochip comprising probe spots, each  
CC containing many identical probes. The probes are nucleotide sequences of  
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
CC least one includes a segment of at least 20 bases identical with, or  
CC complementary to, a segment of an open reading frame (orf) of Escherichia  
CC coli K12. The biochip is used for specific detection of gene expression  
CC in K12 and for determining the gene expression pattern, e.g. for  
CC diagnostic determination of which E. coli strains are present in the gut,  
CC and to determine the effects of e.g. growth media on gene expression. The  
CC biochip provides as comprehensive as possible detection of the K12  
CC genome, with simultaneous analysis of many different genes with a single

CC device, and comparison of gene expression between K12 and its mutants or  
CC other E. coli strains in a single experiment. Apart from qualitative and  
CC quantitative information about gene expression, it also allows  
CC measurements of population densities for the various strains. The use of  
CC synthetic oligonucleotides for preparation of probes allows free  
CC variation in probe length and ensures high purity (and thus selectivity,  
CC reactivity and reproducibility); also synthetic probes are generally  
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to  
CC ACD81540 represent oligonucleotide probes used with the biochip described  
CC in the invention

SQ Sequence 100 BP; 19 A; 25 C; 33 G; 23 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 8; Length 100;  
Best Local Similarity 88.9%; Pred. No. 1.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGTAGTTCAGCGCGGAGC 19  
|||||  
8 GGTAGTTCAGCGGAGAGC 25

Db

RESULT 8  
ADU78696/c  
ID ADU78696 standard; DNA; 20 BP.

XX ADU78696;

XX

XX 27-JUN-2005 (first entry)

XX

DE Antisense oligonucleotide, SEQ ID 69.

XX

XX Neuroprotective; Antidepressant; Neuroleptic; Tranquillizer;  
KM Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;  
KM Cardiovascular-Gen.; Antiartherosclerotic; Antilipemic;  
KM Alzheimer's disease; neurological disorder; phosphatase; enzyme;  
KM antisense; ss.

XX

OS Homo sapiens.

XX

PN US2004226056-A1.

XX

PD 11-NOV-2004.

XX

PF 09-FEB-2004; 2004US-00776013.

XX

PR 22-DEC-1998; 98US-0113534P.

XX

PR 12-MAR-1999; 99US-0124120P.

XX

PR 30-JUN-1999; 99US-0141243P.

XX

PR 21-DEC-1999; 99US-0046613P.

XX

PR 17-OCT-2000; 2000US-0240790P.

XX

PR 13-JUL-2001; 2001US-0304775P.

XX

PR 10-SEP-2001; 2001US-00948904.

XX

PR 12-OCT-2001; 2001US-00975072.

XX

PR 15-JUL-2002; 2002US-00194967.

XX

PA (MYRI-) MYRIAD GENETICS INC.

XX

PI Roch J, Bartel P, Heichman K;

XX

DR WPI; 2004-794772/78.

XX

XX Selecting agents useful for treating Alzheimer's disease comprises  
PT selecting agents useful for treating Alzheimer's disease, comprising a  
PT biological activity related to focal adhesion kinase 2 function with or  
PT without the test agent.

XX

PS Disclosure; SEQ ID NO 69; 247pp; English.

XX

XX The present invention relates to a method for selecting agents that are  
CC potentially useful for the treatment of Alzheimer's disease. The method  
CC comprises selecting Focal Adhesion Kinase 2 (FAK2) with a test agent and  
CC measuring a biological activity related to FAK2 function in the presence

CC and absence of the test agent. The method is useful for screening  
CC compounds or agents that can be used to treat neurological disorders,  
CC ailments and diseases including mild cognitive impairment, depression,  
CC schizophrenia, obsessive-compulsive disorder, bipolar disorder, and  
CC neurodegenerative diseases and disorders and motor neuron diseases and  
CC disorders such as Alzheimer's disease, Parkinson's disease, dementia with  
CC Lewy bodies, amyotrophic lateral sclerosis or Lou Gehrig's disease,  
CC Alpers' disease, Leigh's disease, Pelizaeus-Wertheimer disease,  
CC Olivopontocerebellar atrophy, Friedreich's ataxia, leukodystrophies, Rett  
CC syndrome, Ramsay Hunt syndrome type II, and Down's syndrome, as well as  
CC for treating or preventing other diseases such as distalipidemia, diabetes,  
CC obesity, cardiovascular diseases such as atherosclerosis and coronary  
CC heart disease. Also disclosed is the coding sequence for a novel human  
CC phosphatase called PN7740 (ADU78628 and ADU78629). PN7740 contains a  
CC protein phosphatase 2C domain, which likely acts to dephosphorylate  
CC specific phospho-serine or phospho-threonine residues on particular  
CC protein substrates. Although the precise role played by protein  
CC phosphatase 2C in Alzheimer's disease pathogenesis has yet to be  
CC defined, the inventors have discovered that fragments of PN7740 interact  
CC with the first phosphotyrosine binding domain (PTB) domain of Fe65 (also  
CC known as APMB1/710) or amyloid beta (A4) precursor protein-binding, and  
CC family B, member 1, isoform E9 (710)), suggesting that PN7740 may well be  
CC involved somehow. Fe65 is known to interact with the cytosolic C-terminal  
CC region of Amyloid beta (A4) precursor protein (APP) and APP metabolism is  
CC critical to the pathogenesis of Alzheimer's disease, because it leads to  
CC the release of either toxic A-beta or trophic secreted APP (sAPP)  
CC metabolites. The present sequence is an antisense oligonucleotide which  
CC can be used in antisense therapy for Alzheimer's disease.

Query Match	72.0%	Score 14.4	DB 13	Length 20
Best Local Similarity	93.8%	Pred. No. 2.4e+03		
Matches 15, Conservative	0	Mismatches 1	Indels 0	Gaps 0

```

Qy      3 GTAGTCAGCGCGAG 18
          |||||
Db      18 GTAGTCATGCGGAG 3

```

RESULT 9  
ADU78697/c  
ID ADU78697 standard; DNA; 20 BP.

ADU78697;

DT 27-JAN-2005 (first entry)

DE Antisense oligonucleotide, SEQ ID 70.

KM Neuroprotective; Antidepressant; Neuroleptic; Tranquillizer;  
 KM Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;  
 KM Cardiovascular-Cen.; Antitartaric; Antilipemic;  
 KM Alzheimer's disease; neurological disorder; phosphatase; enzyme;  
 KM antisenesc; ss.

**Homo sapiens.**

US2004226056-A1

PD 11-NOV-2004  
yy

PF 09-FEB-2004; 2004US-00776013.  
XY

PR 22-DEC-1998; 98US-0113534P.  
PR 12-MAR-1999; 99US-0124120P.

PR	30-JUN-1999;	99US-0141243P.
PR	21-DEC-1999;	99US-00466139.

PR 17-OCT-2000; 2000US-0240790P.  
PR 13-JUL-2001; 2001US-0304775P.

PR 10-SEP-2001; 2001US-00948904.  
PR 12-OCT-2001; 2001US-00975072.

PK 13-JUL-2002; 200205-00194967.

XX (MYRI-) MYRIAD GENETICS INC.  
PA  
XX  
XX  
PI Roch J, Bartel P, Heichman K,  
XX  
XX  
DR WPI; 2004-794772/78.

PT Selecting agents useful for treating Alzheimer's disease comprises  
PT contacting focal adhesion kinase 2 with a test agent and measuring  
PT biological activity related to focal adhesion kinase 2 function with or  
PT without the test agent.

PS Disclosure; SEQ ID NO 70; 247pp; English.

The present invention relates to a method for selecting agents that are potentially useful for the treatment of Alzheimer's disease. The method comprises contacting Focal Adhesion Kinase 2 (FAK2) with a test agent and measuring a biological activity related to FAK2 function in the presence and absence of the test agent. The method is useful for screening compounds or agents that can be used to treat neurological disorders, ailments and diseases including mild cognitive impairment, depression, schizophrenia, obsessive-compulsive disorder, bipolar disorder, and neurodegenerative diseases and disorders and motor neuron diseases and disorders such as Alzheimer's disease, Parkinson's disease, dementia with Lewy bodies, amyotrophic lateral sclerosis or Lou Gehrig's disease, Alpers' disease, Leigh's disease, Pelizaeus-Wertheft disease, Olivopontocerebellar atrophy, Friedreich's ataxia, leukodystrophies, Rett syndrome, Ramsay Hunt syndrome type II, and Down's syndrome, as well as for treating or preventing other diseases such as distalpendia, diabetes, obesity, cardiovascular diseases such as atherosclerosis and coronary heart disease. Also disclosed is the coding sequence for a novel human phosphatase called PN7740 (ADU8628 and ADU8629). PN7740 contains a protein phosphatase 2C domain, which likely acts to dephosphorylate specific phospho-serine or phospho-threonine residues on particular protein substrates. Although the precise role played by protein phosphatase 2Cs in Alzheimer's disease pathogenesis has yet to be defined, the inventors have discovered that fragments of PN7740 interact with the first phosphorylation binding domain (PTB) domain of Pe65 (also known as APPB1/710) or amyloid beta (A4) precursor protein-binding, family B, member 1, isoform B9 (710), suggesting that PN7740 may well be involved somehow. Pe65 is known to interact with the cytosolic C-terminal region of Amyloid beta (A4) precursor protein (APP) and APP metabolism is critical to the pathogenesis of Alzheimer's disease, because it leads to the release of either toxic Aβeta or trophic secreted APP (sAPP) metabolites. The present sequence is an antisense oligonucleotide which can be used in antisense therapy for Alzheimer's disease.

**SQ** Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match	72.0%	Score 14.4	DB 13	Length 20
Best Local Similarity	93.8%	Pred. No. 2.4e+03		
Matches 15, Conservative	0	Mismatches 1	Indels 0	Gaps 0

```

QY      3 GTAGTCAGGCGGAG 18
          |||||
Db     16 GTAGTCATGCGGAG 1

```

RESULT 10  
AA174524/C  
ID AA174524 standard; DNA; 51 BP

AC AAI74524;  
VY

DT 09-NOV-2001 (first entry)  
XY

DE Human silent SNP containing nucleic acid SEQ:1465  
XY

KM Human; single nucleotide polymorphism; SNP; genome; gene therapy,  
 protein therapy; vaccine; probe; diagnostic assay; detection;  
 KM

OS Homo sapiens

```
XX XX MO200140521-A2.
XX PN
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000WO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX PI WPI; 2001-356160/37.
XX DR
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy.
XX PS Claim 1; Page 502; 2653pp; English.
XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX CC AA53114 to AA53329 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
XX CC therapy, and in vaccine production. (I) and the polypeptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of polymorphic polypeptides. For
XX CC example, (I) may be used to treat disorders by rectifying mutations or
XX CC deletions in a patient's genome that affect the activity of polypeptides
XX CC by expressing inactive proteins or to supplement the patients own
XX CC production of polypeptide. Additionally, (I) and its complementary
XX CC sequences may also be used as DNA probes in diagnostic assays to detect
XX CC and quantitate the presence of similar nucleic acids in samples, and
XX CC therefore which patients may be in need of restorative therapy. The
XX CC polypeptides encoded by (I) may be used as antigens in the production of
XX CC antibodies specific for polymorphic polypeptides. The antibodies may also
XX CC be used to down regulate expression and activity. The antibodies may also
XX CC be used as diagnostic agents for detecting the presence of polymorphic
XX CC polypeptides in samples
XX SQ
XX Sequence 51 BP; 10 A; 19 C; 10 G; 12 T; 0 U; 0 Other;
XX
Query Match 71.0%; Score 14.2; DB 4; Length 51;
Best Local Similarity 84.2%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGTAGTTGAGCGCGGAGC 19
Db 28 GGGTGGTACAGCGCGGAGC 10
RESULT 11
ABN52875/c
ID ABN52875 standard; DNA; 65 BP.
XX AC ABN52875;
XX
XX 15-JUL-2002 (first entry)
XX DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25623.
XX XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX KM splice variant; transcriptome; oligonucleotide library; ss.
XX OS Mus musculus.
XX OS WO200210449-A2.
XX PN
XX PD 07-FEB-2002.
XX PF 20-JUL-2001; 2001WO-1B001903.
XX XX
```

```
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX XX
XX PA (COMP-) COMPUGEN INC.
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX PI WPI; 2002-257383/30.
XX DR
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX PT selectively hybridize to mRNAs transcribed from a transcription unit of a
XX PT genome, useful for detecting tissue-, pathology-, and developmental-
XX PT specific genes.
XX PS Example 1; SEQ ID NO 25623; 47pp; English.
XX CC The present invention describes oligonucleotide libraries for detecting
XX CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
XX CC transcriptome comprises messenger RNAs transcribed from multiple
XX CC transcription units that populate a genome. The library comprises several
XX CC oligonucleotides, each capable of hybridising selectively to a set of
XX CC messenger RNAs transcribed from a given transcription unit of the genome,
XX CC which encodes one or more messenger RNA splice variants. The
XX CC oligonucleotide libraries are useful for detecting mRNAs from a
XX CC biological sample, in expression profiling studies, in qualitatively or
XX CC quantitatively characterising the corresponding transcriptome, and in
XX CC detecting RNA transcripts and splice variants of human or animal
XX CC transcriptomes. The libraries may also be used as specialised mini
XX CC libraries to detect transcripts of a sub-transcriptome under a particular
XX CC biological or pathological state, and so allowing the detection of tissue
XX CC - and pathology-specific genes such as those genes only expressed in
XX CC specific tissue under a specific pathological condition; to detect
XX CC developmental specific genes; and to detect RNA transcripts and splice
XX CC variants of a transcriptome of a patient suffering from a particular
XX CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
XX CC rats, humans and mice, which are used in the exemplification of the
XX CC present invention. N.B. The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ
XX Sequence 65 BP; 19 A; 19 C; 13 G; 14 T; 0 U; 0 Other;
XX
Query Match 71.0%; Score 14.2; DB 6; Length 65;
Best Local Similarity 84.2%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGTAGTTGAGCGCGGAGCG 20
Db 65 GGTAGTTCCTGTCGGAGCG 47
RESULT 12
AAF75497/c
ID AAF75497 standard; DNA; 95 BP.
XX AC AAF75497;
XX
XX 14-MAY-2001 (first entry)
XX DE Codon-optimised HPV6 E2 fragment 6M.
XX XX Human papillomavirus; HPV; HPV6a; HPV18; L1; E2; E7; E1;
XX KM antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX OS Human papillomavirus.
XX OS Synthetic.
XX OS WO200114416-A2.
XX PN
XX PD 01-MAR-2001.
XX PF 21-AUG-2000; 2000WO-US022932.
XX XX
```

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PR 25-AUG-1999; 99US-0150728P.
PR 07-JUN-2000; 2000US-0210143P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Neoper MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
XX
XX MPI; 2001-218428/22.
XX
XX Novel synthetic polynucleotide encoding human papillomavirus (HPV)
XX protein or mutated HPV protein useful as anti-HPV vaccines, comprises
XX optimized-codons for expression of the viral proteins in human host
XX cells.
XX
XX Example 6; Fig 23; 119pp; English.
XX
XX The present sequence is an oligomer which was used in the assembly of one
XX of a number of synthetic polynucleotides that encode a human
XX papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
XX mutated HPV proteins have reduced protein function as compared to wild
XX type proteins but maintain immunogenicity. The proteins comprise codons
XX for optimised expression in humans. The polynucleotides are useful as a
XX vaccine which provides effective immunoprophylaxis against papillomavirus
XX infection through stimulation of neutralising antibody and cell-mediated
XX immunity
XX
XX Sequence 95 BP; 23 A; 36 C; 23 G; 13 T; 0 U; 0 Other;
XX
XX Query Match 71.0%; Score 14.2; DB 4; Length 95;
XX Best Local Similarity 84.2%; Pred. No. 3.4e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 GGTAAGTCAGCGCGGAGCG 20
DB 92 GATCGTTACGCGCGTAGCG 74

RESULT 13
AA75498
ID AA75498 standard; DNA; 96 BP.
XX
XX AA75498;
XX
XX 14-MAY-2001 (first entry)
XX
XX Codon-optimised HPV6 E2 fragment 6N.
XX
XX Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
XX antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX
XX Human papillomavirus.
XX Synthetic.
XX
XX WO200114416-A2.
XX
XX 01-MAR-2001.
XX
XX 21-AUG-2000; 2000WO-US022932.
XX
XX 25-AUG-1999; 99US-0150728P.
XX PR 07-JUN-2000; 2000US-0210143P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Neoper MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
XX
XX MPI; 2001-218428/22.
XX
XX Novel synthetic polynucleotide encoding human papillomavirus (HPV)
XX protein or mutated HPV protein useful as anti-HPV vaccines, comprises
XX optimized-codons for expression of the viral proteins in human host
XX cells.
XX

```

```

PS Example 6; Fig 23; 119pp; English.
XX
XX The present sequence is an oligomer which was used in the assembly of one
XX of a number of synthetic polynucleotides that encode a human
XX papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
XX mutated HPV proteins have reduced protein function as compared to wild
XX type proteins but maintain immunogenicity. The proteins comprise codons
XX for optimised expression in humans. The polynucleotides are useful as a
XX vaccine which provides effective immunoprophylaxis against papillomavirus
XX infection through stimulation of neutralising antibody and cell-mediated
XX immunity
XX
XX Sequence 96 BP; 13 A; 23 C; 40 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 71.0%; Score 14.2; DB 4; Length 96;
XX Best Local Similarity 84.2%; Pred. No. 3.4e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 GGTAAGTCAGCGCGGAGCG 20
DB 73 GATCGTTACGCGCGTAGCG 91

RESULT 14
ABS52695
ID ABS52695 standard; RNA; 74 BP.
XX
XX ABS52695;
XX
XX 15-NOV-2002 (first entry)
XX
XX Elongator tRNA Aaa-CA.
XX
XX Translation; ss; cell-free translation system; insulin; tRNA;
XX growth hormone; erythropoietin; ribosome display; mRNA display.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX FT 1..7
XX FT misc_binding
XX FT /tag= a
XX FT /bound_molecy= "Nucleotides 71-65 of the present
XX FT sequence"
XX FT
XX FT modified_base
XX FT /tag= b
XX FT /note= "Shown as S4U in the specification"
XX FT
XX FT stem_loop
XX FT /tag= c
XX FT /note= "OTHER= D"
XX FT
XX FT misc_difference
XX FT /tag= d
XX FT /label= OTHER
XX FT /note= "OTHER= D"
XX FT
XX FT misc_difference
XX FT /tag= e
XX FT /label= OTHER
XX FT /note= "OTHER= D"
XX FT
XX FT stem_loop
XX FT /tag= e
XX FT /label= OTHER
XX FT /note= "OTHER= D"
XX FT
XX FT misc_difference
XX FT /tag= f
XX FT /label= OTHER
XX FT /note= "OTHER= Q"
XX FT
XX FT modified_base
XX FT /tag= g
XX FT /note= "16A"
XX FT
XX FT misc_difference
XX FT /tag= h
XX FT /label= OTHER
XX FT /note= "OTHER= Psi"
XX FT
XX FT modified_base
XX FT /tag= i
XX FT /label= Smg
XX FT
XX FT stem_loop
XX FT /tag= j
XX FT /label= Smg
XX FT

```

```
FT misc_difference 55 /*tag= k
FT /*tag= j
FT /label= OTHER
FT /note= "OTHER= Psi"
FT misc_binding 65. .71
FT /*tag= 1
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XX
XX MO200259293-A2.
XX
XX 01-AUG-2002.
XX
XX 25-JAN-2002; 2002WO-US002344.
XX
XX 25-JUN-2001; 2001US-0264147P.
XX
XX (FORS/) FORSTER A C.
XX (BLAC/) BLACKLOW S C.
XX
XX Forster AC, Blacklow SC;
XX
XX MPI; 2002-608454/65.
XX
XX A new reconstituted cell-free translation system comprising translation
XX factors and tRNA species capable of translating exogenously added mRNAs,
XX useful for the synthesis of peptides or protein ligands or catalysts,
XX e.g. inulin.
XX
XX Disclosure; Fig 14; 83pp; English.
XX
XX This invention relates to a novel reconstituted cell-free translation
XX system comprising translation factors and transfer ribonucleic acid
XX (tRNA) species which translate exogenously added messenger RNA (mRNA)
XX with highly selective incorporation at each codon to form a peptide or a
XX peptidomimetic product when the system includes one or more tRNA species
XX charged with a synthetic amino acid or amino acid analogue. The
XX translation system of the invention is useful for the synthesis of
XX peptide or protein ligands or catalysts, such as inulin, growth hormone
XX or erythropoietin, and for pure ribosome display and pure mRNA display
XX selection experiments. The translation process provides a simplified,
XX highly purified system that offers potentially improved routes to all
XX peptides and proteins currently synthesised by alternative routes. This
XX overcomes the limitations of the prior art, e.g. difficulty in
XX maintaining purified components and trace contaminants or inefficient
XX processivity. There are several advantages associated with performing
XX peptide and protein display in a pure system, such as an expected lack of
XX post-translational modification of peptides, lack of proteases which
XX often cause protein degradation problem and a lack of competition from
XX CC contaminants in the selection steps. The present sequence represents the
XX CC Cys tRNA molecule used in an example of the cell free translation method
XX of the invention
XX
XX Sequence 74 BP; 15 A; 17 C; 21 G; 1 T; 15 U; 5 Other;
XX
XX Query Match 70.0%; Score 14; DB 6; Length 74;
XX Best Local Similarity 68.8%; Pred. No. 4.2e+03;
XX Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 3 GTAGTTCAGCGCGGAG 18
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DB 7 GUAGUUCAGNCGGNAG 22
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RESULT 15
ADA14190
ID ADA14190 standard; DNA; 66 BP.
XX
XX ADA14190;
AC
XX 20-NOV-2003 (first entry)
DT
XX
DE C3 nucleic acid ligand sequence SEQ ID NO:139.
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XX
XX detection; photoreactive nucleic acid ligand; photocrosslink;
XX solid support; HIV; gp120; photocrosslinking nucleic acid ligand; ss.
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XX Synthetic.
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XX Key Location/Qualifiers
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XX /*tag= a
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XX /note= "5'-amino-c6-g"
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XX MO2003070984-A1.
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XX 28-AUG-2003.
XX
XX 10-FEB-2003; 2003WO-US004142.
XX
XX 15-FEB-2002; 2002US-0357297P.
XX 01-APR-2002; 2002US-00114187.
XX 26-JUL-2002; 2002US-0398666P.
XX 02-AUG-2002; 2002US-0400759P.
XX
XX (SOMA-) SOMALOGIC INC.
XX
XX Gold L, Zichi DA, Smith JD, Schneider DJ, Greef C;
XX
XX MPI; 2003-697627/66.
XX
XX Detecting the presence of a target molecule suspected of being contained
XX in a test mixture, where the target molecule is a protein contacting the
XX PT solid support with a Universal Protein Stain and detecting the presence
XX of target molecule.
XX
XX Example 4; Fig 3; 136pp; English.
XX
XX The present invention describes a method for detecting the presence of a
XX target molecule suspected of being contained in a test mixture, where the
XX target molecule is a protein. The method comprises: (a) providing a solid
XX support, comprising a photoreactive nucleic acid ligand having specific
XX affinity for the target protein and that binds specifically to the target
XX molecule through non-Watson-Crick interactions; (b) contacting the solid
XX support with the test mixture suspected of containing the target
XX molecule, where a nucleic acid ligand-target molecule complex is formed
XX if the target molecule is present; (c) irradiating the solid support,
XX where the nucleic acid ligand-target molecule complex photocrosslinks;
XX (d) removing non-specifically bound material from the solid support; (e)
XX contacting the solid support with a universal protein stain (UPS),
XX comprising one or more reagents that label proteins with a detectable
XX moiety; and (f) detecting the presence of the target molecule by
XX detecting the presence of the detectable moiety on the solid support.
XX Also described: (1) a biochip comprising an array of nucleic acid ligands
XX attached to a solid support; (2) attaching a nucleic acid ligand to a
XX solid support; (3) simultaneously measuring the dose-response
XX characteristics of species of photocrosslinking nucleic acid ligands,
XX each of which having specific affinity for a cognate target protein, and
XX CC to HIV gp120. The method is useful for detecting the presence of a target
XX CC molecule suspected of being contained in a test mixture, where the target
XX CC molecule is a protein. The present sequence represents a
XX CC photocrosslinking nucleic acid ligand oligonucleotide, which is used in
XX CC an example from the present invention.
XX
XX Sequence 66 BP; 15 A; 17 C; 22 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 69.0%; Score 13.8; DB 9; Length 66;
XX Best Local Similarity 88.2%; Pred. No. 5.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 GGCTAGTTCAGCGCGGA 17  
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Db 36 GGCTAGTTCAGCGCGGA 52  
|||

Search completed: December 24, 2005, 12:28:57  
Job time : 172.4 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
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C 3	14.2	71.0	97	10	CN802XYN	AL216336 Tetraodd
C 4	14	70.0	100	6	CD959631	CD959631 SW_16 Gg
C 5	13.8	69.0	70	10	CG918269	CG918269 CH240_14
C 6	13.8	69.0	95	6	CD533699	CD533699 3BE1 Atab
C 7	13.8	69.0	89	8	T72387	T72387 YC71d12.x1
C 8	13.6	68.0	62	9	AZ377853	AZ377853 1M0132E21
C 9	13.6	68.0	31	9	AZ920486	AZ920486 1006020AR
C 10	13.6	68.0	69	1	AJ744102	AJ744102 AJ744102
C 11	13.6	68.0	92	9	BH412029	BH412029 1007024HD
C 12	13.6	68.0	96	7	CK112469	CK112469 S008BA02 F
C 13	13.4	67.0	98	10	CG473325	CG473325 OST736 M
C 14	13.2	66.0	38	9	AZ440246	AZ440246 1M0231A18
C 15	13.2	66.0	51	1	AI033458	AI033458 ow94h01.s
C 16	13.2	66.0	51	3	BM431597	BM431597 1DU024E12
C 17	13.2	66.0	60	10	CN802XYN	AL215203 Tetraodd
C 18	13.2	66.0	65	10	AL216274	AL216274 Tetraodd
C 19	13.2	66.0	85	10	CL604005	CL604005 CH240_17
C 20	13	65.0	92	10	BX896637	BX896637 ArabidOPP
C 21	12.8	64.0	23	3	BM388474	BM388474 5009.0-4545
C 22	12.8	64.0	25	8	L32042	L32042 H0MKP2E8A H

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C	27	12.8	64.0	95	5	B0218404
C	28	12.6	63.0	50	1	A1U04217
C	29	12.6	63.0	56	10	BX983419
C	30	12.6	63.0	64	10	CG705429
C	31	12.6	63.0	65	10	CG705453
C	32	12.6	63.0	66	10	AG189248
C	33	12.6	63.0	66	10	CG713805
C	34	12.6	63.0	67	6	CA333624
C	35	12.6	63.0	69	5	B0761873
C	36	12.6	63.0	75	11	CR128533
C	37	12.6	63.0	77	1	A0022596
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C	44	12.6	63.0	86	8	DN484908
C	45	12.6	63.0	88	1	AW302675

## ALIGNMENTS

## RESULT 1

BH609118/c

**LOCUS**

## DEFINITION

**ACCESSION**

**VERSION**

## REFERENCES

ORGANISM

## REFERENCE

## AUTHORS

**TITLE**

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COMMENT

## FEATURES

**SOURCE**

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ORIGIN

Query Ma

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### Matches

Qy

1

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RESULT 2  
AA406204/c 97 bp mRNA linear EST 17-MAY-1997  
LOCUS z65d04.s1 Soares testis NHT Homo sapiens cDNA IMAGE:742855  
DEFINITION 3' similar to SM:UUKM.BOVIN P42026 NADH-UBIQUINONE OXIDOREDUCTASE  
20 KD SUBUNIT PRECURSOR ;, mRNA sequence.  
AA406204  
ACCESSION AA406204.1 GI:2064185  
VERSION EST.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 97)  
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,  
Kucaba,T., Lacy,M., Le,N., Lennon,G., Maira,M., Martin,J.,  
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,  
White,Y., Wylie,T., Waterston,R. and Wilson,R.  
WashU-Merck EST Project 1997  
JOURNAL Unpublished (1997)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watsn.wustl.edu  
This clone is available royalty-free through LNLN ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand  
Seq primer: -4mln3 fwd. RT from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..97  
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/db\_xref="GDB:5929850"  
/db\_xref="taxon:9606"  
/clone="IMAGE:742855"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5].  
TCTTACCAATCTGAGTGGGAGCGCGCCATTTTCTTTTCTTTT 3'.  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
Query Match 71.0%; Score 14.2; DB 1; Length 97;  
Best Local Similarity 84.2%; Pred. No. 4.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GGTAGTTCAGCGCGAGCG 20  
DB 42 GGAAGATCAAGCGGAGCG 24

RESULT 3  
CNS02VXN 97 bp DNA linear GSS 01-SEP-2000  
LOCUS Tetradon nigroviridis genome survey sequence T7 end of clone  
DEFINITION 175B09 of library G from Tetradon nigroviridis, genomic survey  
sequence.  
ACCESSION AL216356

VERSION AL216356.1 GI:7875175  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetradon nigroviridis  
ORGANISM Tetradon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;  
Tetradontidae; Tetradontidae; Tetradon.  
REFERENCE 1  
Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,M. and Weissenbach,J.  
Estimate of human gene number provided by genome-wide analysis  
using Tetradon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)  
10835645  
JOURNAL  
PUBMED  
REFERENCE 2  
Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C.,  
Fizames,C., Fischer,C., Bouneau,L., Billaule,A., Quetier,F.,  
Saurin,M., Bernot,A. and Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetradon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)  
10899143  
JOURNAL  
PUBMED  
REFERENCE 3 (bases 1 to 97)  
Genoscope.  
Direct Submision  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetradon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetradon.  
Location/Qualifiers  
1..97  
/organism="Tetradon nigroviridis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:99883"  
/clone="175B09"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COAG175CA05LP1  
end : 17"

ORIGIN  
Query Match 71.0%; Score 14.2; DB 10; Length 97;  
Best Local Similarity 84.2%; Pred. No. 4.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GGTAGTTCAGCGCGAGCG 20  
DB 55 GGTCTTCAGCGGAGCG 73

RESULT 4  
CD959631/c 100 bp mRNA linear EST 15-JUL-2003  
LOCUS SCW 46 Genetag2 Zea mays cDNA, mRNA sequence.  
DEFINITION CD959631  
ACCESSION CD959631.1 GI:32807397  
VERSION EST.  
KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 100)  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
33, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genome programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).  
Location/Qualifiers

## FEATURES

source

1..100  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="mixtured"  
/db\_xref="taxon:4577"  
/clone\_1ib="Genet92"

## ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 100;  
Best Local Similarity 100.0%; Pred. No. 5.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 TAGTTCAGCGCGGA 17  
|||||  
Db 33 TAGTTCAGCGCGGA 20

RESULT 5  
CG918269/c 70 bp DNA linear GSS 12-DEC-2003  
LOCUS CH240\_142F20.TU CHORI-240 Bos taurus genomic clone CH240\_142F20,  
DEFINITION genomic survey sequence.  
ACCESSION CG918269  
VERSION CG918269.1 GI:39777952  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 70)  
Costa, J.N., Mota, M. and Caetano, A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_142F20.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasilia  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetanoc@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
Bases shown have phred quality value equal to or higher than 20.  
For BAC library availability, please contact Pieter de Jong  
([pdejong@mail.choi.org](mailto:pdejong@mail.choi.org)).  
Clones may be purchased from BACPAC Resources  
([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 142 Row: F Column: 20  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 70.  
Location/Qualifiers

## FEATURES

source

1..70  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_142F20"

/sex="Male"  
/cell\_type="Blood"  
/clone\_1ib="CHORI-240"  
/note="Vector: pTARBA01.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99315; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 70;  
Best Local Similarity 88.2%; Pred. No. 6.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GGAGTTCAGCGCGGA 17  
|||||  
Db 30 GGAGTTCAGCGCGGA 14

RESULT 6  
CD533699/c 85 bp mRNA linear EST 31-DEC-2003  
LOCUS 33E1 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA  
DEFINITION 3', mRNA sequence.  
ACCESSION CD533699  
VERSION CD533699.1 GI:40453711  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (chale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 85)  
Guo, Y., Cai, Z. and Gan, S.  
Transcriptome of Arabidopsis leaf senescence  
Plant Cell Environ. 27 (5), 521-549 (2004)  
Contact: Susheng Gan  
Department of Horticulture  
Cornell University  
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA  
Tel: 607 254 5418  
Fax: 607 255 0599  
Email: sg288@cornell.edu  
Insert Length: 85 Std Error: 0.00  
Seq primer: 17  
POLYA-No.

## FEATURES

source

Location/Qualifiers  
1..85  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/ecotype="landsberg erecta"  
/db\_xref="taxon:3702"  
/tissue\_type="Leaf"  
/dev\_stage="Yellow Leaf with Greenish Base Area"  
/lab\_host="E. coli"  
/clone\_1ib="Arabidopsis Leaf Senescence Library"  
/note="Organ: Rosette leaf; Vector: pBluscript SKII+;  
Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5  
and #6 (counted from the bottom) were harvested and  
immediately frozen in liquid N2. The leaves were visibly  
yellow excepted for the leaf base areas that were still  
greenish."

## ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 85;  
Best Local Similarity 78.9%; Pred. No. 6.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 GGAGTTCAGCGCGGAGC 20  
|||||  
Db 75 GGAGTTCAGCGCGGAGC 57

RESULT 7  
TT2387/c

LOCUS	T72387	99 bp	mRNA	linear	EST 01-MAR-1995
DEFINITION	yc17id12.r1 Strata gene liver (#937224) Homo sapiens cDNA clone IMAGE:86135' similar to gb:X06985_1nal HEME OXYGENASE 1 (HUMAN); , mRNA sequence.				
ACCESSION	T72387				
VERSION	T72387.1	GI:686908			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 99) Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Glen, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaekis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Maria, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)				
AUTHORS	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu				
TITLE	Insert Size: 43				
JOURNAL	High quality sequence states: 1 High quality sequence stops: 1				
PUBMED	Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality				
COMMENT	Seq primer: M13Rp1 High quality sequence stop: 1. Location/Qualifiers <pre>1..99 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:503192" /db_xref="taxon:9606" /clone="IMAGE:86135" /sex="male" /dev_stage="49 years old" /lab_host="SOLR cells (kanamycin resistant)" /clone_lib="Stratagene liver (#937224)" /note="Organ: liver; Vector: pluscript SK; Site: 1; ECOR1; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5' CTCCAGTTTTTTTTTTTTTTTTT 3'"</pre>				
FEATURES	<p>source</p> <p>Query Match 69.0%; Score 13.8; DB 8; Length 99;</p> <p>Best Local Similarity 78.9%; Pred. NO. 6.5e+04;</p> <p>Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p> <p>OY 2 GGTAATTCAAGCGGAGCG 20</p> <p>Db 49 GGGAGTTCATGCGGNNCG 31</p>				
RESULT 8	A2377853/c				
LOCUS	A2377853	32 bp	DNA	linear	GSS 02-OCT-2000
DEFINITION	IM0132B21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0132B21 F, genomic survey sequence.				
ACCESSION	A2377853				
VERSION	A2377853.1	GI:10491553			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				

ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 32) Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weis University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0132 row: E column: 21 Seq primer: CGTGTAAACGACGCGCAGT Class: plasmid High quality sequence stop: 32.
FEATURES	Location/Qualifiers 1..32 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGC1M0132E21" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_1kb="Mouse 10kb plasmid UGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1473114[gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted vector DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN	' Query Match 68.0%; Score 13.6; DB 9; Length 32; Best Local Similarity 80.0%; Pred. No. 8.1e+04; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY	1 GCGTAGTTCAGCGCGGACGC 20       
DB	20 GGATTAAGCCAGCGCGGACGC 1
RESULT 9	AZ920486 61 bp DNA linear GSS 17-DEC-2001
AZ920486/c	
LOCUS	AZ920486 61 bp DNA linear GSS 17-DEC-2001
DEFINITION	1006020A02.x1 1006 - Rescuemu Grid G Zea mays genomic, genomic survey sequence.
ACCESSION	AZ920486
VERSION	AZ920486.1 GI:13391189
KEYWORDS	GSS.

SOURCE  
ORGANISM Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 61)  
Walbot, V.  
Maize genomic sequences found using engineered RescuerMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 723 8221  
Email: walbot@stanford.edu  
Plate: 1006020 ROW: 38  
Class: transposon-tagged.  
Location/Qualifiers  
1..61  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/issue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="11006 - RescuerMu Grid G"  
/note="Organ: leaf; Vector: RescuerMu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
RescuerMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescuerMu, go to the web  
site 'www.zmdb.iastate.edu' and follow the links for  
'RescuerMu.' Grid G was grown at Stanford in 2000. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

ORIGIN  
Query Match 68.0%; Score 13.6; DB 9; Length 61;  
Best Local Similarity 80.0%; Pred. No. 8.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGCTAGTTCAGCGGAGCG 20  
|||||  
DB 61 GGCTAGTTTGGCGGCGCG 42

FEATURES  
source  
1..61  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/issue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="11006 - RescuerMu Grid G"  
/note="Organ: leaf; Vector: RescuerMu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
RescuerMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescuerMu, go to the web  
site 'www.zmdb.iastate.edu' and follow the links for  
'RescuerMu.' Grid G was grown at Stanford in 2000. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

RESULT 10  
AJ744102 69 bp mRNA linear EST 17-FEB-2005  
LOCUS AJ744102.1 riken1 gallus gallus CDNA clone 22K1382, mRNA sequence.  
DEFINITION AJ744102  
ACCESSION AJ744102.1 GI:53909461  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianidae; Gallus.  
1 (bases 1 to 69)  
Caldwell, R.B., Kleerek, A.M., Arakawa, H., Bezubov, Y., Zaim, J.,  
Fiedler, P., Kutter, S., Blagoder, A., Kosovska, D., Koser, M.,  
Plachy, J., Carninci, P., Hayashizaki, Y. and Buerstedde, J.M.,  
Full-length cDNAs from chicken bursal lymphocytes to facilitate  
gene function analysis  
Genome Biol. 6 (1), R6 (2005)  
JOURNAL PUBMED  
PUBMED 15642098  
COMMENT  
Contact: Caldwell RB  
GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie

FEATURES  
source  
Location/Qualifiers  
1..69  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="22K1382"  
/cell\_type="bursal lymphocyte"  
/dev\_stage="2-3 weeks old"  
/clone\_lib="riken1"  
/note="CB inbred strain"

ORIGIN  
Query Match 68.0%; Score 13.6; DB 1; Length 69;  
Best Local Similarity 80.0%; Pred. No. 8.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGCTAGTTCAGCGGAGCG 20  
|||||  
DB 35 GAGGGGCTCAGCGGAGCG 16

FEATURES  
source  
1..92  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/issue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1007 - RescuerMu Grid H"  
/note="Organ: leaf; Vector: RescuerMu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
RescuerMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescuerMu, go to the web  
site 'www.zmdb.iastate.edu' and follow the links for  
'RescuerMu.' Grid H was grown at Berkeley in 2001. DNA  
was extracted from leaf punches, double digested using  
BamHI and BglII, and ligated to form circular plasmids.  
DH10B cells were transformed and then screened on LB  
plates with ampicillin."

ORIGIN  
Query Match 68.0%; Score 13.6; DB 9; Length 92;

RESULT 11  
BH412029 92 bp DNA linear GSS 12-DEC-2001  
LOCUS BH412029/c  
DEFINITION 1007024H03.y1 1007 - RescuerMu Grid H Zea mays genomic, genomic  
survey sequence.  
ACCESSION BH412029  
VERSION BH412029.1 GI:17584839  
KEYWORDS  
SOURCE  
ORGANISM Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 92)  
Walbot, V.  
Maize genomic sequences found using engineered RescuerMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 723 8221  
Email: walbot@stanford.edu  
Plate: 1007024 column: 14  
Class: transposon-tagged.  
Location/Qualifiers  
1..92  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/issue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1007 - RescuerMu Grid H"  
/note="Organ: leaf; Vector: RescuerMu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
RescuerMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescuerMu, go to the web  
site 'www.zmdb.iastate.edu' and follow the links for  
'RescuerMu.' Grid H was grown at Berkeley in 2001. DNA  
was extracted from leaf punches, double digested using  
BamHI and BglII, and ligated to form circular plasmids.  
DH10B cells were transformed and then screened on LB  
plates with ampicillin."





/strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCTM0231A18"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGGCTM library"  
 /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 38;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGAGTTCAGCGGAGC 19  
 |||||  
 Db 30 GGAAITTAGCGAGAGC 13

RESULT 15  
 AI033458 51 bp mRNA linear EST 28-AUG-1998  
 LOCUS ow94h01.91 Soares fetal\_liver\_spleen\_INFLS\_S1 Homo sapiens cDNA  
 DEFINITION clone IMAGE:1654513 3' similar to gb:M81181  
 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);, mRNA  
 sequence.

ACCESSION AI033458  
 VERSION AI033458.1 GI:3254411  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 51)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strauberg, Ph.D.  
 Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert length: 400 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amerham  
 High quality sequence stop: 1.  
 Location/Qualifiers

## FEATURES

1..51  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1654513"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal liver spleen\_INFLS\_S1"  
 /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)  
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
 This is a subtracted version of the original Soares fetal  
 liver spleen INFLS library. 1st strand cDNA was primed  
 with a Pac I - oligo(dT) primer [5',  
 AACCTGAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified p773 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 1; Length 51;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTAGTTCAGCGGAGCG 20  
 |||||  
 Db 33 GTAGCTCAGCTGAGCTG 50

Search completed: December 24, 2005, 18:28:32  
 Job time : 1575 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds  
(without alignments)  
739.111 Million cell updates/sec

Title: US-09-296-264-6  
Perfect score: 20  
Sequence: 1 gggatgcagcgcgagcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/1 COMB. seq: \*  
2: /cgn2\_6/ptodata/1/ina/5 COMB. seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A COMB. seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B COMB. seq: \*  
5: /cgn2\_6/ptodata/1/ina/H COMB. seq: \*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB. seq: \*  
7: /cgn2\_6/ptodata/1/ina/PP COMB. seq: \*  
8: /cgn2\_6/ptodata/1/ina/RE COMB. seq: \*  
9: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.6	68.0	88	3	US-09-513-999C-13933
2	13.4	67.0	42	3	US-08-879-565-9
3	13.4	67.0	63	2	US-08-530-492-6
4	13.4	67.0	73	3	US-08-906-517-6
5	13.4	67.0	73	2	US-07-982-712-12
6	13.2	66.0	28	2	US-08-408-656-7
7	13.2	66.0	28	6	PCT-US95-03602-7
8	13.2	66.0	33	2	US-08-432-871C-14
9	13.2	66.0	33	3	US-09-270-956-14
10	13.2	66.0	75	3	US-09-513-999C-34512
11	13.2	66.0	97	3	US-09-513-999C-17808
12	12.8	64.0	21	3	US-09-262-773-105
13	12.8	64.0	40	3	US-09-830-337-6
14	12.8	64.0	48	2	US-08-391-000-11
15	12.8	64.0	48	2	US-08-741-931-11
16	12.8	64.0	50	3	US-10-131-827-2780
17	12.8	64.0	60	3	US-09-144-428-62
18	12.8	64.0	88	3	US-09-513-999C-36170
19	12.6	63.0	25	3	US-09-396-196G-55656
20	12.6	63.0	38	3	US-09-771-035A-42
21	12.6	63.0	100	3	US-09-621-976-8298
22	12.4	62.0	24	2	US-08-508-088-5
23	12.4	62.0	24	2	US-09-009-925-5
24	12.4	62.0	27	3	US-09-314-847A-13

25	12.4	62.0	27	3	US-10-037-677A-15	Sequence 15, Appl
26	12.4	62.0	62	3	US-09-935-338-71	Sequence 71, Appl
27	12.4	62.0	65	2	US-08-453-104-11	Sequence 11, Appl
28	12.4	62.0	65	2	US-08-694-824-11	Sequence 11, Appl
29	12.4	62.0	73	2	US-08-453-104-20	Sequence 20, Appl
30	12.4	62.0	73	2	US-08-694-824-20	Sequence 20, Appl
31	12.4	62.0	99	3	US-09-407-605-86	Sequence 86, Appl
32	12.2	61.0	20	3	US-09-344-529-15	Sequence 15, Appl
33	12.2	61.0	20	3	US-09-907-884-30	Sequence 30, Appl
34	12.2	61.0	25	2	US-08-412-376-3	Sequence 3, Appl
35	12.2	61.0	25	2	US-08-859-998-1021	Sequence 1021, Ap
36	12.2	61.0	25	3	US-08-646-273-32	Sequence 32, Appl
37	12.2	61.0	25	3	US-09-225-928-1021	Sequence 1021, Ap
38	12.2	61.0	25	3	US-09-225-201B-1021	Sequence 1021, Ap
39	12.2	61.0	25	3	US-09-396-196G-53377	Sequence 53377, A
40	12.2	61.0	29	3	US-10-083-246A-128	Sequence 128, App
41	12.2	61.0	31	6	PCT-US92-10792-29	Sequence 29, Appl
42	12.2	61.0	70	3	US-09-871-579-2	Sequence 2, Appl
43	12.2	61.0	70	3	US-09-871-579-14	Sequence 14, Appl
44	12.2	61.0	72	3	US-09-871-579-7	Sequence 7, Appl
45	12.2	61.0	74	3	US-09-621-976-12304	Sequence 12304, A

## ALIGNMENTS

RESULT 1  
US-09-513-999C-13933/C  
Sequence 13933, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Ductert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513, 999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 13933  
LENGTH: 88  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-13933

Query Match 68.0%; Score 13.6; DB 3; Length 88;  
Best Local Similarity 80.0%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGATGTCAGCGGAGCG 20  
Db 85 GCGAAGTCAGCGGAGCG 66

RESULT 2  
US-08-879-565-9  
Sequence 9, Application US/08879565A  
Patent No. 6093573  
GENERAL INFORMATION:  
APPLICANT: Beamier, Lesa J.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Eisenberg, David  
TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF  
TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN  
FILE REFERENCE: 1103/11034US01  
CURRENT APPLICATION NUMBER: US/08/879, 565A  
CURRENT FILING DATE: 1997-06-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
OTHER INFORMATION: Oligonucleotide complementary to SEQ ID NO:8  
US-08-879-565-9

Query Match 67.0%; Score 13.4; DB 3; Length 42;  
Best Local Similarity 93.3%; Pred. No. 2.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTTCAGCGCGGACG 20  
DB 3 GTTCAGCGCGGACG 17

## RESULT 3

US-08-530-492-6  
Sequence 6, Application US/0850492  
Patent No. 5689052

## GENERAL INFORMATION:

APPLICANT: Brown, Sherri M.  
APPLICANT: Dean, Duff A.  
APPLICANT: Fromm, Michael E.  
APPLICANT: Sanders, Patricia R.  
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced  
TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For  
NUMBER OF INVENTIONS: Preparation Thereof  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESS: Dennis R. Hoerner, Jr., Monsanto Co. B44F  
STREET: 700 Chesterfield Parkway No. 5689052ch  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA

ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/530,492  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/172,333  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10605)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6099  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: DNA (synthetic)  
US-08-530-492-6

Query Match 67.0%; Score 13.4; DB 2; Length 63;  
Best Local Similarity 93.3%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTCAGCGCGGACG 19  
DB 26 AGTTCAGCGCGGACG 40

RESULT 4  
US-08-906-517-6  
Sequence 6, Application US/08906517  
Patent No. 6180774

## GENERAL INFORMATION:

APPLICANT: Brown, Sherri M.  
APPLICANT: Dean, Duff A.  
APPLICANT: Fromm, Michael E.  
APPLICANT: Sanders, Patricia R.  
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced  
TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For  
NUMBER OF INVENTIONS: Preparation Thereof  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESS: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA

ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,517  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: NOBT:170  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-474-7577  
TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-906-517-6

Query Match 67.0%; Score 13.4; DB 3; Length 63;  
Best Local Similarity 93.3%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTCAGCGCGGACG 19  
DB 26 AGTTCAGCGCGGACG 40

RESULT 5  
US-07-982-712-12  
Sequence 12, Application US/07982712  
Patent No. 5436391

GENERAL INFORMATION:  
APPLICANT: Hiroya FUJIMOTO, Kimiko ITOH  
APPLICANT: Mikihito YAMAMOTO, and Ko SHIMAMOTO  
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous  
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb

Query Match 67.0%; Score 13.4; DB 2; Length 63;  
Best Local Similarity 93.3%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/992,712  
FILING DATE: 19921127  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 73 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-07-982-712-12

Query Match 67.0%; Score 13.4; DB 2; Length 73;  
Best Local Similarity 93.3%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTCAGCGCGGAGC 19  
DB 29 AGTCAGAGGAGC 43

RESULT 6  
US-08-408-656-7  
Sequence 7, Application US/08408656  
Patent No. 5674683  
GENERAL INFORMATION:  
APPLICANT: KOOL, Eric T.  
TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530-0239  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,656  
FILING DATE: 21-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9373  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: circular  
US-08-408-656-7

Query Match 66.0%; Score 13.2; DB 2; Length 28;  
Best Local Similarity 83.3%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGGAG 18  
DB 6 GGGTGCTCCAGAGGAG 23

RESULT 7  
PCT-US95-03602-7  
Sequence 7, Application PC/TUS9503602  
GENERAL INFORMATION:  
APPLICANT: Research Corporation Technologies, Inc.  
TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530-0239  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03602  
FILING DATE: 21-MAR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9373  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
PCT-US95-03602-7

Query Match 66.0%; Score 13.2; DB 6; Length 28;  
Best Local Similarity 83.3%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGGAG 18  
DB 6 GGGTGCTCCAGAGGAG 23

RESULT 8  
US-08-432-871C-14/C  
Sequence 14, Application US/08432871C  
Patent No. 5877010  
GENERAL INFORMATION:  
APPLICANT: Loeb, Lawrence A.  
APPLICANT: Black, Margaret B.  
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle

STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,871C  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 240052.409C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..33  
US-08-432-871C-14

Query Match 66.0%; Score 13.2; DB 2; Length 33;  
Best Local Similarity 83.3%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGGAG 18  
||||| ||||| |||||  
Db 26 GGGTAGCAGCAGGAGGAG 9

RESULT 9  
US-09-270-956-14/C  
Sequence 14, Application US/09270956  
Patent No. 6451571  
GENERAL INFORMATION:  
APPLICANT: Loeb, Lawrence A.  
APPLICANT: Black, Margaret E.  
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/270,956  
FILING DATE: 17-MAR-1999  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 240052.409C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..33)  
US-09-270-956-14

Query Match 66.0%; Score 13.2; DB 3; Length 33;  
Best Local Similarity 83.3%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGGAG 18  
||||| ||||| |||||  
Db 26 GGGTAGCAGCAGGAGGAG 9

RESULT 10  
US-09-513-999C-34512/C  
Sequence 34512, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Duciart, A.  
APPLICANT: Dumas Milne Edwards, J.B.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59. US2. REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 34512  
LENGTH: 75  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-34512

Query Match 66.0%; Score 13.2; DB 3; Length 75;  
Best Local Similarity 83.3%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGGAG 18  
||||| ||||| |||||  
Db 68 GGGTAGTGAGGAGGAGGAG 51

RESULT 11  
US-09-513-999C-17808  
Sequence 17808, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duciart, A.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59. US2. REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 17808  
LENGTH: 97  
TYPE: DNA  
ORGANISM: Homo sapiens



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/741,931  
FILING DATE: 31-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/391,000  
FILING DATE: 21-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Neuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 028750-123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-741-931-11

Query Match 64.0%; Score 12.8; DB 2; Length 48;  
Best Local Similarity 87.5%; Pred. No. 4.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TAGTTCAGGCGGGAGC 19  
|||||||  
Db 17 TAGTTCAGGCGGTAGC 2

Search completed: December 24, 2005, 18:36:28  
Job time : 48.1 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-6  
Perfect score: 20  
Sequence: 1 gggtagtcagcgagcgagcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20  
Maximum DB seq length: 100.

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications NA Main:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-6
2	20	100.0	20	3	US-09-296-264-31
3	18	90.0	30	6	US-10-263-162-59
4	14.4	72.0	20	8	US-10-776-013-69
5	14.4	72.0	20	8	US-10-776-013-70
6	14.2	71.0	25	10	US-11-036-317-78024
7	14.2	71.0	25	10	US-11-036-317-531280
8	14.2	71.0	65	3	US-09-908-975-25623
9	14.2	71.0	95	9	US-10-728-131-115
10	14.2	71.0	96	9	US-10-728-131-116
11	13.8	69.0	25	7	US-10-719-956-405220
12	13.8	69.0	25	7	US-10-719-956-224531
13	13.8	69.0	25	9	US-10-956-157-187244
14	13.8	69.0	25	10	US-11-060-756-179496
15	13.8	69.0	57	9	US-10-790-273-6
16	13.6	68.0	25	10	US-11-036-317-953755
17	13.6	68.0	37	8	US-10-865-978-26
18	13.6	68.0	25	8	US-10-719-900-395307
19	13.4	67.0	25	8	US-10-162-743-9
20	13.4	67.0	42	7	US-10-960-853-13
21	13.4	67.0	25	7	US-10-719-956-117106
22	13.2	66.0	25	7	US-10-719-956-421274
23	13.2	66.0	25	7	US-10-719-956-421274

24	13.2	66.0	25	8	US-10-719-900-215966	Sequence 215966,
25	13.2	66.0	25	8	US-10-719-900-378428	Sequence 378428,
26	13.2	66.0	25	9	US-10-843-527-5709	Sequence 5709, Ap
27	13.2	66.0	25	9	US-10-843-527-6198	Sequence 6198, Ap
28	13.2	66.0	25	9	US-10-843-527-231979	Sequence 231979,
29	13.2	66.0	25	9	US-10-843-527-232468	Sequence 232468,
30	13.2	66.0	25	10	US-11-036-317-78914	Sequence 78914, A
31	13.2	66.0	25	10	US-11-036-317-538383	Sequence 538383,
32	13.2	66.0	25	10	US-11-036-317-812158	Sequence 812158,
33	13.2	66.0	31	8	US-10-638-464-12	Sequence 12, Appl
34	13.2	66.0	60	3	US-09-908-975-9754	Sequence 9754, Ap
35	13.2	66.0	60	3	US-09-908-975-22705	Sequence 22705, A
36	13.2	66.0	65	3	US-09-908-975-2370	Sequence 2370, Ap
37	13.2	66.0	65	3	US-09-908-975-28457	Sequence 28457, A
38	13.2	66.0	70	6	US-10-403-232-34	Sequence 34, Appl
39	13.2	66.0	94	3	US-09-783-530-6363	Sequence 6363, Ap
40	13	65.0	25	7	US-10-719-956-40713	Sequence 40713, A
41	13	65.0	25	9	US-10-843-527-119022	Sequence 119022,
42	13	65.0	25	9	US-10-843-527-119155	Sequence 119155,
43	12.8	64.0	25	5	US-10-211-059-236	Sequence 236, App
44	12.8	64.0	25	5	US-10-211-059-237	Sequence 237, App
45	12.8	64.0	25	5	US-10-211-059-238	Sequence 238, App

#### ALIGNMENTS

```

RESULT 1
US-09-296-264-6
; Sequence 6, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; FILE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-6

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGGTAGTCAGCGGAGCG 20
Db 1 GGGTAGTCAGCGGAGCG 20

RESULT 2
US-09-296-264-31/C
; Sequence 31, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; FILE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791

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EARLIER FILING DATE: 1998-04-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Human  
US-09-296-264-31

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTAGTTCAGCGCGGAGCG 20  
Db 20 GGGTAGTTCAGCGCGGAGCG 1

RESULT 3  
US-10-263-162-59/c

Sequence 59, Application US/10263162  
Publication No. US20030186868A1  
GENERAL INFORMATION:  
APPLICANT: Rosenbaum, et al.  
TITLE OF INVENTION: Anti-Angiogenic Peptides  
FILE REFERENCE: REG 810  
CURRENT APPLICATION NUMBER: US/10/263,162  
CURRENT FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: 60/326,712  
PRIOR FILING DATE: 2001-10-03  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 59  
LENGTH: 30  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-263-162-59

Query Match 90.0%; Score 18; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTAGTTCAGCGCGGAGCG 20  
Db 30 GTAGTTCAGCGCGGAGCG 13

RESULT 4  
US-10-776-013-69/c

Sequence 69, Application US/10776013  
Publication No. US20040226056A1  
GENERAL INFORMATION:  
APPLICANT: MYRIAD GENETICS, INC.  
APPLICANT: Koch, Jean-Marc  
APPLICANT: Bartel, Paul  
APPLICANT: Heichman, Karen  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND  
TITLE OF INVENTION: DISEASES  
FILE REFERENCE: 1600.24  
CURRENT APPLICATION NUMBER: US/10/776,013  
CURRENT FILING DATE: 2004-02-09  
PRIOR APPLICATION NUMBER: 09/948904  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: 09/466139  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/113534  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/124120  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/141243  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: 09/975072  
PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240790  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 10/194967  
PRIOR FILING DATE: 2002-07-15  
PRIOR APPLICATION NUMBER: 60/304775  
PRIOR FILING DATE: 2001-07-13  
NUMBER OF SEQ ID NOS: 695  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 69  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-776-013-69

Query Match 72.0%; Score 14.4; DB 8; Length 20;  
Best Local Similarity 93.8%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTAGTTCAGCGCGGAG 18  
Db 18 GTAGTTCAGCGCGGAG 3

RESULT 5  
US-10-776-013-70/c

Sequence 70, Application US/10776013  
Publication No. US20040226056A1  
GENERAL INFORMATION:  
APPLICANT: MYRIAD GENETICS, INC.  
APPLICANT: Koch, Jean-Marc  
APPLICANT: Bartel, Paul  
APPLICANT: Heichman, Karen  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND  
TITLE OF INVENTION: DISEASES  
FILE REFERENCE: 1600.24  
CURRENT APPLICATION NUMBER: US/10/776,013  
CURRENT FILING DATE: 2004-02-09  
PRIOR APPLICATION NUMBER: 09/948904  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: 09/466139  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/113534  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/124120  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/141243  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: 09/975072  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/240790  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 10/194967  
PRIOR FILING DATE: 2002-07-15  
PRIOR APPLICATION NUMBER: 60/304775  
PRIOR FILING DATE: 2001-07-13  
NUMBER OF SEQ ID NOS: 695  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 70  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-776-013-70

Query Match 72.0%; Score 14.4; DB 8; Length 20;  
Best Local Similarity 93.8%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTAGTTCAGCGCGGAG 18  
Db 16 GTAGTTCAGCGCGGAG 1

RESULT 6

US-11-036-317-78024/c  
; Sequence 78024, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; PRIOR FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 78024  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-78024

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTAGTTCAGCGCGGAGC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 20 GAGCAGCTCAGCGCGGAGC 2

RESULT 7  
US-11-036-317-531280/c  
; Sequence 531280, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; PRIOR FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 531280  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-531280

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTAGTTCAGCGCGGAGC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 20 GAGCAGCTCAGCGCGGAGC 2

RESULT 8  
US-09-908-975-25623/c  
; Sequence 25623, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: PAIGLER, Simon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975

CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25623  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-25623

Query Match 71.0%; Score 14.2; DB 3; Length 65;  
Best Local Similarity 84.2%; Pred. No. 3.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGTAGTTCAGCGCGGAGC 20  
| | | | | | | | | | | | | | | | | | | | |  
Db 65 GGTAGTTCCTGTGGAGCG 47

RESULT 9  
US-10-728-131-115/c  
; Sequence 115, Application US/10728131  
; Publication No. US20050075303A1  
; GENERAL INFORMATION:  
; APPLICANT: Neepet, Michael P.  
; APPLICANT: McClements, William L.  
; APPLICANT: Jansen, Kathryn U.  
; APPLICANT: Schultz, Loren D.  
; APPLICANT: Chen, Ling  
; APPLICANT: Wang, Xin-min  
; TITLE OF INVENTION: SYNTHETIC HUMAN PAPILLOMAVIRUS GENES  
; FILE REFERENCE: 20413YCA  
; CURRENT APPLICATION NUMBER: US/10/728,131  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: 09/642,405  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: PCT/US00/22932  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 60/210,143  
; PRIOR FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: 60/150,728  
; PRIOR FILING DATE: 1999-08-25  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 95  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Codon-Optimized HPV6 E2 fragment  
US-10-728-131-115

Query Match 71.0%; Score 14.2; DB 9; Length 95;  
Best Local Similarity 84.2%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGTAGTTCAGCGCGGAGC 20  
| | | | | | | | | | | | | | | | | | | | |  
Db 92 GATGCTTCAGCGCGGAGC 74

RESULT 10  
US-10-728-131-116  
; Sequence 116, Application US/10728131  
; Publication No. US20050075303A1  
; GENERAL INFORMATION:  
; APPLICANT: Neepet, Michael P.  
; APPLICANT: McClements, William L.  
; APPLICANT: Jansen, Kathryn U.  
; APPLICANT: Schultz, Loren D.

```
/ APPLICANT: Chen, Ling
/ TITLE OF INVENTION: SYNTHETIC HUMAN PAPILLOMAVIRUS GENES
/ FILE REFERENCE: 20413YCA
/ CURRENT FILING DATE: 2003-12-04
/ PRIOR APPLICATION NUMBER: 09/542,405
/ PRIOR FILING DATE: 2000-08-21
/ PRIOR APPLICATION NUMBER: PCT/US00/22932
/ PRIOR FILING DATE: 2000-08-21
/ PRIOR APPLICATION NUMBER: 60/210,143
/ PRIOR FILING DATE: 2000-06-07
/ PRIOR APPLICATION NUMBER: 60/150,728
/ PRIOR FILING DATE: 1999-08-25
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 116
/ LENGTH: 96
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Codon-Optimized HPV6 E2 fragment
US-10-728-131-116

Query Match          71.0%; Score 14.2; DB 9; Length 96;
Best Local Similarity 84.2%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GGTAGTTCAGCGCGGCGG 20
DB      73 GATCGTTTCAGCGCGGCGG 91

RESULT 11
US-10-719-956-405220/c
/ Sequence 405220, Application US/10719956
/ Publication No. US20040146910A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002-11-20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 405220
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-719-956-405220

Query Match          69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GTAGTTCAGCGCGGAGC 19
DB      17 GTAGTTCAGCGCGAGC 1

RESULT 12
US-10-719-900-224531
/ Sequence 224531, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808

/ PRIOR FILING DATE: 2002-11-20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 224531
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-224531

Query Match          69.0%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GTAGTTCAGCGCGGAGC 19
DB      6 GTCGTTCAGGAGGAGC 22

RESULT 13
US-10-956-157-187244/c
/ Sequence 187244, Application US/10956157
/ Publication No. US20050118625A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William
/ TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
/ TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
/ FILE REFERENCE: 031896-043000 (AM 101081)
/ CURRENT APPLICATION NUMBER: US/10/956,157
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 319805
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 187244
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Probe Sequence
US-10-956-157-187244

Query Match          69.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGTAGTTCAGCGCGGAG 18
DB      17 GGTAGTTCAGGAGGAGC 1

RESULT 14
US-11-060-756-179496/c
/ Sequence 179496, Application US/11060756
/ Publication No. US20050221354A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William Martin
/ TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
/ TITLE OF INVENTION: Target Genes
/ FILE REFERENCE: AM101083 (031896-042000)
/ CURRENT APPLICATION NUMBER: US/11/060,756
/ CURRENT FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 303284
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 179496
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: probe
US-11-060-756-179496

Query Match          69.0%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGTAGTTCAGCGCGGAG 18
DB      17 GGTAGTTCAGCGCGGAG 18
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Db 17 GGTAGTTCAGGAGGCAG 1

RESULT 15  
US-10-790

US-10-790-273-6  
; Sequence 6, Application US/10790273  
; Publication No. US20050191710A1  
; GENERAL INFORMATION.

GENERAL INFORMATION:

APPLICANT: Hanrahan, John W.

APPLICANT: Luo, Yishan

FILE REFERENCE: MCI-0037

FILE REFERENCE: MGU-0027  
CURRENT ADDITION NUMBER:

CURRENT FILING DATE: 2004-03-01  
CURRENT APPLICATION NUMBER: US/10/790,273

NUMBER OF SEQ ID NOS: 10  
; CURRENT FILING DATE: 2004-03-01

; NUMBER OF SEQ  
; SOFTWARE: Pat

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; SOFTWARE: PatentIn version 3.1.1
; SEO ID NO 6

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; SEQ ID NO 6  
; LENGTH: 57

! LENGTH: 57  
! TYPE: DNA

ORGANISM:

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; ORGANISM: Artificial sequence
;
FEATURE:

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OTHER IN

US-10-790-273-6

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Query Match	69.0%	Score 13.8	DB 9	Length 57
Best Local Similarity	88.2%	Pred. No. 5.3e+03		
Matches 15, Conservative	0	Mismatches 2	Indels 0	Gaps 0

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Oy      3 GTAGTTCAGGCCGGAGC   19  
         |||||  
Db     22 GTCGTTCAAGCCCGGAC   38
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Search completed: December 25, 2005, 04:14:22  
Job time : 338.6 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds

(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20

Sequence: 1 595tagtcagcgagcgagcg 20

Scoring table: IDENTITY\_NTC

Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.8	69.0	25	US-11-121-849-39004	Sequence 39004, A
C 2	13.4	67.0	25	US-11-121-849-11305	Sequence 11305,
C 3	13.2	66.0	21	US-10-770-726-5453	Sequence 5453, Ap
C 4	13.2	66.0	21	US-10-770-726-5454	Sequence 5454, Ap
C 5	13.2	66.0	25	US-11-121-849-247302	Sequence 247302,
C 6	13.2	66.0	25	US-11-121-849-490840	Sequence 490840,
C 7	13.2	66.0	25	US-11-121-849-514561	Sequence 514561,
C 8	13.2	66.0	25	US-11-121-849-191523	Sequence 191523,
C 9	12.8	64.0	25	US-11-121-849-11984	Sequence 11984, A
C 10	12.8	64.0	25	US-11-121-849-242741	Sequence 242741,
C 11	12.8	64.0	25	US-11-121-849-332708	Sequence 332708,
C 12	12.8	64.0	25	US-11-121-849-332709	Sequence 332709,
C 13	12.8	64.0	25	US-11-121-849-332710	Sequence 332710,
C 14	12.8	64.0	25	US-11-121-849-488425	Sequence 488425,
C 15	12.8	64.0	25	US-11-121-849-488424	Sequence 488424,
C 16	12.6	63.0	25	US-11-121-849-58824	Sequence 58824, A
C 17	12.6	63.0	25	US-11-121-849-58825	Sequence 58825, A
C 18	12.6	63.0	25	US-11-121-849-59759	Sequence 59759, A
C 19	12.6	63.0	25	US-11-121-849-59760	Sequence 59760, A
C 20	12.6	63.0	25	US-11-121-849-360118	Sequence 360118,
C 21	12.6	63.0	25	US-11-121-849-466071	Sequence 466071,
C 22	12.6	63.0	25	US-11-121-849-615229	Sequence 615229,
C 23	12.6	63.0	25	US-11-121-849-629144	Sequence 629144,

C 24	12.6	63.0	25	US-11-121-849-660189	Sequence 660189,
C 25	12.4	62.0	25	US-11-121-849-13534	Sequence 13534, A
C 26	12.4	62.0	25	US-11-121-849-358636	Sequence 358636,
C 27	12.4	62.0	25	US-11-121-849-467927	Sequence 467927,
C 28	12.2	61.0	25	US-11-121-849-56129	Sequence 56129, A
C 29	12.2	61.0	25	US-11-121-849-176620	Sequence 176620,
C 30	12.2	61.0	25	US-11-121-849-176621	Sequence 176621,
C 31	12.2	61.0	25	US-11-121-849-176622	Sequence 176622,
C 32	12.2	61.0	25	US-11-121-849-176623	Sequence 176623,
C 33	12.2	61.0	25	US-11-121-849-176624	Sequence 176624,
C 34	12.2	61.0	25	US-11-121-849-176898	Sequence 176898,
C 35	12.2	61.0	25	US-11-121-849-176899	Sequence 176899,
C 36	12.2	61.0	25	US-11-121-849-176900	Sequence 176900,
C 37	12.2	61.0	25	US-11-121-849-176901	Sequence 176901,
C 38	12.2	61.0	25	US-11-121-849-268934	Sequence 268934,
C 39	12.2	61.0	25	US-11-121-849-325562	Sequence 325562,
C 40	12.2	61.0	25	US-11-121-849-350301	Sequence 350301,
C 41	12.2	61.0	25	US-11-121-849-653557	Sequence 653557,
C 42	12.2	61.0	41	US-11-032-236-2	Sequence 2, Appl
C 43	12	60.0	25	US-11-121-849-731174	Sequence 731174, A
C 44	12	60.0	25	US-11-121-849-241316	Sequence 241316,
C 45	12	60.0	25	US-11-121-849-529576	Sequence 529576,

#### ALIGNMENTS

RESULT 1  
US-11-121-849-39004/c  
; Sequence 39004, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 39004  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-39004

Query Match  
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;  
Matches 15; Conservative 0; Pred. No. 5.2e+02;  
Mismatch 2; Indels 0; Gaps 0;

Qy 3 GTAGCTCAGCGCGAGC 19  
Db 17 GTAGCTCAGCGCGAGC 1

RESULT 2  
US-11-121-849-113305/c  
; Sequence 113305, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 113305

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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-849-113305

Query Match
Best Local Similarity 93.3%; Pred. No. 8.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTACGGCGGAGC 19
DB 16 AGTTACGCTGGAGC 2

RESULT 3
US-10-770-726-5453/C
; Sequence 5453, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5453
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-770-726-5453

Query Match
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTAGTTCAGCGCGAGCG 20
DB 21 GTAGATCATCGCGAGCG 4

RESULT 4
US-10-770-726-5454/C
; Sequence 5454, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5454
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
; US-10-770-726-5454

Query Match
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTAGTTCAGCGCGAGCG 20
DB 19 GTAGATCATCGCGAGCG 2

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-849-247302/C
; Sequence 247302, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247302
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-849-247302

Query Match
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGAG 18
DB 20 GTGTATTTCAGCGCGAG 3

RESULT 6
US-11-121-849-490840/C
; Sequence 490840, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 490840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-849-490840

Query Match
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTAGTTCAGCGCGAGCG 20
DB 18 GTAGTTCAGCGCGAGCG 1

RESULT 7
US-11-121-849-514561/C
; Sequence 514561, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
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; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 514561
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-514561

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GGTAGTTCAGCGCGGAGC 19
Db      19 GGAGTTCAGCGCGGAGC 2

RESULT 8
US-11-121-849-191523/c
; Sequence 191523, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 191523
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-191523

Query Match      65.0%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GTTCAGCGCGGAGC 18
Db      18 GTTCAGCGCGGAGC 6

RESULT 9
US-11-121-849-11984/c
; Sequence 11984, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 11984
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-11984

Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      5 AGTTCAGCGCGGAGC 20
Db      16 ACTTCAGGTGGAGCC 1

RESULT 10
US-11-121-849-242741
; Sequence 242741, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 242741
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-242741

Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 TAGTTCAGCGCGGAGC 19
Db      6 TAGTTCAGCGCGGAGC 21

RESULT 11
US-11-121-849-332708/c
; Sequence 332708, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 332708
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-332708

Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 TAGTTCAGCGCGGAGC 19
Db      20 TGGTTCAGGCTGGAGC 5

RESULT 12
US-11-121-849-332709/c
; Sequence 332709, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
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FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 332709
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-332709

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TAGTTCAGCGCGGAGC 19
DB 16 TGGTTCAGGCTGAGC 3

RESULT 13
US-11-121-849-332710/c
Sequence 332710, Application US/11/121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 332710
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-332710

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TAGTTCAGCGCGGAGC 19
DB 16 TGGTTCAGGCTGAGC 1

RESULT 14
US-11-121-849-488425/c
Sequence 488425, Application US/11/121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 488425
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-488425
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Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TAGTTCAGCGCGGAGC 19
DB 16 TAGTTGAGCGCGGAGC 1

RESULT 15
US-11-121-849-498584
Sequence 498584, Application US/11/121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 498584
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-498584

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GGTAGTTCAGCGCGGA 17
DB 4 GGTATTTGAGGCTGGA 19

Search completed: December 25, 2005, 04:37:03
Job time : 136.3 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 : Search time 582 Seconds  
(without alignments)  
1953.383 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gtgccagcagcagcagcactg 20

Scoring table: IDENTITY\_NUC

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*\n2: gb\_in:\*\n3: gb\_env:\*\n4: gb\_om:\*\n5: gb\_ov:\*\n6: gb\_pat:\*\n7: gb\_ph:\*\n8: gb\_pr:\*\n9: gb\_ro:\*\n10: gb\_scs:\*\n11: gb\_sy:\*\n12: gb\_un:\*\n13: gb\_vl:\*\n14: gb\_hhg:\*\n15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211665 Antisense
2	15.4	77.0	50	6	AX430850 Sequence
3	14.8	74.0	50	6	CQ002433 Sequence
4	14.2	71.0	42	6	AX231094 Sequence
5	14.2	71.0	42	6	AX231098 Sequence
6	14.2	71.0	42	6	AX231555 Sequence
7	14.2	71.0	42	6	AX232206 Sequence
8	14.2	71.0	42	6	AX233340 Sequence
9	14.2	71.0	91	8	HSTINOSX01
10	13.8	69.0	26	6	BD084096 Human Induc
11	13.8	69.0	100	6	CQ000039 Sequence
12	13.8	69.0	100	6	CQ001129 Sequence
13	13.6	68.0	30	6	CQ082140 Sequence
14	13.6	68.0	50	6	CQ000889 Sequence
15	13.6	68.0	51	6	AR444776 Sequence
16	13.4	67.0	51	6	AX157921 Sequence
17	13.4	67.0	51	6	AX157922 Sequence
18	13.4	67.0	99	10	G34988 DBX human S

c 19	13.4	67.0	100	6	CQ055901 Sequence
c 20	13.4	67.0	100	6	CQ075146 Sequence
c 21	13.4	67.0	100	6	CQ106093 Sequence
c 22	13.4	67.0	100	6	CQ144785 Sequence
c 23	13.4	67.0	100	6	CQ180232 Sequence
c 24	13.4	67.0	100	6	CQ204623 Sequence
c 25	13.4	67.0	100	6	CQ227975 Sequence
c 26	13.4	67.0	100	6	CQ266129 Sequence
c 27	13.4	67.0	100	6	CQ303173 Sequence
c 28	13.4	67.0	100	6	CQ340406 Sequence
c 29	13.2	66.0	27	6	AX306740 Sequence
c 30	13.2	66.0	28	6	AX306741 Sequence
c 31	13.2	66.0	28	6	AR130372 Sequence
c 32	13.2	66.0	28	6	AR455456 Sequence
c 33	13.2	66.0	39	6	AX663324 Sequence
c 34	13.2	66.0	51	6	AX115349 Sequence
c 35	13.2	66.0	76	6	AR121636 Sequence
c 36	13.2	66.0	76	6	E55383 Process for
c 37	13.2	66.0	90	6	AX306734 Sequence
c 38	13.2	66.0	100	10	HSR308722 Homo sapi
c 39	13	65.0	92	15	ATH525570 Arabidops
c 40	13	65.0	92	15	ATH525987 Arabidops
c 41	13	65.0	92	15	ATH528787 Arabidops
c 42	12.8	64.0	27	6	133657 Sequence 6
c 43	12.8	64.0	30	6	158430 Sequence 14
c 44	12.8	64.0	31	6	158435 Sequence 19
c 45	12.8	64.0	55	6	113710 Sequence 16

## ALIGNMENTS

RESULT 1  
LOCUS BD211665 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION BD211665.1 GI:33021435  
KEYWORDS JP 2002512793-A/8.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1 (bases 1 to 20)

AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.

TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

JOURNAL Patent: JP 2002512793-A 8 08-MAY-2002;  
GENSENSE TECHNOLOGIES INC

COMMENT OS Homo sapiens (human)

PN JP 2002512793-A/8

PD 08-MAY-2002

PF 23-APR-1999 JP 2000545999

PR 23-APR-1998 US 60/082791

PI JIM A WRIGHT, AIPING H YOUNG, YOON S LEE

PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC

CC Antisense oligonucleotide sequence of neuropilin and method of using the

CC same for controlling cell proliferation

FH key Location/Qualifiers

FT source 1..20 /organism='Homo sapiens (human)'.  
Location/Qualifiers

FEATURES 1..20 /organism='Homo sapiens'  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 83;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GTGCCAGCCAGAGCGACTG 20

Db 1 GTGCCAGCCAGAGCGACTG 20

RESULT 2  
AX30850/c  
LOCUS AX30850 50 bp RNA linear PAT 28-JUN-2002  
DEFINITION Sequence 4 from Patent WO0240994.  
ACCESSION AX30850  
VERSION AX30850.1 GI:21655915  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
AUTHORS Mesrobian, E., Shoham, S., Soreq, H. and Sklan, E.  
TITLE System and method for assaying drugs  
JOURNAL Patent: WO 0240994-A 4 23-MAY-2002;  
YISSUM RES DEV CO (IL)  
FEATURES  
source 1..50  
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/mol\_type="unassigned RNA"  
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ORIGIN  
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Best Local Similarity 94.1%; Pred. No. 1.4e+04;  
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QY 2 TGCCAGCCAGAGCGAC 18  
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50 TGCCAGCCAGAGCGAC 34

Db 50 TGCCAGCCAGAGCGAC 34

RESULT 3  
CQ002433/c  
LOCUS CQ002433 50 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 1073 from Patent WO0147944.  
ACCESSION CQ002433  
VERSION CQ002433.1 GI:41009065  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
JOURNAL methods of use thereof  
PATENT: WO 0147944-A 1073 05-JUL-2001;  
Curagen Corporation (US)  
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Best Local Similarity 88.9%; Pred. No. 2.6e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCAGAGCGACT 19

Db 49 GTGCCAGCCAGCGCCT 32  
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49 GTGCCAGCCAGCGCCT 32

RESULT 4  
AX231094  
LOCUS AX231094 42 bp DNA linear PAT 11-SEP-2001  
DEFINITION Sequence 490 from Patent WO0162787.  
ACCESSION AX231094  
VERSION AX231094.1 GI:15592450  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
AUTHORS Herath, H.M., Parekh, R.B., Rohlf, C.O., Terrett, J.A. and Tyson, K.L.  
TITLE Diagnosis and treatment of bipolar affective disorder  
JOURNAL Patent: WO 0162787-A 490 30-AUG-2001;  
Oxford Glycosciences (UK) Limited (GB)  
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Best Local Similarity 84.2%; Pred. No. 5.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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|||||  
7 GTGCCAGCCAGAGCGACT 25

Db 7 GTGCCAGCCAGAGCGACT 25

RESULT 5  
AX231098  
LOCUS AX231098 42 bp DNA linear PAT 11-SEP-2001  
DEFINITION Sequence 494 from Patent WO0162787.  
ACCESSION AX231098  
VERSION AX231098.1 GI:15592454  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
AUTHORS Herath, H.M., Parekh, R.B., Rohlf, C.O., Terrett, J.A. and Tyson, K.L.  
TITLE Diagnosis and treatment of bipolar affective disorder  
JOURNAL Patent: WO 0162787-A 494 30-AUG-2001;  
Oxford Glycosciences (UK) Limited (GB)  
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Best Local Similarity 84.2%; Pred. No. 5.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCGACT 19  
|||||  
1 GTGCCAGCCAGAGCGACT 19

Db 7 GTGCCATCGAGAGCGACT 25

RESULT 6  
AX231555 42 bp DNA linear PAT 11-SEP-2001  
LOCUS Sequence 453 from Patent WO0163294.  
ACCESSION AX231555  
VERSION AX231555.1 GI:15592461  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 Herath,H.M., Parekh,R.B. and Rohlf,C.  
AUTHORS Diagnosis of bipolar affective disorder (bad) and unipolar  
TITLE depression  
JOURNAL Patent: WO 0163294-A 453 30-AUG-2001;  
Oxford Glycosciences (UK) Limited (GB)  
FEATURES  
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1 GTGCCATCGAGAGCGACT 19  
7 GTGCCATCGAGAGCGACT 25

Db 7 GTGCCATCGAGAGCGACT 25

RESULT 7  
AX232206 42 bp DNA linear PAT 11-SEP-2001  
LOCUS Sequence 484 from Patent WO0163293.  
ACCESSION AX232206  
VERSION AX232206.1 GI:15592539  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 Herath,H.M., Parekh,R.B. and Rohlf,C.O.  
AUTHORS Diagnosis and treatment of schizophrenia  
TITLE Patent: WO 0163293-A 484 30-AUG-2001;  
Oxford Glycosciences (UK) Limited (GB)  
FEATURES  
source location/Qualifiers  
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ORIGIN

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Best Local Similarity 84.2%; Pred. No. 5.2e+04;  
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7 GTGCCATCGAGAGCGACT 25

Db 7 GTGCCATCGAGAGCGACT 25

RESULT 8  
AX233340 42 bp DNA linear PAT 11-SEP-2001  
LOCUS Sequence 664 from Patent WO0162785.  
ACCESSION AX233340  
VERSION AX233340.1 GI:15592679  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 Herath,H.M., Parekh,R.B., Rohlf,C.C., Terrett,J.A. and Tyson,K.L.  
AUTHORS Protein and gene and their use for diagnosis and treatment of  
TITLE schizophrenia  
JOURNAL Patent: WO 0162785-A 664 30-AUG-2001;  
Oxford Glycosciences (UK) Limited (GB)  
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Best Local Similarity 84.2%; Pred. No. 5.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
1 GTGCCATCGAGAGCGACT 19  
7 GTGCCATCGAGAGCGACT 25

Db 7 GTGCCATCGAGAGCGACT 25

RESULT 9  
HSINOSX01 91 bp DNA linear PRI 27-JAN-1998  
LOCUS Human inducible nitric oxide synthase (iNOS) pseudogene, exon 1.  
DEFINITION U65689  
ACCESSION U65689  
VERSION U65689.1 GI:1621317  
KEYWORDS  
SEGMENT 1 of 11  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 (bases 1 to 91)  
AUTHORS Park,C.S., Park,R., Lee,H.S., Lee,H.Y. and Krishna,G.  
TITLE Direct Submission  
JOURNAL Submitted (31-JUL-1996) Section of Chemical Pharmacology, National  
Institutes of Health, Bethesda, MD 20892, USA  
2 (bases 1 to 91)  
AUTHORS Park,C.S., Lee,H.S., Lee,H.Y. and Krishna,G.  
TITLE An unprocessed pseudogene of inducible nitric oxide synthase gene  
in human  
JOURNAL Nitric Oxide 1 (4), 294-300 (1997)  
PUBMED 9441901

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30. 91  
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intron

Query Match  
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DB 34 GTGCCAGCGCAGCGTCT 52

RESULT 10  
LOCUS BD084096 26 bp DNA linear PAT 27-AUG-2002  
DEFINITION Human pancreatic cancer antigen.  
ACCESSION BD084096  
VERSION BD084096.1 GI:22629706  
KEYWORDS JP 2001340081-A/3.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Kawakami,H., Akada,M. and Fujita,T.  
TITLE Human pancreatic cancer antigen  
JOURNAL Patent: JP 2001340081-A 3 11-DEC-2001;  
KEIO UNIVERSITY  
COMMENT OS Artificial Sequence  
PN JP 2001340081-A/3  
PD 11-DEC-2001  
PF 31-MAY-2000 JP 2000161930  
PI HIROSHI KAWAKAMI,MASANORI AKADA,TOMONOSHU FUJITA PC  
C12N15/00,A01K67/027,A61K38/00,A61K39/395,A61K45/00,A61P35/00, PC  
C07K14/00,  
PC C07K14/47,C07K16/18,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC  
,C12N5/10,C12Q1/02,  
PC C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/577//C12P21/02,  
PC C12P21/08,  
PC (C12N15/09,C12R1:91),(C12N5/10,C12R1:91),(C12P21/02,C12R1:91),  
PC C12N15/00,  
PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91) CC  
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DB 1 TGCCAGCGCAGAGATAC 17

RESULT 11  
LOCUS CQ000039/c 100 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 11501 from Patent EP1260592.  
ACCESSION CQ000039  
VERSION CQ000039.1 GI:41006413  
KEYWORDS  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Escherichia.  
REFERENCE 1  
AUTHORS Donner,H., Drescher,B., Huber,A. and Weber,J.  
TITLE Bioclip  
JOURNAL Patent: EP 1260592-A 11501 27-NOV-2002;  
MMG - Biotech AG (DE)  
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1. 100  
/organism="Escherichia coli"  
/mol\_type="unassigned DNA"  
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/note="mtr b0625 U00096 complement(656778\_657161)"  
ORIGIN  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 70 TGCCAGCGCAGCGAC 54

RESULT 12  
LOCUS CQ001129/c 100 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 12591 from Patent EP1260592.  
ACCESSION CQ001129  
VERSION CQ001129.1 GI:41007767  
KEYWORDS  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Escherichia.  
REFERENCE 1  
AUTHORS Donner,H., Drescher,B., Huber,A. and Weber,J.  
TITLE Bioclip  
JOURNAL Patent: EP 1260592-A 12591 27-NOV-2002;  
MMG - Biotech AG (DE)  
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ORIGIN  
Query Match  
Best Local Similarity 69.0%; Score 13.8; DB 6; Length 100;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCGCAGCGAC 18  
DB 36 TGCCAGCGCAGTCCGCC 20

RESULT 13  
LOCUS CQ821440/c 30 bp DNA linear PAT 21-JUN-2004  
DEFINITION Sequence 11 from Patent EP1428875.  
ACCESSION CQ821440  
VERSION CQ821440.1 GI:49019139  
KEYWORDS

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   other sequences; artificial sequences.
AUTHORS     1
            Boutin,P., Dubois,S., Dina,C. and Froguet,P.
TITLE       Method of diagnosis of obesity
JOURNAL     Patent: EP 1428875-A 11 16-JUN-2004;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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    /note="Description of Artificial Sequence: Primer to
    amplify SNP 1.6 kb"

ORIGIN

Query Match      68.0%; Score 13.6; DB 6; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GTGCCAGCCAGAGCGACTG 20
        |||||
Db      29 GCGCCTGCGCCAGAGCGCCTG 10

RESULT 14
LOCUS       CQ008899/c              50 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION  Sequence 7539 from Patent WO0147944.
ACCESSION   CQ008899
VERSION     CQ008899.1 GI:41015621
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Shinkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0147944-A 7539 05-JUL-2001;
            Curen Corporation (US)
FEATURES
  source
    1..50
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
    /note="Nucleotide deleted between bases 25 and 26
    Accession number cg44034179"

ORIGIN

Query Match      68.0%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GTGCCAGCCAGAGCGACTG 20
        |||||
Db      27 GTGCCAGCCAGCGCTAGTG 8

RESULT 15
LOCUS       AR444776/c              51 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION  Sequence 1187 from patent US 6670464.
ACCESSION   AR444776
VERSION     AR444776.1 GI:42672555
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.

```

```

REFERENCE   1 (bases 1 to 51)
AUTHORS     Shinkets,R.A. and Leach,M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: US 6670464-A 1187 30-DEC-2003;
            Curen Corporation; New Haven, CT
FEATURES
  source
    1..51
    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN

Query Match      68.0%; Score 13.6; DB 6; Length 51;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GTGCCAGCCAGAGCGACTG 20
        |||||
Db      33 GTGCCAGCCAGAGCCACAG 14

Search completed: December 24, 2005, 14:06:12
Job time : 585 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 : Search time 171.4 Seconds  
(without alignments)  
777.677 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gtgccagccagagcagctg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues  
Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: geneseqn19808.\*  
2: geneseqn19908.\*  
3: geneseqn20008.\*  
4: geneseqn20018.\*  
5: geneseqn20028.\*  
6: geneseqn20038.\*  
7: geneseqn20048.\*  
8: geneseqn20058.\*  
9: geneseqn20068.\*  
10: geneseqn20078.\*  
11: geneseqn20088.\*  
12: geneseqn20098.\*  
13: geneseqn20108.\*  
14: geneseqn20118.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AA231438 Human neu
2	20	100.0	20	9	ADA74690 GTT3608 a
3	15.4	77.0	50	6	ABK90054 Human ace
4	14.8	74.0	50	4	AA127865 Human SNP
5	14.2	71.0	42	4	AA12579 DNA encod
6	14.2	71.0	42	4	AA542471 Schlizophr
7	14.2	71.0	42	4	AA543073 RST AAS26
8	14.2	71.0	42	12	AD079046 Schlizophr
9	14	70.0	41	12	ADH05972 Gene poly
10	14	70.0	41	12	ADH91759 1-beta-me
11	14	70.0	80	2	AAQ11150 Probe GTR
12	13.8	69.0	26	6	ABA97968 Human pan
13	13.8	69.0	36	8	AA155205 Pshhl-Ffl
14	13.8	69.0	71	14	ADV87091 Non-speci
15	13.8	69.0	100	8	ACD80225 E. coli K
16	13.8	69.0	100	8	ACD81315 E. coli K
17	13.6	68.0	21	13	ADU43644 Knock-dow
18	13.6	68.0	29	3	AAA47678 Primer (S
19	13.6	68.0	30	12	ADP27364 Human 5'

C	20	13.6	68.0	31	2	AA38710 Human gen
C	21	13.6	68.0	50	4	AA134331 Human SNP
C	22	13.6	68.0	51	3	AA77504 Human typ
C	23	13.4	67.0	51	4	AA174309 Human b11
C	24	13.4	67.0	51	4	AA174308 Human b11
C	25	13.4	67.0	100	4	AA121013 Probe #10
C	26	13.4	67.0	100	4	ABA66085 Human foe
C	27	13.4	67.0	100	4	AA146266 Probe #14
C	28	13.4	67.0	100	4	ABA48205 Human bre
C	29	13.4	67.0	100	4	ABA33162 Probe #11
C	30	13.4	67.0	100	4	AAK40250 Human bon
C	31	13.4	67.0	100	4	AAK14509 Human bra
C	32	13.4	67.0	100	4	AB339824 Human 11v
C	33	13.4	67.0	100	5	AA106730 Probe #67
C	34	13.4	67.0	100	6	AB314287 Human gen
C	35	13.2	66.0	25	9	AC135993 Human m1c
C	36	13.2	66.0	27	6	ABK16832 Human pro
C	37	13.2	66.0	27	6	ABK16831 Human pro
C	38	13.2	66.0	27	12	ADG82567 Human end
C	39	13.2	66.0	28	2	AA748247 HSV chym1
C	40	13.2	66.0	28	4	AA502243 Cytosolic
C	41	13.2	66.0	28	4	AA502251 Reverse P
C	42	13.2	66.0	32	14	ADK69401 Bifidobac
C	43	13.2	66.0	33	6	ABA9259 Human end
C	44	13.2	66.0	34	3	AA64022 PCR prime
C	45	13.2	66.0	34	3	AA64024 PCR prime

## ALIGNMENTS

RESULT 1	AA231438	AA231438 standard; DNA; 20 BP.
ID	AA231438	
XX	AA231438;	
AC	AA231438;	
XX		
DT	07-FEB-2000	(first entry)
XX		
DE	Human neuropilin mRNA specific antisense oligo GTT3608.	
XX		
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;	
KX	papilloma; diabetic retinopathy; antisense; ss.	
OS	Synthetic.	
XX		
OS	Homo sapiens.	
XX		
PN	W09955855-A2.	
XX		
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA000324.
XX		
PR	23-APR-1998;	98US-0082791P.
XX		
PA	(GENE-) GENESENSE TECHNOLOGIES INC.	
XX		
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI; 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for	
PT	treating cancer.	
XX		
PS	Claim 4; Page 16; 57pp; English.	
XX		
CC	Sequences AA231431-460 represent antisense oligonucleotides which inhibit	
CC	human neuropilin expression. The antisense oligonucleotides can be used	
CC	to inhibit the growth or metastasis of a mammalian tumor and inhibit	
CC	neovascularisation. The oligonucleotides may be used to treat various	
CC	forms of cancers or tumors, such as sarcomas, melanomas, adenomas,	
CC	carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of	
CC	the mouth, throat, larynx and lung, genitourinary cancers such as	

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
CC cancer, head and neck cancers, and nervous system cancers, as well as  
CC benign lesions such as papillomas. The methods may be used to treat  
CC neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration

XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGCACTG 20  
Db 1 GTGCCAGCCAGAGCACTG 20

RESULT 2  
ADA74690  
ID ADA74690 standard; DNA; 20 BP.

XX ADA74690;  
XX 20-NOV-2003 (first entry)

DE GT13608 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
KM cytostatic; growth; tumour metastasis; angiogenesis; gene therapy;  
XX GT13608; antisense; human; ss.

OS Homo sapiens.

PN US2003083274-A1.

XX 01-MAY-2003.

PD 22-APR-1999; 99US-00296264.

XX 23-APR-1998; 98US-0082791P.

PA (WRIGHT) WRIGHT J A.  
PA (YOUNG) YOUNG A H.  
PA (LEEVY) LEEVY S.

XX Wright JA, Young AH, Lee VS;

DR WPI; 2003-576622/54.

PT New antisense oligonucleotide that inhibits neuropilin expression, useful  
PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
PT mammalian tumor.

PS Claim 1; Page 5; 27pp; English.

XX The invention relates to a novel antisense oligonucleotide that inhibits  
CC the expression of neuropilin, also known as VEGF165R (vascular  
CC endothelial growth factor receptor). The oligonucleotide of the invention  
CC demonstrates cytostatic activity and may be useful for inhibiting the  
CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in  
CC mammals. Furthermore, the oligonucleotide may be utilised during gene  
CC therapy. The current sequence is that of the GT13608 antisense  
CC oligonucleotide of the invention which is targeted to human neuropilin  
CC mRNA.

XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGCACTG 20

Db 1 GTGCCAGCCAGAGCACTG 20

RESULT 3  
ABK90054/C  
ID ABK90054 standard; RNA; 50 BP.

XX ABK90054;

XX 05-NOV-2002 (first entry)

DE Human acetylcholinesterase (ACHE) mRNA probe.

XX Nervous system; drug assay; acetylcholinesterase; AChE; brain;  
KM isoform variance; AChE blocker; muscarinic receptor; M1; M2;  
KM pyridostigmine; muscarinic receptor blocker; scopolamine;  
KM M1 receptor blocker; pirenzepine; anxiety; post-traumatic stress;  
KM Alzheimer's disease; muscle malfunctioning; neurodegenerative disorder;  
KM xenobiotic damage; panic; neuromuscular disorder; Parkinson's disease;  
KM Huntington's chorea; muscle fatigue; multiple chemical sensitivity;  
KM autism; multiple sclerosis; Sjogren's disease; human; probe; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX modified\_base 1..50

XX /\*tag= b

XX /mod\_base= OTHER

XX /note= "OTHER= 2-O-methylated"

XX /\*tag= a

XX /mod\_base= OTHER

XX /note= "OTHER= labelled with 5'-biotin"

XX WO200240994-A2.

XX 23-MAY-2002.

XX 14-NOV-2001; 2001WO-11001051.

XX 14-NOV-2000; 2000US-0247970P.

XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

XX Soreq H, Meshorer E, Sklan E, Shoham S;

XX WPI; 2002-490152/52.

XX Evaluating effect of drugs on nervous system by comparing effect of drug

XX PT on acetylcholinesterase, AChE activity in brain of test animal following

XX PT challenge by AChE blocker and comparing it with control group.

XX Example; Page 55; 114pp; English.

XX The present invention relates to a method and system for evaluating an  
CC effect on the nervous system of a test drug. The method comprises  
CC comparing the effect of the drug on acetylcholinesterase (AChE) catalytic  
CC activity or isoform variance in a brain of a test animal following a  
CC challenge by an AChE blocker or a blocker of AChE and muscarinic  
CC receptors M1 and M2 (e.g. pyridostigmine) and comparing this effect with  
CC that of a known agent, preferably a non-selective muscarinic receptor  
CC blocker (e.g. scopolamine) or a specific M1 receptor blocker (e.g.  
CC pirenzepine). The method is useful for evaluating an effect on the  
CC nervous system of a test drug, including drugs for the treatment of  
CC anxiety conditions, post-traumatic stress, Alzheimer's disease, muscle  
CC malfunctioning, neurodegenerative disorders, damage resulting from  
CC exposure to xenobiotics, panic, neuromuscular disorders, Parkinson's  
CC disease, Huntington's chorea, muscle fatigue, multiple chemical  
CC sensitivity, autism, multiple sclerosis and Sjogren's disease. The  
CC present sequence represents a probe for human AChE mRNA

XX Sequence 50 BP; 5 A; 17 C; 16 G; 0 T; 12 U; 0 Other;

Query Match 77.0%; Score 15.4; DB 6; Length 50;  
Best Local Similarity 94.1%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGCCGAGCCGAGCGAC 18  
Db 50 TCCCGAGCCGAGCGAC 34

RESULT 4  
AAL27865/c  
ID AAL27865 standard; DNA; 50 BP.

AC AAL27865;  
DT 24-JAN-2002 (first entry)  
DE Human SNP oligonucleotide #1073.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX complement related protein; cytochrome; kinase; cytokine; interferon;  
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX multifactorial disease; autoimmune disease; infection;  
XX nervous system disease; ss.

OS Homo sapiens.  
PN WO200147944-A2.

PD 05-JUL-2001.  
PF 28-DEC-2000; 2000WO-US035498.

PR 28-DEC-1999; 99US-0173419P.  
PR 27-DEC-2000; 2000US-0017341S.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI: 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.

PS Claim 1; Page 1687; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid protein, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms

XX Sequence 50 BP; 3 A; 14 C; 24 G; 9 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 4; Length 50;  
Best Local Similarity 88.9%; Pred. No. 4.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCCGAGCCGAGCGACT 19  
Db 49 TGCCGAGCCGAGCGCGCT 32

RESULT 5  
AAS12579  
ID AAS12579 standard; DNA; 42 BP.

AC AAS12579;  
XX

DT 03-JAN-2002 (first entry)

DE DNA encoding peptide sequence #1 identified from DPI-45 and DPI-213.

XX Human; depression associated protein isoform; tryptic digest peptide;  
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic; DPI-213;  
XX manic-depressive illness; schizoaffective disorder; DPI-45; ds.

XX Homo sapiens.

FH Key location/Qualifiers  
FT CDS 1..42  
FT /\*tag= a

FT /product= "Peptide sequence #1 from DPI-45 and DPI-213"  
FT /note= "This sequence lacks both start and stop codons"

PN WO200162787-A1.

PD 30-AUG-2001.

PF 23-FEB-2001; 2001WO-GB000786.

PR 24-FEB-2000; 2000GB-00004412.

PR 08-DEC-2000; 2000GB-00030050.

PR 12-DEC-2000; 2000US-0254830P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI: 2001-570626/64.

XX P-PSDB; AAU28402.

PT Novel nucleic acid encoding a protein associated with bipolar affective  
PT disorder, which is used for diagnosis, prophylaxis and therapy of  
PT neuropsychiatric disorders, such as bipolar affective disorder.

PS Claim 1; Page 145; 153pp; English.

XX The present invention relates to the identification of depression  
CC associated protein isoforms (DPIs), particularly the tryptic digest  
CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
CC described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar  
CC affective disorder) subjects, whilst other DPIs (AAU28626-AAU28687) are  
CC increased in BAD subjects. Also described are peptide sequences  
CC identified from DPI-45 and DPI-213 and the nucleic acid sequences they are  
CC encoded by. The sequences of the invention are useful for clinical  
CC screening, diagnosis, prognosis, therapy and prophylaxis of  
CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,  
CC BP), manic-depressive illnesses, attention deficit disorders,  
CC schizoaffective disorders, and unipolar affective disorders. The present  
CC DNA sequence encodes for peptide sequence #1 identified from DPI-45 and  
CC DPI-213

XX Sequence 42 BP; 6 A; 12 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 42;  
Best Local Similarity 84.2%; Pred. No. 8.8e+03;

Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	GTGCCAGCCAGAGCGACT	19						
Db	7	GTGGCCATCGAGAGCGACT	25						
RESULT 6									
AA542471									
ID	AA542471	standard;	DNA;	42	BP.				
XX	AA542471;								
AC	18-DEC-2001	(first entry)							
DT									
XX									
XX	Schizophrenia-Associated Protein Isoform (SPI) 238/240 peptide DNA #1.								
DE									
XX	Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;								
KM	neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma; ds.								
XX									
OS	Homo sapiens.								
XX									
PN	WO200162785-A2.								
PD	30-AUG-2001.								
XX									
XX	23-FEB-2001; 2001WO-GB000792.								
PF									
PR	24-FEB-2000; 2000GB-00004415.								
FR	28-DEC-2000; 2000US-00750395.								
XX	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.								
PA									
XX									
PI	Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;								
XX									
DR	WPI; 2001-570624/64.								
XX	P-PSDB; AAU25420.								
PT	New schizophrenia associated protein isoforms and encoding nucleic acid								
PT	molecules, useful for treatment, diagnosis and prognosis of schizophrenia								
PT	and screening for potential drugs for treatment and new drug targets.								
XX									
PS	Disclosure; Page 80; 148bp; English.								
XX									
CC	The sequence represents DNA encoding a schizophrenia-associated protein								
CC	isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240								
CC	are detectable in cerebrospinal fluid, serum or plasma and are useful								
CC	markers of schizophrenia. The sequences can be used for treatment and								
CC	diagnosis of schizophrenia, screening, prognosis, monitoring the results								
CC	of therapy, identifying patients most likely to respond to a particular								
CC	therapy and identification of new targets for drug treatment. SPI DNA is								
CC	useful as a nucleic acid probe to detect the presence of nucleic acids or								
CC	SPI								
XX									
XX	Sequence 42 BP; 6 A; 12 C; 15 G; 9 T; 0 U; 0 Other;								
Qy									
Query Match		71.0%;	Score 14.2;	DB 4;	Length 42;				
Best Local Similarity		84.2%;	Pred. No. 8	8e+03;					
Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
1	GTGCCAGCCAGAGCGACT	19							
7	GTGGCCATCGAGAGCGACT	25							
RESULT 7									
AA543073									
ID	AA543073	standard;	DNA;	42	BP.				
XX									
AC	AA543073;								
XX									
DT	18-DEC-2001	(first entry)							

DE	EST	AAS26679/A1589129	encoding	Peptide #1.
XX	Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;			
XX	DP; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;			
KW	CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;			
KW	attention deficient disorder; schizoaffective disorder; AAS26679; ss;			
KW	unipolar affective disorder; EST; expressed sequence tag; A1589129.			
XX				
OS	Homo sapiens.			
XX				
PN	MO200163294-A2.			
XX				
PD	30-AUG-2001.			
XX				
PF	23-FEB-2001; 2001WO-GB000791.			
XX				
PR	24-FEB-2000; 2000GB-00004412.			
PR	08-DEC-2000; 2000GB-00030050.			
PR	12-DEC-2000; 2000US-0254830P.			
XX				
PA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.			
XX				
PI	Herath HMAc, Parekh RB, Rohlf C;			
XX				
DR	WPI; 2001-582081/65.			
XX	P-PsDB; AAU26555.			
XX				
PT	Preparation for diagnosing or treating bipolar affected disorder (BAD) or			
PT	unipolar depression, or for screening for modulators, comprises a BAD-			
PT	associated protein isoform.			
XX				
PS	Disclosure; Page 74; 163pp; English.			
XX				
CC	The invention relates to a preparation comprising an isolated Bipolar			
CC	Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are			
CC	used to screen, diagnose or prognose of BAD or unipolar depression,			
CC	determine the stage or severity of BAD or unipolar depression, identify a			
CC	subject at risk of developing BAD or unipolar depression, or monitor the			
CC	effect of therapy in a subject. They are also used to screen for or			
CC	identify agents that interact with a DPI. These agents, antibodies			
CC	against the DPIs, and nucleic acids encoding the DPIs are used to treat			
CC	or prevent BAD or unipolar depression. Diseases that can be treated are			
CC	attention deficient disorder, a schizoaffective disorder, a bipolar or a			
CC	unipolar affective disorder. The DPIs are used in proteomics. The			
CC	proteomic approach of using DPIs for screening, diagnosis or prognosis of			
CC	BAD or unipolar depression overcomes the problems of using gene			
CC	expression analysis, such as not being able to obtain central nervous			
CC	system (CNS) tissue from a living patient under normal circumstances. The			
CC	present sequence is part of a PCR fragment generated from two EST			
CC	(expressed sequence tags) sequences AAS26679 and A1589129, which express			
XX	DIPs			
XX				
SO	Sequence 42 BP; 6 A; 12 C; 15 G; 9 T; 0 U; 0 Other;			
XX				
QY	Query Match 71.0%; Score 14.2; DB 4; Length 42;			
DB	Best Local Similarity 84.2%; Pred. No. 8.8e+03;			
	Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.			
	1 GAGCCAGCCAGAGCGACT 19			
	7 GTGGCCATCGAGAGCGACT 25			
RESULT 8				
ADO79046				
ID	ADO79046 standard; DNA; 42 BP.			
XX				
XX	ADO79046;			
XX				
DT	26-AUG-2004 (first entry)			
XX				
DE	Schizophrenia-Associated Protein Isoform (SPI) DNA seqid 664.			
XX				

KW neuroleptic; Schizophrenia; immunospecific binding;  
 KW Schizophrenia-Associated Protein Isoform; SPI; schizophrenia screening;  
 KW Schizophrenia diagnosis; schizophrenia prognosis;  
 KW Schizophrenia treatment; drug development; cerebrospinal fluid; human;  
 ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004110938-A1.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 23-FEB-2001; 2001US-00791377.  
 XX  
 PR 24-FEB-2000; 2000GB-00044156.  
 PR 28-DEC-2000; 2000US-00750395.  
 XX  
 PA (PARE/) PAREKH R B.  
 PA (HERA/) CHANDRASIRI HERATH H M A.  
 PA (ROHL/) ROHLFF C.  
 PA (TERR/) TERRETT J A.  
 PA (TYSON/) TYSON K L.  
 XX  
 PI Parekh RB, Chandrasiri Herath HMA, Rohlff C, Terrett JA, Tyson KL;  
 XX  
 DR WPI: 2004-440403/41.  
 DR P-PSDB; ADO79047.  
 XX  
 PT New isolated nucleic acid molecule, useful for diagnosing Schizophrenia,  
 PT for monitoring the effectiveness of Schizophrenia treatment or for  
 PT screening agents for treating Schizophrenia.  
 XX  
 PS Disclosure; SEQ ID NO 664; 170bp; English.  
 XX  
 CC The invention describes an isolated nucleic acid molecule (I) that  
 CC hybridises to two short nucleic acid sequences and the 1515 amino acid  
 CC sequence fully defined in the specification. Also described are: a  
 CC preparation comprising an isolated peptide coded for by the nucleic acid  
 CC molecule above, or comprising an isolated human protein comprising one or  
 CC more of the following sequences: Glu-Leu-Asp-Val-Leu-Gln-Gly-Arg, and Gly  
 CC -Ile-Leu-Ile-Leu-Gln-Gln-Asp-Thr-Leu-Gly-Arg; methods for  
 CC diagnosing Schizophrenia; antibodies capable of immunospecific binding to  
 CC a Schizophrenia-Associated Protein Isoform (SPI); methods of treating  
 CC Schizophrenia; and methods of screening for agents that modulate a  
 CC characteristic (e.g., expression or binding activity) of an SPI, an SPI  
 CC analogue, or an SPI-related polypeptide. The nucleic acid molecule and  
 CC encoded proteins, as well as the methods and compositions are useful for  
 CC screening, diagnosing, and prognosing Schizophrenia, for monitoring the  
 CC effectiveness of Schizophrenia treatment, for identifying patients most  
 CC likely to respond to a particular therapeutic treatment and for  
 CC developing drug. They are also useful for screening modulators of  
 CC Schizophrenia-Associated Protein Isoform useful for treating  
 CC Schizophrenia. This sequence encodes a schizophrenia-associated protein  
 CC isoform.  
 CC  
 SQ Sequence 42 BP; 6 A; 12 C; 15 G; 9 T; 0 U; 0 Other;  
 XX  
 Query Match 71.0%; Score 14.2; DB 12; Length 42;  
 Best Local Similarity 84.2%; Pred. No. 8.8e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GTGCCAGCCAGAGCACT 19  
 DB 7 GTGCCAGCCAGAGCACT 25  
 XX  
 RESULT 9  
 ADH05972/C  
 ID ADH05972 standard; DNA; 41 BP.  
 AC ADH05972;  
 XX  
 DT 11-MAR-2004 (first entry)

XX  
 DE Gene polymorphism detection method-related primer/probe #938.  
 KW gene polymorphism detection; primer; probe; SNP analysis;  
 KW single nucleotide polymorphism analysis; drug selection; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003097877-A1.  
 XX  
 PD 27-NOV-2003.  
 XX  
 PF 16-MAY-2003; 2003WO-JP006141.  
 XX  
 PR 17-MAY-2002; 2002JP-00143185.  
 PR 17-OCT-2002; 2002JP-00303528.  
 XX  
 PA (RIKE ) RIKEN KK.  
 PA (NAKA/) NAKAMURA Y.  
 PA (SEKI/) SEKINE A.  
 PA (IIDA/) IIDA A.  
 PA (SAIT/) SAITO S.  
 XX  
 PI Nakamura Y, Sekine A, Iida A, Saito S;  
 XX  
 DR WPI: 2004-012542/01.  
 XX  
 PT Detecting gene polymorphism for single nucleotide polymorphism analysis  
 PT and drug selection.  
 XX  
 PS Claim 2; SEQ ID NO 938; 166bp; Japanese.  
 XX  
 CC The invention comprises a method for detecting gene polymorphisms, the  
 CC method involves constructing an oligonucleotide primer and/or probe  
 CC containing the polymorphism site in a receptor gene or its complementary  
 CC sequence, amplifying that part and detecting it with the probe and/or  
 CC primer. The method of the invention is useful for the analysis of SNPs  
 CC and in drug selection. The present DNA sequence represents a primer/probe  
 CC of the invention.  
 CC  
 SQ Sequence 41 BP; 10 A; 9 C; 12 G; 9 T; 0 U; 1 Other;  
 XX  
 Query Match 70.0%; Score 14; DB 12; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGCCAGCCAGAG 14  
 DB 37 GTGCCAGCCAGAG 24  
 XX  
 RESULT 10  
 ADH91759/C  
 ID ADH91759 standard; DNA; 41 BP.  
 AC ADH91759;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE 1-beta-methylcarbapenem compound-related human DNA sequence #938.  
 DE  
 XX  
 KW 1-beta-methylcarbapenem compound; antimicrobial; bacterial infection;  
 KW respiratory infection; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003095454-A1.  
 XX  
 PD 20-NOV-2003.  
 XX  
 PF 14-MAY-2003; 2003WO-JP006028.  
 XX  
 DT 14-MAY-2002; 2002JP-00138448.

```
XX (SANY ) SANKYO CO LTD.
PA Kobayashi Y, Ashida Y, Uchida T, Kojima K;
XX WPI; 2004-081882/08.
XX
XX New carapenem compounds resistant to beta-lactamase (except metallo-beta
PT -lactamase), useful for treating microbial infections especially
PT respiratory infections.
XX
XX Disclosure; SEQ ID NO 938; 726bp; Japanese.
XX
XX The invention comprises 1-beta-methylcarapenem compounds which are
CC useful as antimicrobials to treat bacterial infections, especially
CC respiratory infections in warm-blooded animals (e.g. humans). The present
CC human DNA sequence is included in the sequence listing of this patent.
XX
XX
SQ Sequence 41 BP; 10 A; 9 C; 12 G; 9 T; 0 U; 1 Other;

Query Match          70.0%; Score 14; DB 12; Length 41;
Best Local Similarity 100.0%; Pred.No.1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGCCAGCCAGCAG 14
DB      37 GTGCCAGCCAGCAG 24

RESULT 11
AAQ1150
ID AAQ1150 standard; DNA; 80 BP.
XX
XX AAQ1150;
XX
XX 04-JUN-1991 (first entry)
XX
XX Probe GTR-2 based on the 3' end of human and rat GTP sequences.
DE
XX Glucose transporter protein; serum-independence; Chinese Hamster;
XX Insulin-independence; ss.
XX
XX Cricetus sp.
XX
XX MO9103554-A.
XX
XX 21-MAR-1991.
XX
XX
XX 01-SEP-1989; 89US-00402204.
XX
XX 01-SEP-1989; 89US-00402204.
XX
XX 20-JUN-1990; 90US-00541426.
XX
XX (GETH ) GENENTECH INC.
XX
XX Thomas JN, Williams SR;
XX
XX WPI; 1991-102073/14.
XX
XX Transfecting eukaryotic cells with a replicable vector - comprising
PT nucleic acid sequence encoding a GTP operably linked to control sequences
PT recognised by transfected cells.
XX
XX
XX Example 1; Page 20; 58pp; English.
XX
XX A cDNA library was prepared in lambda gt10 from total cellular RNA from
CC CHO-PR4 cells. The library was screened with 3 probes (GTR1- GTR-3) based
CC on highly conserved regions of the known rat and human facilitative GTP
CC sequences (Birbaum et al., Proc. Natl. Acad. Sci. USA, 83:5784-
CC 5788, (1986); Mueckler et al., Science, 223:941-945, (1985)). One positive
CC plaque was identified (out of 150000), replated and screened with probes
CC GTR-1 and GTR-3. Phage DNA was prepared from one of the positive plaques
CC and its 2.5kb cDNA insert excised using EcoRI. The insert was ligated
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```
CC into pRK5 and transformed into E.coli strain SR101. Recombinant clones
CC were picked for sequencing and the complete CHO GTP-encoding sequence
CC determined. See also AAQ11148-9 and AAQ11151
XX
XX
SQ Sequence 80 BP; 18 A; 23 C; 28 G; 11 T; 0 U; 0 Other;

Query Match          70.0%; Score 14; DB 2; Length 80;
Best Local Similarity 100.0%; Pred.No.1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCAGCCAGAGCGCAGC 18
DB      50 CCAGCCAGAGCGCAGC 63

RESULT 12
ABA97968
ID ABA97968 standard; DNA; 26 BP.
XX
XX ABA97968;
XX
XX 25-APR-2002 (first entry)
XX
XX Human pancreatic cancer antigen related PCR primer SEQ ID NO 3.
DE
XX Human pancreatic cancer; antigen; oesophageal cancer; colon cancer;
XX Human; pancreatic cancer; antigen; oesophageal cancer; colon cancer;
XX breast cancer; PCR primer; ss.
XX
XX Synthetic.
XX
XX JP2001340081-A.
XX
XX 11-DEC-2001.
XX
XX 31-MAY-2000; 2000JP-00161930.
XX
XX 31-MAY-2000; 2000JP-00161930.
XX
XX (KEIO-) GH KEIO GIJUKU.
XX
XX WPI; 2002-144963/19.
XX
XX New DNA encoding a human pancreatic cancer antigen protein for treating
PT and diagnosing cancer, especially pancreatic, esophagus, colon and breast
PT cancer.
XX
XX
XX Example; Page 10; 20pp; Japanese.
XX
XX The invention relates to a DNA (ABA97973) encoding a human pancreatic
CC cancer antigen protein (AB808656) or a protein consisting of the amino
CC acid sequence of human pancreatic antigen protein in which at least one
CC amino acid is deleted, replaced or added and having immunity-inducing
CC activity. The antigen and the DNA are useful for treating and diagnosing
CC pancreatic cancer, oesophagus cancer, colon cancer and breast cancer. The
CC present sequence is that of a PCR primer, useful to the invention
XX
XX
SQ Sequence 26 BP; 10 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match          69.0%; Score 13.8; DB 6; Length 26;
Best Local Similarity 88.2%; Pred.No.1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGCCAGCCAGAGCAGC 18
DB      1 TGCCAGCCAGAGATAC 17

RESULT 13
AAL55205/c
ID AAL55205 standard; RNA; 36 BP.
XX
XX AAL55205;
XX
```

DT 01-MAY-2003 (first entry)  
 XX  
 DE pshn1-Ff1 RNA oligomer, SEQ ID NO 10.  
 XX  
 KM Cytostatic; RNA interference; RNAi agent; non-embryonic mammal;  
 XX gene therapy; vaccination; vaccine; animal model; cancer; enzyme; ss.  
 OS Unidentified.  
 XX  
 PN WO2003010180-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 19-JUL-2002; 2002WO-US022869.  
 XX  
 PR 23-JUL-2001; 2001US-0307411P.  
 XX 27-FEB-2002; 2002US-0360664P.  
 XX  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Kay M, Mc Caffrey A;  
 XX  
 DR WPI; 2003-229634/22.  
 XX  
 PT Reducing coding sequence expression in a target cell of a non-embryonic  
 PT mammal, useful for producing animal models of RNA virus infection or in  
 PT therapeutic applications, comprises administering to the mammal an RNA  
 PT interference agent.  
 XX  
 PS Disclosure; Page 63; 65pp; English.  
 XX  
 CC The invention relates to a novel method for reducing expression of a  
 CC coding sequence in a target cell of a non-embryonic mammal. The method  
 CC comprises administering to the mammal an RNA interference (RNAi) agent  
 CC specific for the coding sequence to reduce expression of the coding  
 CC sequence. The RNAi agent is useful for modulating, i.e., reducing, the  
 CC coding sequence expression in a target cell of a non-embryonic mammal  
 CC used in academic, research or therapeutic applications, e.g. gene therapy  
 CC or vaccination applications. Academic or research applications include  
 CC producing animal models of RNA virus infection, determining potential  
 CC targets for pharmaceuticals, understanding normal and pathological events  
 CC associated with development, determining signaling pathways responsible  
 CC for post-natal development or ageing, or identifying gene function in non  
 CC embryonic mammals. The method is useful for treating different  
 CC conditions in which the modulation of target gene expression in a  
 CC mammalian host is desired, e.g. cancer. This polynucleotide sequence  
 CC represents a pshn1-Ff1 RNA oligomer relating to the RNAi agents of the  
 CC invention  
 XX  
 SQ Sequence 36 BP; 6 A; 8 C; 11 G; 0 T; 11 U; 0 Other;  
 XX  
 QY Query Match 69.0%; Score 13.8; DB 8; Length 36;  
 XX Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 DB 3 GCCCAGCCGAGCGACT 19  
 XX |||||  
 DB 30 GCCCAGCCGAGCGACT 14  
 XX |||||  
 XX  
 RESULT 14  
 ADV87091  
 ID ADV87091 standard; DNA; 71 BP.  
 XX  
 AC ADV87091;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DE Non-specific shRNA expression construct DNA insert.  
 XX  
 KM RNA interference; RNAi; probe; gene silencing; short hairpin RNA; shRNA;  
 KM myosin D; ss.  
 XX

OS Synthetic.  
 XX  
 PN WO200411190-A2.  
 XX  
 PD 23-DEC-2004.  
 XX  
 PF 26-MAY-2004; 2004WO-US016844.  
 XX  
 PR 27-MAY-2003; 2003US-0473809P.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Mittal V, Kumar R;  
 XX  
 DR WPI; 2005-040085/04.  
 XX  
 PT Determining whether an RNAi probe can inhibit expression of a target gene  
 PT by detecting expression of a target-reporter fusion construct, useful for  
 PT high-throughput screens to identify effective RNAi probes.  
 XX  
 PS Example 1; SEQ ID NO 50; 59pp; English.  
 XX  
 CC The invention provides a reliable and quantitative approach for the rapid  
 CC and efficient identification of an effective RNAi probe (e.g. a short  
 CC interfering RNA (siRNA) or short hairpin RNA (shRNA)) against any gene,  
 CC and for selecting the best RNAi probe from among a group of RNAi  
 CC candidates. This method may be used for high-throughput screens, e.g.  
 CC based on microarray cell transfections, of RNAi probes. The method is  
 CC based upon introduction into a target cell of both an RNAi probe and a  
 CC cognate target-reporter fusion expression construct, where expression of  
 CC the target-reporter fusion may be easily quantitated based upon the  
 CC reporter. The ability of an RNAi probe to suppress target-reporter fusion  
 CC expression, as quantified by reporter expression, specifically correlates  
 CC with the ability of the identified RNAi probe to effectively suppress  
 CC expression of the cognate endogenous gene. The present sequence is that  
 CC of the 3'-5' strand of a double-stranded DNA insert of a non-specific  
 CC shRNA expression construct. This shRNA was compared with mouse myod-  
 CC specific shRNA expression constructs in examples from the invention.  
 XX  
 SQ Sequence 71 BP; 23 A; 19 C; 16 G; 13 T; 0 U; 0 Other;  
 XX  
 QY Query Match 69.0%; Score 13.8; DB 14; Length 71;  
 XX Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 DB 3 GCCCAGCCGAGCGACT 19  
 XX |||||  
 DB 36 GCCCAGCCGAGCGACT 52  
 XX |||||  
 XX  
 RESULT 15  
 ACD80225/C  
 ID ACD80225 standard; DNA; 100 BP.  
 XX  
 AC ACD80225;  
 XX  
 DT 19-SEP-2003 (first entry)  
 XX  
 DE E. coli K12 MG1655 biochip probe SEQ ID 11501.  
 XX  
 KM Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 PN EP1260592-A1.  
 XX  
 PD 27-NOV-2002.  
 XX  
 PF 17-MAY-2001; 2001EP-00112179.  
 XX  
 PR 17-MAY-2001; 2001EP-00112179.  
 XX  
 PA (MWGB-) MWG-BIOTECH AG.  
 XX







musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 64;  
Best Local Similarity 89.5%; Pred. No. 1.2e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCCACGACGAGCGACTG 20  
|||||  
Db 31 TGCCACGACGAGCGACTG 49

RESULT 2 85 bp mRNA linear EST 10-FEB-1998  
AA797827  
LOCUS vy04003.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA  
DEFINITION clone IMAGE:1294445 5' similar to SW:YKNO.YEAST Q03103 HYPOTHETICAL  
65.0 KD PROTEIN IN COX14 5'REGION PRECURSOR. ; mRNA sequence.

ACCESSION AA797827  
VERSION AA797827.1 GI:2860782  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Merrin, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheinberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:675493

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev1 ET from Amersham  
High quality sequence stop: 1.

## FEATURES

source  
1..85  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1294445"  
/issue\_type="macrohage"  
/dev\_stage="WEHI-3 cell line"

/lab\_host="SOLR (kanamycin resistant)"  
/clone\_1ib="Stratagene mouse macrophage (#937306)"  
/note="Organ: blood; Vector: pBluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb.  
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAAATTCGACGACGAG  
3' ~3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGT 3'."

## ORIGIN

Query Match 76.0%; Score 15.2; DB 1; Length 85;  
Best Local Similarity 85.0%; Pred. No. 2.3e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCACGACGAGCGACTG 20  
|||||  
Db 66 GTGCCACGACGAGCGACTG 47

RESULT 3 70 bp mRNA linear GSS 01-OCT-2003  
CG552451  
LOCUS OST161696 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST161696,  
DEFINITION mRNA sequence.

ACCESSION CG552451  
VERSION CG552451.1 GI:37339038  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 70)

Zambrowicz, B.P., Abidin, A., Ramirez-Solis, R., Richter, L.J., Piggett, J., Beltrandro, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.O., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W., Jr., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Marzesh, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
14610273

COMMENT Contact: Zambrowicz BP

OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: [materials@lexgen.com](mailto:materials@lexgen.com)  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

## FEATURES

source  
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/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST161696"  
/cell\_type="embryonic stem cell"  
/clone\_1ib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 75.0%; Score 15; DB 10; Length 70;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CAGCCAGAGCGACTG 20  
|||||  
Db 20 CAGCCAGAGCGACTG 34

RESULT 4  
CG476131/c

LOCUS CG476131 94 bp mRNA linear GSS 01-OCT-2003  
 DEFINITION OST5407 Mus musculus 129sv/Ev Mus musculus cDNA clone OST5407, mRNA sequence.

ACCESSION CG476131  
 VERSION CG476131.1 GI:37227020  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 94)  
 Zambrowicz, B.P., Abuh, A., Ramirez-Solis, R., Richter, L.J., Pigott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jang, C., Key, B.W., Jr., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D., Payne, R., Porter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Slichtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.  
 Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 14610273

COMMENT Contact: Zambrowicz BP  
 OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: materials@lexgen.com  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap.

FEATURES  
 source Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
 /clone="OST5407"  
 /cell\_type="embryonic stem cell"  
 /clone\_11b="Mus musculus 129sv/Ev"

ORIGIN  
 Query Match 71.0%; Score 14.2; DB 10; Length 94;  
 Best Local Similarity 84.2%; Pred. No. 6.7e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGCGACT 19  
 |||||  
 83 GTGCCAGCCAGCGACT 65

Db

RESULT 5  
 LOCUS DQ045724 51 bp DNA linear GSS 02-JUN-2005  
 DEFINITION Pan troglodytes PALM gene, VIRUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ045724  
 VERSION DQ045724.1 GI:66896939  
 KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pan.  
 1 (bases 1 to 51)  
 Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B., Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civeello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.  
 A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees  
 (er) PLOS Biol. 3 (6), E170 (2005)  
 15869325  
 2 (bases 1 to 51)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 PUBMED  
 REFERENCE

AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B., Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civeello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES  
 source Location/Qualifiers  
 1..51  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 <1..>51  
 /gene="PALM"  
 /locus\_tag="HC11484"

ORIGIN  
 Query Match 69.0%; Score 13.8; DB 11; Length 51;  
 Best Local Similarity 88.2%; Pred. No. 1e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCAGCGCGCTG 20  
 |||||  
 24 CCCAGCAGCGCGCTG 40

Db

RESULT 6  
 LOCUS AI037190/c 64 bp mRNA linear EST 26-JUN-1998  
 DEFINITION uds6a09.y1 Sugano mouse liver mila Mus musculus cDNA clone IMAGE:1450264 5' similar to SW:YHLL\_EBV P03181 HYPOPHYSICAL BHLFI PROTEIN. ;, mRNA sequence.

ACCESSION AI037190  
 VERSION AI037190.1 GI:3260881  
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 64)  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
 The WashU-HMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LIND; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:923580

Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: custom primer used  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..64  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1450264"  
 /sex="female"  
 /dev\_stage="adult"

FEATURES  
 source

/lab host="DH108"  
 /clone lib="Sugano mouse liver mlia"  
 /note="Ogan: liver; Vector: pME185-FL3; Site 1: DraIII  
 (CACTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA  
 was primed with an oligo (dT) primer  
 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was  
 ligated to a DraIII adaptor (TGTGGCCCTACTGG), digested  
 and cloned into distinct DraIII sites of the pME185-FL3  
 vector (5' site CACTGTG; 3' site CACCATGTG). XhoI should  
 be used to isolate the cDNA insert. Size selection was  
 performed to exclude fragments <1.5kb. Library  
 constructed by Dr. Sumio Sugano (University of Tokyo  
 Institute of Medical Science). Custom primers for  
 sequencing: 5' end primer CTCTGCTTAAAGCTGGC and 3' end  
 primer CCACTGCGACGTGACGACA."

## ORIGIN

Query Match 69.0%; Score 13.8; DB 1; Length 64;  
 Best Local Similarity 88.2%; Pred. No. 1e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGACGCA 17  
 |||||  
 Db 44 GAGACCGACGACGACGA 28

RESULT 7 98 bp mRNA linear GSS 02-OCT-2003  
 CG637147 OST362774 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST362774,  
 LOCUS mRNA sequence.  
 DEFINITION CG637147  
 CG637147.1 GI:37460996  
 GSS.  
 VERSION Mus musculus (house mouse)  
 KEYWORDS Mus musculus  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
 Piggett, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
 Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
 Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-O., Markesich, D.,  
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z.,  
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
 Zhu, Q., Person, C. and Sands, A.T.  
 Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

JOURNAL  
 PUBMED 14610273  
 COMMENT Contact: Zambrowicz BP  
 OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: materials@lexgen.com  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;352(6676):608-11)  
 Class: Gene Trap.  
 Location/Qualifiers  
 1..98  
 /organism="Mus musculus"  
 /mol\_type="RNA"  
 /strain="129Sv/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST362774"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

FEATURES  
 source

## ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 98;  
 Best Local Similarity 88.2%; Pred. No. 1e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCAGACGAC 18  
 |||||  
 Db 96 TGCCAGCCAGACGAC 80

RESULT 8 55 bp DNA linear GSS 05-OCT-2000  
 A2487430 1M0317A10F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 LOCUS clone UGCGM0317A10 F, genomic survey sequence.  
 DEFINITION

ACCESSION A2487430  
 VERSION A2487430.1 GI:10655167  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 55)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0317 row: A column: 10  
 Seq primer: CGTGTGTAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 55.

FEATURES  
 source

1..55  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCGM0317A10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydridynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g14732114[gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 55;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCAGCTG 20  
 |||  
 30 GAGCCAGCCAGAGGTGAGTG 49

RESULT 9  
 B2586465 60 bp DNA linear GSS 17-DEC-2002  
 DEFINITION 3590\_1\_16\_1\_H09.2EL\_Y\_1 3590 - RescueMu Grid M Zea mays genomic,  
 genomic survey sequence.  
 ACCESSION B2586465  
 VERSION B2586465.1 GI:27221526  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 60)

REFERENCE  
 AUTHORS Walbot,V.  
 TITLE Maize genomic sequences found using engineered RescueMu transposon  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 3590\_1\_16\_1 column: 4  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..60  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="mixed BackGround W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="3590 - RescueMu Grid M"  
 /note="Organ: leaf; Vector: RescueMu (engineered from  
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
 RescueMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescueMu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'RescueMu.' Grid M was grown at University of Arizona in  
 2001. DNA was extracted from leaf punches, double digested  
 using BamHI and BglII, and ligated to form circular  
 plasmids. DH10B cells were transformed and then screened  
 on LB plates with ampicillin."

ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 60;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCAGCTG 20  
 |||  
 14 GTGCCAGCTGAGCCCTG 33

RESULT 10  
 AK197036 76 bp mRNA linear HTC 23-NOV-2004  
 LOCUS Mus musculus cDNA, clone:Y1G0123M15, strand:minus,  
 DEFINITION reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000040111, based

on BLAT search.

ACCESSION AK197036  
 VERSION AK197036.1 GI:56021213  
 KEYWORDS HTC; ASSETS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 Watabiki,A., Waki,K., Hayatsu,N., Shiraki,T., Kondo,S.,  
 Nakamura,M., Sasaki,D., Arakawa,T., Kawai,J., Harbers,M.,  
 Hayashizaki,Y. and Carninci,P.  
 Libraries enriched for alternatively spliced exons reveal splicing  
 patterns in melanocytes and melanomas  
 Nat. Methods 1, 233-239 (2004)

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 2 (bases 1 to 76)  
 Arakawa,T., Carninci,P., Fukuda,S., Harbers,M., Hayatsu,N.,  
 Horii,F., Imotani,K., Kawai,J., Kondo,S., Murata,M., Nakamura,M.,  
 Nomura,K., Ohno,M., Sasaki,D., Shiraki,T., Waki,K., Watabiki,A. and  
 Hayashizaki,Y.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 Direct Submission  
 Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa, 230-0045, Japan (E-mail:genome-res@gs.c.riken.jp,  
 URL: http://genome.gsc.riken.jp, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)

COMMENT  
 Alternative Splicing Libraries (ASLs) are prepared by: Preparing  
 of single-stranded DNA using a RNA template from full length cDNA  
 libraries, hybridizing of  
 single-stranded DNAs, removing of remaining single-stranded DNA,  
 digesting of regions comprising double-stranded DNA by a set of 4  
 bp-cutters, capturing of DNA hybrids with loop structures  
 (alternative spliced exon), ligation of Y-shaped primers to  
 isolated DNA hybrids with loop structures, PCR amplification of  
 ligation products and their cloning into pFUCI vector. (reference).  
 Location/Qualifiers  
 1..76  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone\_lib="Y1G0123M15"  
 /cell\_line="mixture of B16-F10Y and melan-c"  
 /cell\_type="mixture of melanoma cell and melanocyte cell"  
 /clone\_lib="Alternative Splicing Library L1"  
 /note="strand:minus, reference:ENSEMBL:Mouse-Transcript-  
 ENST:ENSMUST0000040111, based on BLAT search"

ORIGIN

Query Match 68.0%; Score 13.6; DB 4; Length 76;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCAGCTG 20  
 |||  
 52 GTGCTCTGCCAGAGCATCTG 33

RESULT 11  
 AZ946089 20 bp DNA linear GSS 27-APR-2001  
 LOCUS 2M0207A13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0207A13 R, genomic survey sequence.  
 ACCESSION AZ946089  
 VERSION AZ946089.1 GI:13812898  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb  
 COMMENT Plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0207 row: A column: 13  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers  
 1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCM0207A13"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
 /note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gll4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
 Query Match 67.0%; Score 13.4; DB 9; Length 20;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+05;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 5 CCAGCCAGAGCGACT 19  
 |||||  
 |||||  
 Db 18 CCAGCCAGAGCGATT 4

RESULT 12  
 DN460399/c 73 bp mRNA linear EST 09-MAR-2005  
 LOCUS EST956198 Sequencing ESTs from loblolly pine embryos Pinus taeda  
 DEFINITION cDNA clone RPIHY11 5' end, mRNA sequence.  
 DN460399  
 ACCESSION DN460399.1 GI:60666823  
 VERSION  
 KEYWORDS EST.  
 SOURCE Pinus taeda (loblolly pine)  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 73)  
 AUTHORS Buell, C.R., Zheng, L., Cowles, A. and Cairney, J.  
 TITLE Sequencing of ESTs from loblolly pine embryonic libraries  
 JOURNAL Unpublished (2004)  
 COMMENT CONTACT: C. Robin Buell  
 Plant Genomics Group  
 The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: rbuell@tigr.org  
 This clone is available through TIGR. Please contact pine@tigr.org for further information  
 Seq primer: ATT TAG GTG ACA CTA TAG.  
 Location/Qualifiers  
 1..73  
 /organism="Pinus taeda"  
 /mol\_type="mRNA"  
 /cultivar="7-56 mother tree, open-pollinated tree from, Lyons, Georgia, USA"  
 /db\_xref="taxon:3352"  
 /clone="RPIHY11"  
 /lab\_host="E.coli DH10B-TonA"  
 /clone\_lib="Sequencing ESTs from loblolly pine embryos"  
 /note="Organ: Zygotic Embryo and Megagametophyte. Somatic Embryo; Vector: pCMV-SPORT 6.1; Site\_1: Nct1; Site\_2: EcoRV; tissue: whole megagametophytes isolated from pine seeds, whole embryos excised from these megagametophytes, whole somatic embryos and suspensor tissue from tissue culture, isolated from cell line A12. Pooled RNA from zygotic embryos, megagametophytes, and somatic embryos was used for library construction. Pine cones were harvested weekly from open-pollinated 7-56 mother trees, collections megagametophytes were first isolated from pine seeds, and whole embryos excised from these megagametophytes each was flash frozen. Embryo development was assessed using the system of Pullman et al (Pullman GS, Johnson S, Peter G, Cairney J, Xu N. 2003. Loblolly Pine somatic embryogenesis: development of a maturation medium and resulting embryo quality. Plant Cell Reports 21:747-758 (<http://link.springer.de/link/service/journals/00299/content/03/00556/>). For photographs see Clavatta et al 2001. (Clavatta VE, Morillon R, Pullman GS, Christopels M, Cairney J. 2001. An aquaglycoperin is abundantly expressed early in the development of the suspensor and the embryo proper of loblolly pine (Pinus taeda L.). Plant Physiol. 127: 1556-1567 (<http://www.plantphysiol.org/cgi/content/full/127/4/1556>))."

ORIGIN  
 Query Match 67.0%; Score 13.4; DB 8; Length 73;  
 Best Local Similarity 93.3%; Pred. No. 1.6e+05;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 TGCCAGCCAGAGCG 16  
 |||||  
 |||||  
 Db 50 TGCCAGCCAGAGCG 36

RESULT 13  
 AZ475290 86 bp DNA linear GSS 04-OCT-2000  
 LOCUS 1M0293H07F Mouse 10kb plasmid UGGC1M library Mus musculus genomic  
 DEFINITION clone UGGC1M0293H07 F, genomic survey sequence.  
 AZ475290  
 ACCESSION AZ475290.1 GI:10633415  
 VERSION  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 86)

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, S., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niedermaier, A., and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

## FEATURES

## source

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0293 row: H column: 07  
Seq primer: CGTGTGAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 86.  
Location/Qualifiers

1..86

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0293H07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42uv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 67.0%; Score 13.4; DB 9; Length 86;  
Best Local Similarity 93.3%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCCACCGCAGGC 15  
Db 34 GTGCCACCGCAGGC 48

## RESULT 14

CL271491/c

## LOCUS

DEFINITION

Ggal\_73c\_PR\_C06 Ggal\_PR-1 Gallus gallus genomic clone  
Ggal\_73c\_PR\_C06, genomic survey sequence.

## ACCESSION

CL271491

## VERSION

KEYWORDS

SOURCE

GSS  
Gallus gallus (chicken)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

## REFERENCE

1 (bases 1 to 89)

## AUTHORS

Wicker, T., Robertson, J. S., Schulze, S. R., Fellus, F. A., Magrini, V.,  
Morrison, V. A., Mardis, E. R., Wilson, R. K., Peterson, D. G.,  
Paterson, A. H., and Ivarte, R.

## TITLE

The repetitive landscape of the chicken genome  
Genome Res. 15 (1), 126-136 (2005)

## JOURNAL

PUBMED

## COMMENT

Contact: Paterson AH  
Plant Genome Mapping Laboratory  
University of Georgia, Center for Applied Genetic Technologies  
Riverbend Research Laboratory, Room 162, 110 Riverbend Road,  
Athens, GA 30602 USA  
Tel: 7065830169  
Fax: 7065830160  
Email: paterson@ga.edu  
Sequence from middle repetitive (MR) Cot fraction, Cot 10-100  
Class: Hydroxyapatite-fractionated DNA.

## FEATURES

## source

1..89

/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9031"  
/clone="Ggal\_73c\_PR\_C06"  
/sex="female"  
/clone\_lib="Ggal\_PR-1"  
/note="Produced by Cot-based cloning and sequencing  
(CBCS)"

## ORIGIN

Query Match 67.0%; Score 13.4; DB 10; Length 89;  
Best Local Similarity 93.3%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCCACCGCAGGC 15  
Db 38 GTGCCACCGCAGGC 24

## RESULT 15

CB884871

LOCUS

DEFINITION

CB884871 94 bp mRNA linear EST 14-AUG-2003  
M15038 Hamster Bluescript Dp11 library Mesocricetus auratus cDNA  
similar to outer dense fibre of sperm tails 2 (ODF2), mRNA  
sequence.

ACCESSION

CB884871

VERSION

KEYWORDS

SOURCE

ORGANISM

Mesocricetus auratus (golden hamster)  
EST.  
CB884871.1 GI:30086661  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Cricetidae; Cricetinae; Mesocricetus.  
1 (bases 1 to 94)  
Oduru, S., Campbell, J. L., Karr, S., Hendry, W. J., Khan, S. A. and  
Williams, S. C.

## TITLE

JOURNAL

PUBMED

COMMENT

Contact: Simon C. Williams  
Department of Cell Biology and Biochemistry  
Texas Tech University Health Science Center  
3601 4th Street, Lubbock, TX 79430, USA  
Tel: 806 743 2524  
Fax: 806 743 2990  
Email: simon.williams@ttuhs.ttuhs.edu  
Insert Length: 94 Std Error: 0.00  
Seq primer: T7  
High quality sequence stop: 94.  
Location/Qualifiers

## FEATURES

## source

1..94  
/organism="Mesocricetus auratus"  
/mol\_type="mRNA"

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/db_xref="raxon:10036"
/bex="male"
/tissue_type="testis"
/dev_stage="adult"
/clone_lib="Hamster Bluescript DpniI library"
/notes="library prepared by insertion of DpniI
digested hamster testis cDNA into pbluescript, BamHI digested
vector."

```

ORIGIN

	Query Match	Score	Length
	67.0%	13.4	94
	Best Local Similarity	93.3%	DB 6
	Best Local Similarity	Pred. No. 1.6e+05	
Matches	14; Conservative	0; Mismatches	1; Indels
			Gaps
OY	2 TGGCCAGCCAGCG 16		
DB	58 TGGCCAGCTAGGCG 72		

Search completed: December 24, 2005, 18:28:36  
Job time : 1576 secs





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; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42233
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-42233
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Query Match          72.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      4 CCCAGCCAGAGCGACT 19
         |||||
Db       1 CCCACGACGAGCGACT 16
```

```

RESULT 3
US-09-396-196G-62691/c
; Sequence 62691, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-62691
```

```

Query Match          72.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

QY      5 CCAGCCAGAGCGACTG 20
         |||||
Db       18 CCAGCCAGAGCGACTG 3
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```

RESULT 4
US-09-396-196G-16382/c
; Sequence 16382, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16382
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-16382
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Query Match          69.0%; Score 13.6; DB 3; Length 25;
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```

Best Local Similarity 88.2%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      1 GTGCCAGCCAGAGCGA 17
         |||||
Db       17 GTGCCAGAGAGAGCGA 1
```

```

RESULT 5
US-09-396-196G-105272/c
; Sequence 105272, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105272
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-105272
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```

Query Match          69.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      3 GCCCAGCCAGAGCGACT 19
         |||||
Db       19 GCCCAGCCAGAGCGACT 3
```

```

RESULT 6
US-09-443-199C-1187/c
; Sequence 1187, Application US/09443199C
; Patent No. 6670464
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A.
; APPLICANT: Leach, Martin
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
; FILE REFERENCE: 15966-534A
; CURRENT APPLICATION NUMBER: US/09/443,199C
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 1272
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 1187
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26)...(0)
; OTHER INFORMATION: 1 of 2 allelic variants (1188 is other entry)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number CG44931270
US-09-443-199C-1187
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```

Query Match          68.0%; Score 13.6; DB 3; Length 51;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 1 GTGCCGAGCCAGCAGCTG 20  
Db 33 GTGCCGAGCCAGCAGCTG 14

RESULT 7  
US-08-658-034-2/c  
Sequence 2, Application US/08658034  
Patent No. 6190657  
GENERAL INFORMATION:  
APPLICANT: Pawelek, John M.  
APPLICANT: Bermudez, David  
APPLICANT: Low, Kenneth Brooks  
TITLE OF INVENTION: VECTORS FOR THE DIAGNOSIS AND TREATMENT  
OF SOLID TUMORS INCLUDING MELANOMA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,034  
FILING DATE: On Even Date Herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Baldwin, Geraldine F.  
REGISTRATION NUMBER: 31,232  
REFERENCE/DOCKET NUMBER: 8002-036  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-658-034-2

Query Match 66.0%; Score 13.2; DB 3; Length 28;  
Best Local Similarity 83.3%; Pred. No. 6.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCCAGCCAGCAGCTG 20  
Db 28 GCCCTGCCATAGCCACTG 11

RESULT 8  
US-09-358-052-2/c  
Sequence 2, Application US/09358052  
Patent No. 6685935  
GENERAL INFORMATION:  
APPLICANT: Pawelek, John M.  
APPLICANT: Bermudez, David  
APPLICANT: Low, Kenneth Brooks  
TITLE OF INVENTION: VECTORS FOR THE DIAGNOSIS AND TREATMENT  
OF SOLID TUMORS INCLUDING MELANOMA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/358,052  
FILING DATE: 21-Jul-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/658,034  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Baldwin, Geraldine F.  
REGISTRATION NUMBER: 31,232  
REFERENCE/DOCKET NUMBER: 8002-036  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-358-052-2

Query Match 66.0%; Score 13.2; DB 3; Length 28;  
Best Local Similarity 83.3%; Pred. No. 6.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCCAGCCAGCAGCTG 20  
Db 28 GCCCTGCCATAGCCACTG 11

RESULT 9  
US-09-348-578-31/c  
Sequence 31, Application US/09348578  
Patent No. 6160089  
GENERAL INFORMATION:  
APPLICANT: HONJO, Masaru  
APPLICANT: UCHIDA, Hiroshi  
APPLICANT: MOCHIZUKI, Kazuya  
APPLICANT: MATSUMOTO, Kazuya  
TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE  
FILE REFERENCE: 029430-421  
CURRENT APPLICATION NUMBER: US/09/348,578  
EARLIER APPLICATION NUMBER: JP 193003/1998  
EARLIER FILING DATE: 1998-07-08  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31  
LENGTH: 76  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
LOCATION: (1)..(76)  
OTHER INFORMATION: Description of Artificial Sequence: Designed DNA sequence to  
OTHER INFORMATION: act as a primer for PCR to produce the latter half of OpA  
OTHER INFORMATION: secretion signal  
US-09-348-578-31

Query Match 66.0%; Score 13.2; DB 3; Length 76;  
Best Local Similarity 83.3%; Pred. No. 7.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCCAGCCAGGACTG 20

DB 25 GCGCAGCCAGACGCGCTG 8

RESULT 10

US-09-699-684-31/C

; Sequence 31, Application US/09699684

; Patent No. 643674

; GENERAL INFORMATION:

; APPLICANT: HONJO, Masaru

; APPLICANT: NAITOH, Naokazu

; APPLICANT: UCHIDA, Hiroshi

; APPLICANT: MOCHIZUKI, Daibuke

; APPLICANT: MATSUMOTO, Kazuya

; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE

; FILE REFERENCE: 029430-421

; CURRENT APPLICATION NUMBER: US/09/699,684

; PRIOR FILING DATE: 2000-10-31

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/348,578

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-07

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 31

; LENGTH: 76

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; LOCATION: (1)..(76)

; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA sequence to

; OTHER INFORMATION: act as a primer for PCR to produce the latter half of Oppa

; OTHER INFORMATION: secretion signal

US-09-699-684-31

Query Match 66.0%; Score 13.2; DB 3; Length 76;  
Best Local Similarity 83.3%; Pred. No. 7.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCCAGCCAGGACTG 20

DB 25 GCGCAGCCAGACGCGCTG 8

RESULT 11

US-09-396-196G-43628

; Sequence 43628, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 43628

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-43628

Query Match 65.0%; Score 13; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGA 13

DB 4 GTGCCAGCCAGA 16

RESULT 12

US-09-396-196G-43629

; Sequence 43629, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 43629

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-43629

Query Match 65.0%; Score 13; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGA 13

DB 2 GTGCCAGCCAGA 14

RESULT 13

US-09-396-196G-61456

; Sequence 61456, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 61456

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-61456

Query Match 65.0%; Score 13; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGA 13

DB 7 GTGCCAGCCAGA 19

RESULT 14

US-09-396-196G-20714/C

; Sequence 20714, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: Alkymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20714  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-20714

Query Match 64.0%; Score 12.8; DB 3; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCAGCCAGAGCACTG 20  
Db 24 CCAGCCAGAGCACTG 9

RESULT 15  
US-07-749-446-6/C  
Sequence 6, Application US/07749446  
Patent No. 5593857

## GENERAL INFORMATION:

APPLICANT: Higaki, Jeffrey N.  
APPLICANT: Tischer, Edmund G.  
APPLICANT: Cordell, Barbara  
APPLICANT: Thompson, Stewart A.  
TITLE OF INVENTION: PRODUCTION OF HOMOGENEOUS CILARY  
TITLE OF INVENTION: NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: California Biotechnology Inc.  
STREET: 2450 Bayshore Parkway  
CITY: Mountain View  
STATE: California  
COUNTRY: USA  
ZIP: 94043

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07749,446  
FILING DATE: 19911008

## CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Shearer, Peter R.  
REGISTRATION NUMBER: 28,117  
REFERENCE/DOCKET NUMBER: PC43:US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-962-5860  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-07-749-446-6

Query Match 64.0%; Score 12.8; DB 2; Length 27;  
Best Local Similarity 87.5%; Pred. No. 1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGCCAGAGCACT 19  
Db 27 CCAGCCAGAGCACT 12

Search completed: December 24, 2005, 18:36:29  
Job time: 49.1 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gtgccacgacagcagcactg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-8
2	15.8	79.0	25	8	US-10-719-900-39761
3	15.8	79.0	25	9	US-10-809-189-16399
4	15.4	77.0	25	8	US-10-719-900-814778
5	15	75.0	25	7	US-10-719-956-247643
6	15	75.0	25	8	US-10-719-900-871237
7	15	75.0	25	10	US-11-036-317-9133
8	15	75.0	25	10	US-11-036-317-39107
9	15	75.0	25	10	US-11-036-317-42520
10	15	75.0	25	10	US-11-036-317-43628
11	14.8	74.0	25	7	US-10-719-956-400453
12	14.8	74.0	25	10	US-11-036-317-456571
13	14.4	72.0	25	8	US-10-719-900-44301
14	14.4	72.0	25	8	US-10-719-900-960417
15	14.4	72.0	25	9	US-10-809-189-42233
16	14.4	72.0	25	9	US-10-809-189-42233
17	14.4	72.0	25	10	US-11-036-317-777729
18	14.4	72.0	25	10	US-11-036-317-854970
19	14.4	72.0	25	10	US-11-036-317-879103
20	14.4	72.0	25	10	US-11-036-317-886387
21	14.4	72.0	25	10	US-11-036-317-932924
22	14.4	72.0	25	10	US-11-036-317-987167
23	14.2	71.0	25	7	US-10-719-956-193314

c	24	14.2	71.0	25	7	US-10-719-956-552832	Sequence 552832,
	25	14.2	71.0	25	7	US-10-719-956-616700	Sequence 616700,
	26	14.2	71.0	25	8	US-10-719-900-39762	Sequence 39762, A
c	27	14.2	71.0	25	8	US-10-719-900-495245	Sequence 495245,
	28	14.2	71.0	25	10	US-11-036-317-400663	Sequence 400663,
	29	14.2	71.0	25	10	US-11-036-317-789908	Sequence 789908,
	30	14.2	71.0	42	3	US-09-791-378-664	Sequence 664, App
	31	14.2	71.0	42	3	US-09-791-393-305	Sequence 306, App
	32	14.2	71.0	42	3	US-09-791-389-306	Sequence 306, App
	33	14.2	71.0	42	3	US-09-791-377-664	Sequence 664, App
	34	14	70.0	25	8	US-10-719-900-479264	Sequence 479264, A
c	35	14	70.0	25	10	US-11-036-317-15574	Sequence 15574, A
	36	13.8	69.0	25	7	US-10-719-956-564652	Sequence 564652,
	37	13.8	69.0	25	8	US-10-719-900-344999	Sequence 344999,
	38	13.8	69.0	25	8	US-10-719-900-814777	Sequence 814777,
c	39	13.8	69.0	25	8	US-10-719-900-881264	Sequence 881264,
c	40	13.8	69.0	25	9	US-10-809-189-16382	Sequence 16382, A
c	41	13.8	69.0	25	9	US-10-809-189-105272	Sequence 105272,
c	42	13.8	69.0	25	10	US-11-036-317-576898	Sequence 576898,
c	43	13.8	69.0	36	6	US-10-259-226-10	Sequence 10, Appl
c	44	13.8	69.0	36	6	US-10-200-002-10	Sequence 10, Appl
c	45	13.6	68.0	25	7	US-10-719-956-125172	Sequence 125172,

#### ALIGNMENTS

RESULT 1  
US-09-296-264-8  
; Sequence 8, Application US/09296264  
; Publication No. US20030083274A1  
; GENERAL INFORMATION:  
; APPLICANT: WRIGHT, Jim A.  
; APPLICANT: YOUNG, Aiping H.  
; APPLICANT: LEE, Yoon S.  
; TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND  
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH  
; FILE REFERENCE: 032396-043  
; CURRENT APPLICATION NUMBER: US/09/296,264  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: US 60/082,791  
; EARLIER FILING DATE: 1998-04-23  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; TYPE: DNA  
; LENGTH: 20  
; ORGANISM: Human  
; US-09-296-264-8

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCACGACGACGACTG 20  
Db 1 GTGCCACGACGACGACTG 20

RESULT 2  
US-10-719-900-39761  
; Sequence 39761, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

```
; SEQ ID NO 39761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-39761
```

```
Query Match          79.0%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 TGCCCGAGCCAGCGACTG 20
         |||||
Db       4 TGCCCGAGCCAGCGACTG 22
```

```
RESULT 3
US-10-809-189-16399/c
; Sequence 16399, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 16399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-16399
```

```
Query Match          79.0%; Score 15.8; DB 9; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GTGCCGAGCCAGCGACT 19
         |||||
Db       20 GTGCCGAGCCAGCGACT 2
```

```
RESULT 4
US-10-719-900-814778
; Sequence 814778, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 814778
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-814778
```

```
Query Match          77.0%; Score 15.4; DB 8; Length 25;
Best Local Similarity 94.1%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 TGCCCGAGCCAGCGAGC 18
         |||||
Db       1 TGCCCGAGCCAGCGAGC 17
```

```
RESULT 5
US-10-719-956-247643
; Sequence 247643, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-247643
```

```
Query Match          75.0%; Score 15; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 CCAGCCAGAGCGAGC 18
         |||||
Db       1 CCAGCCAGAGCGAGC 15
```

```
RESULT 6
US-10-719-900-871237
; Sequence 871237, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 871237
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-871237
```

```
Query Match          75.0%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GTGCCGAGCCAGAGC 15
         |||||
Db       4 GTGCCGAGCCAGAGC 18
```

```
RESULT 7
US-11-036-317-9133/c
; Sequence 9133, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
```



```

; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 9133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-9133

Query Match
Best Local Similarity 75.0%; Score 15; DB 10; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 19 CAGCCAGAGCGACTG 5

RESULT 8
US-11-036-317-39107/c
; Sequence 39107, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 39107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-39107

Query Match
Best Local Similarity 75.0%; Score 15; DB 10; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 23 CAGCCAGAGCGACTG 9

RESULT 9
US-11-036-317-42520/c
; Sequence 42520, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 42520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-42520

Query Match
Best Local Similarity 75.0%; Score 15; DB 10; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 23 CAGCCAGAGCGACTG 9

RESULT 10
US-11-036-317-43628/c
; Sequence 43628, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 43628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-43628

Query Match
Best Local Similarity 75.0%; Score 15; DB 10; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 24 CAGCCAGAGCGACTG 10

RESULT 11
US-10-719-956-400453/c
; Sequence 400453, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 400453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-400453

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGGCGAGCGGCT 19
DB 24 TGCCAGGCGAGCGGCT 7

RESULT 12
US-11-036-317-456571
; Sequence 456571, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
```

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 21 CAGCCAGAGCGACTG 7

RESULT 10
US-11-036-317-43628/c
; Sequence 43628, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 43628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-43628

Query Match
Best Local Similarity 75.0%; Score 15; DB 10; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 24 CAGCCAGAGCGACTG 10

RESULT 11
US-10-719-956-400453/c
; Sequence 400453, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 400453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-400453

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGGCGAGCGGCT 19
DB 24 TGCCAGGCGAGCGGCT 7

RESULT 12
US-11-036-317-456571
; Sequence 456571, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
```

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 456571  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-456571

Query Match 74.0%; Score 14.8; DB 10; Length 25;  
Best Local Similarity 88.9%; Pred. No. 3.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGCCGAGCAGCG 18  
Db 1 GTGCCGAGCAGCG 18

RESULT 13  
US-10-719-900-44301  
Sequence 44301, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 44301  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-44301

Query Match 72.0%; Score 14.4; DB 8; Length 25;  
Best Local Similarity 93.8%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCCGAGCAGCG 16  
Db 7 GTGCCGAGCAGCG 22

RESULT 14  
US-10-719-900-960417/c  
Sequence 960417, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 960417  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-960417

Query Match 72.0%; Score 14.4; DB 8; Length 25;

Best Local Similarity 93.8%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGCCAGGCGACTG 20  
Db 24 CCAGCCAGGCGACTG 9

RESULT 15  
US-10-809-189-42233  
Sequence 42233, Application US/10809189  
Publication No. US20050048531A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 42233  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-809-189-42233

Query Match 72.0%; Score 14.4; DB 9; Length 25;  
Best Local Similarity 93.8%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGCCAGGCGACT 19  
Db 1 CCAGCCAGGCGACT 16

Search completed: December 25, 2005, 04:14:23  
Job time : 338.6 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds  
(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gggccagccagcagcagcagc 20

Scoring table: IDENTITY\_NUC

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

1: /cgn2\_6/prodata/2/pubphn/us08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/prodata/2/pubphn/us06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/prodata/2/pubphn/us07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/prodata/2/pubphn/PCT\_NEW\_PUB.seq:\*  
5: /cgn2\_6/prodata/2/pubphn/us09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/prodata/2/pubphn/us10\_NEW\_PUB.seq:\*  
7: /cgn2\_6/prodata/2/pubphn/us11\_NEW\_PUB.seq:\*  
8: /cgn2\_6/prodata/2/pubphn/us11\_NEW\_PUB.seq2:\*  
9: /cgn2\_6/prodata/2/pubphn/us11\_NEW\_PUB.seq3:\*  
10: /cgn2\_6/prodata/2/pubphn/us60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	79.0	25	US-11-121-849-444117	Sequence 444117,
2	15.2	76.0	25	US-11-121-849-28342	Sequence 28342, A
3	15.2	76.0	25	US-11-121-849-548725	Sequence 548725,
4	14.2	71.0	25	US-11-121-849-548692	Sequence 548692,
5	14	70.0	25	US-11-121-849-429927	Sequence 429927,
6	13.8	69.0	25	US-11-121-849-248643	Sequence 248643,
7	13.8	69.0	25	US-11-121-849-313084	Sequence 313084,
8	13.8	69.0	25	US-11-121-849-340873	Sequence 340873,
9	13.8	69.0	25	US-11-121-849-340915	Sequence 340915,
10	13.8	69.0	25	US-11-121-849-340916	Sequence 340916,
11	13.6	68.0	25	US-11-121-849-195011	Sequence 195011,
12	13.6	68.0	25	US-11-121-849-195074	Sequence 195074,
13	13.6	68.0	25	US-11-121-849-485677	Sequence 485677,
14	13.4	67.0	25	US-11-121-849-94049	Sequence 94049, A
15	13.4	67.0	25	US-11-121-849-593181	Sequence 593181,
16	13.2	66.0	25	US-11-121-849-452270	Sequence 452270,
17	13.2	66.0	25	US-11-121-849-520368	Sequence 520368,
18	13	65.0	25	US-11-121-849-83263	Sequence 83263, A
19	13	65.0	25	US-11-121-849-83264	Sequence 83264, A
20	13	65.0	25	US-11-121-849-280576	Sequence 280576,
21	13	65.0	25	US-11-121-849-291424	Sequence 291424,
22	13	65.0	25	US-11-121-849-438663	Sequence 438663,
23	13	65.0	25	US-11-121-849-474629	Sequence 474629,

C 24	13	65.0	25	US-11-121-849-474630	Sequence 474630,
C 25	13	65.0	25	US-11-121-849-474631	Sequence 474631,
C 26	13	65.0	25	US-11-121-849-489362	Sequence 489362,
C 27	12.8	64.0	25	US-11-121-849-42175	Sequence 42175, A
C 28	12.8	64.0	25	US-11-121-849-112602	Sequence 112602,
C 29	12.8	64.0	25	US-11-121-849-131719	Sequence 131719,
C 30	12.8	64.0	25	US-11-121-849-131720	Sequence 131720,
C 31	12.8	64.0	25	US-11-121-849-132378	Sequence 132378,
C 32	12.8	64.0	25	US-11-121-849-132379	Sequence 132379,
C 33	12.8	64.0	25	US-11-121-849-457604	Sequence 457604,
C 34	12.8	64.0	25	US-11-121-849-518332	Sequence 518332,
C 35	12.8	64.0	25	US-11-121-849-538982	Sequence 538982,
C 36	12.8	64.0	25	US-11-121-849-647201	Sequence 647201,
C 37	12.8	64.0	32	US-10-939-294A-17166	Sequence 17166, A
C 38	12.6	63.0	25	US-11-121-849-29949	Sequence 29949, A
C 39	12.6	63.0	25	US-11-121-849-31672	Sequence 31672, A
C 40	12.6	63.0	25	US-11-121-849-127447	Sequence 127447,
C 41	12.6	63.0	25	US-11-121-849-181631	Sequence 181631,
C 42	12.6	63.0	25	US-11-121-849-191930	Sequence 191930,
C 43	12.6	63.0	25	US-11-121-849-256169	Sequence 256169,
C 44	12.6	63.0	25	US-11-121-849-297509	Sequence 297509,
C 45	12.6	63.0	25	US-11-121-849-297510	Sequence 297510,

#### ALIGNMENTS

RESULT 1  
US-11-121-849-444117  
; Sequence 444117, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 444117  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-444117

Query Match  
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 25;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGCCAGCCAGCAGCAGCTG 20  
Db 5 TGGCCAGCCAGCAGCAGCTG 23

RESULT 2  
US-11-121-849-28342  
; Sequence 28342, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 28342

```
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-28342

Query Match          76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCGAGGACTG 20
    |||||
DB 5 GTGCCAGCCGAGGACTG 24

RESULT 3
US-11-121-849-548725
/ Sequence 548725, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 548725
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-548725

Query Match          76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCGAGGACTG 20
    |||||
DB 6 GTGCCAGCCGAGGACTG 25

RESULT 4
US-11-121-849-548692
/ Sequence 548692, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 548692
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-548692

Query Match          71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCGAGGACT 19
    |||||
DB 7 GTGCCAGCCGAGGACT 25

RESULT 5
US-11-121-849-429927
/ Sequence 429927, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 429927
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-429927

Query Match          70.0%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCCAGCCGAGGC 15
    |||||
DB 2 TGCCAGCCGAGGC 15

RESULT 6
US-11-121-849-248643/C
/ Sequence 248643, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 248643
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-248643

Query Match          69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCGAGGCAC 18
    |||||
DB 17 TGCCAGCCGAGGCAC 1

RESULT 7
US-11-121-849-313084/C
/ Sequence 313084, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
```

PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 313084  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien

US-11-121-849-313084

Query Match 69.0%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCCAGAGCACTG 20  
Db 25 CACAGCCAGAGCACTG 9

RESULT 8

US-11-121-849-340873  
Sequence 340873, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:

APPLICANT: John Palma  
TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 340873  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien

US-11-121-849-340873

Query Match 69.0%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCCAGAGCACTG 20  
Db 4 CCCAGCCAGAGCACTG 20

RESULT 9

US-11-121-849-340915  
Sequence 340915, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:

APPLICANT: John Palma  
TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 340915  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien

US-11-121-849-340915

Query Match 69.0%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCCAGAGCACTG 20  
Db 4 CCCAGCCAGAGCACTG 20

RESULT 10

US-11-121-849-340916  
Sequence 340916, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:

APPLICANT: John Palma  
TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 340916  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien

US-11-121-849-340916

Query Match 69.0%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCCAGAGCACTG 20  
Db 2 CCCAGCCAGAGCACTG 18

RESULT 11

US-11-121-849-195011  
Sequence 195011, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:

APPLICANT: John Palma  
TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 195011  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien

US-11-121-849-195011

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGCACTG 20  
Db 2 GTGCCAGCCAGAGCACTG 21

RESULT 12

US-11-121-849-195074  
Sequence 195074, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:

APPLICANT: John Palma  
TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 195074  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien

US-11-121-849-195074

Query Match 69.0%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 195074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-195074
```

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GTGCCCCAGCCAGAGCGACTG 20
Db 2 GTGACCAGCCAGGGGCAATG 21
```

```
RESULT 13
US-11-121-849-485677
; Sequence 485677, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 485677
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-485677
```

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GTGCCCCAGCCAGAGCGACTG 20
Db 6 GTCCCCAGCCAAAGCCAGTG 25
```

```
RESULT 14
US-11-121-849-94049/c
; Sequence 94049, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94049
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-94049
```

```
Query Match          67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GTGCCCCAGCCAGAGC 15
Db 22 GTGCCCCAGCCAGAGC 8
```

```
RESULT 15
US-11-121-849-593181
; Sequence 593181, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 593181
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-593181
```

```
Query Match          67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CCAGCCAGAGCGACT 19
Db 11 CCAAGCCAGAGCGACT 25
```

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Search completed: December 25, 2005, 04:37:03
Job time : 135.3 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds  
(without alignments)  
1953.383 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20

Sequence: 1 tgaagtcgcggtcggaagtcgc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_in:\*

3: gb\_env:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pr:\*

9: gb\_ro:\*

10: gb\_srb:\*

11: gb\_sy:\*

12: gb\_un:\*

13: gb\_vi:\*

14: gb\_hsg:\*

15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	BD211666	BD211666 Antisense
2	15.2	76.0	60	CQ552983	CQ552983 Sequence
3	15.2	76.0	100	AX999601	AX999601 Sequence
4	15	75.0	24	A57512	A57512 Sequence 4
5	15	75.0	24	A57514	A57514 Sequence 6
6	15	75.0	24	AR052978	AR052978 Sequence
7	15	75.0	24	AR052980	AR052980 Sequence
8	14.8	74.0	48	A28016	A28016 Sequence
9	14.8	74.0	48	A28017	A28017 pCD4-FVCD3
10	14.4	72.0	60	CQ551412	CQ551412 Sequence
11	14.4	72.0	100	AJ08144	AJ08144 Homo sapi
12	14.2	71.0	30	AR106307	AR106307 Sequence
13	14.2	71.0	30	AR110116	AR110116 Sequence
14	14.2	71.0	30	AR126277	AR126277 Sequence
15	14.2	71.0	30	BD075492	BD075492 Secretory
16	14.2	71.0	50	BD172352	BD172352 Secreted
17	14.2	71.0	50	BD172671	BD172671 Secreted
18	14.2	71.0	50	BD172990	BD172990 Secreted

19	14.2	71.0	50	BD173309	BD173309 Secreted
20	14.2	71.0	50	BD175343	BD175343 Secretory
21	14.2	71.0	50	CQ008337	CQ008337 Sequence
22	14.2	71.0	50	CQ008339	CQ008339 Sequence
23	14.2	71.0	50	CQ008340	CQ008340 Sequence
24	14.2	71.0	50	AR410721	AR410721 Sequence
25	14.2	71.0	50	AR439085	AR439085 Sequence
26	14.2	71.0	50	AR473105	AR473105 Sequence
27	14.2	71.0	50	AR527091	AR527091 Sequence
28	14.2	71.0	50	AR566124	AR566124 Sequence
29	14.2	71.0	50	AR592142	AR592142 Sequence
30	14.2	71.0	50	AR604416	AR604416 Sequence
31	14.2	71.0	50	AR605002	AR605002 Sequence
32	14.2	71.0	50	AR613667	AR613667 Sequence
33	14.2	71.0	50	AR635838	AR635838 Sequence
34	14.2	71.0	50	AR650567	AR650567 Sequence
35	14.2	71.0	50	AR657508	AR657508 Sequence
36	14.2	71.0	50	AX697560	AX697560 Sequence
37	14.2	71.0	51	CQ005584	CQ005584 Sequence
38	14.2	71.0	51	CQ008338	CQ008338 Sequence
39	14.2	71.0	51	AX161940	AX161940 Sequence
40	14.2	71.0	66	CS016537	CS016537 Sequence
41	14.2	71.0	68	BD105319	BD105319 Method fo
42	14.2	71.0	77	BD105318	BD105318 Method fo
43	14.2	71.0	82	AY282610	AY282610 Symasgite
44	14.2	71.0	82	AY270944	AY270944 Homo sapi
45	14.2	71.0	85	AF318496	AF318496 Scutiger

#### ALIGNMENTS

RESULT 1  
BD211666  
LOCUS  
DEFINITION  
Antisense oligonucleotide sequence of neuropilin and method of  
using the same for controlling cell proliferation.

ACCESSION  
BD211666.1 GI:33021436

VERSION  
JP 2002512793-A/9.

KEYWORDS  
Homo sapiens (human)

SOURCE  
Homo sapiens

ORGANISM  
Homo sapiens

REFERENCE  
Wright,J.A., Young,A.H. and Lee,Y.S.

AUTHORS  
Wright,J.A., Young,A.H. and Lee,Y.S.

TITLE  
Antisense oligonucleotide sequence of neuropilin and method of  
using the same for controlling cell proliferation

JOURNAL  
Patent: JP 2002512793-A 9 08-MAY-2002;

COMMENT  
GENSENSE TECHNOLOGIES INC

OS  
Homo sapiens (human)

PN  
JP 2002512793-A/9

PD  
08-MAY-2002

PF  
23-APR-1999 JP 2000545999

PR  
23-APR-1998 US 60/082791

PI  
JIM A WRIGHT,ALPING H YOUNG,YOON S LEE

PC  
C12N15/09,A61K31/711,A61K48/00,A61J35/00,C12N15/00 CC

Antisense oligonucleotide sequence of neuropilin and method of  
using the same for controlling cell proliferation

CC  
same for controlling cell proliferation

FM  
key

FT  
source

FT  
source

FEATURES  
source

location/Qualifiers

1..20

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 6; Length 20;

```

Matches      20; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY
1 TGAGGTGCGGTTGAGAGTGC 20
|||||
Db
1 TGAGGTGCGGTTGAGAGTGC 20

RESULT 2
LOCUS      CQ552983
DEFINITION Sequence 22618 from Patent WO0210449.
ACCESSION  CQ552983
VERSION     CQ552983.1 GI:41519410
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE
AUTHORS    Shoshan, A., Maeserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE      Oligonucleotide library for detecting rna transcripts and splice
            variants that populate a transcritpome
JOURNAL     Patent: WO 0210449-A 22618 07-FEB-2002;
            Compugen Inc. (US)
FEATURES
source      location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

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Best Local Similarity 85.0%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
1 TGAGGTGCGGTTGAGAGTGC 20
|||||
Db
25 TGAGGTGCTGTGTGATGTCC 44

RESULT 3
LOCUS      AX999601
DEFINITION Sequence 11064 from Patent EP1260592.
ACCESSION  AX999601
VERSION     AX999601.1 GI:41005947
KEYWORDS
SOURCE      Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE
AUTHORS    Donner, H., Drescher, B., Huber, A. and Weber, J.
TITLE      Biochip
JOURNAL     Patent: EP 1260592-A 11064 27-NOV-2002;
            MMG - Biotech AG (DE)
FEATURES
source      Location/Qualifiers
            1..100 /organism="Escherichia coli"
            /mol_type="unassigned DNA"
            /db_xref="taxon:562"
            /note="B1980 B1981 U00096 complement(2050646__2051350)"

ORIGIN
Query Match      76.0%; Score 15.2; DB 6; Length 100;
Best Local Similarity 85.0%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
1 TGAGGTGCGGTTGAGAGTGC 20
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Db
31 TGAGGTGCGCGAGGAATGC 50

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RESULT 4
LOCUS      A57512/c
DEFINITION Sequence 4 from Patent WO9632483.
ACCESSION  A57512
VERSION     A57512.1 GI:3713370
KEYWORDS
SOURCE      unidentified
            unclassified sequences.
ORGANISM    unidentified
            unclassified sequences.

REFERENCE
AUTHORS    Masucci, M.G.
TITLE      IMMUNE-EVADING PROTEINS
JOURNAL     Patent: WO 9632483-A 4 17-OCT-1996;
            MASUCCI MARIA GRAZIA (SE)
COMMENT     Other publication AU 5284296 961030.
            Location/Qualifiers
            1..24 /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:3264"

ORIGIN
Query Match      75.0%; Score 15; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
2 GAGGTGCGGTTGGA 16
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Db
15 GAGGTGCGGTTGGA 1

RESULT 5
LOCUS      A57514/c
DEFINITION Sequence 6 from Patent WO9632483.
ACCESSION  A57514
VERSION     A57514.1 GI:3713372
KEYWORDS
SOURCE      unidentified
            unclassified sequences.
ORGANISM    unidentified
            unclassified sequences.

REFERENCE
AUTHORS    Masucci, M.G.
TITLE      IMMUNE-EVADING PROTEINS
JOURNAL     Patent: WO 9632483-A 6 17-OCT-1996;
            MASUCCI MARIA GRAZIA (SE)
COMMENT     Other publication AU 5284296 961030.
            Location/Qualifiers
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ORIGIN
Query Match      75.0%; Score 15; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
2 GAGGTGCGGTTGGA 16
|||||
Db
15 GAGGTGCGGTTGGA 1

RESULT 6
LOCUS      AR052978/c
DEFINITION Sequence 7 from patent US 5833991.
ACCESSION  AR052978
VERSION     AR052978.1 GI:5977840
KEYWORDS
SOURCE      Unknown.

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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Masucci,M.G.  
TITLE Glycine-containing sequences conferring invisibility to the immune system  
JOURNAL Patent: US 5833991-A 7 10-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
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ORIGIN  
Query Match 75.0%; Score 15; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGAA 16  
15 GAGGTGCGGGTGAA 1

RESULT 7  
LOCUS AR052980 24 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 10 from patent US 5833991.  
ACCESSION AR052980  
VERSION AR052980.1 GI:5977842  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Masucci,M.G.  
TITLE Glycine-containing sequences conferring invisibility to the immune system  
JOURNAL Patent: US 5833991-A 10 10-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

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Query Match 75.0%; Score 15; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGAA 16  
15 GAGGTGCGGGTGAA 1

RESULT 8  
LOCUS A28016 48 bp DNA linear PAT 03-OCT-1995  
DEFINITION PC04-FPCD3 construction oligo 2119.  
ACCESSION A28016  
VERSION A28016.1 GI:1248563  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Karjalainen,K., Lanzavecchia,A. and Trautnecker,A.  
TITLE Chimeric polypeptides  
JOURNAL Patent: EP 0505908-A 11 30-SEP-1992;  
F. HOFFMANN-LA ROCHE AG  
FEATURES Location/Qualifiers  
source 1..48  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 48;  
Best Local Similarity 88.9%; Pred. No. 4.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGAAAGTG 19  
16 GAGGTGCGGGTGAAAGTG 33

RESULT 9  
LOCUS A28017 48 bp DNA linear PAT 03-OCT-1995  
DEFINITION PC04-FPCD3 construction oligo 2120.  
ACCESSION A28017  
VERSION A28017.1 GI:1248564  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Karjalainen,K., Lanzavecchia,A. and Trautnecker,A.  
TITLE Chimeric polypeptides  
JOURNAL Patent: EP 0505908-A 12 30-SEP-1992;  
F. HOFFMANN-LA ROCHE AG  
FEATURES Location/Qualifiers  
source 1..48  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 48;  
Best Local Similarity 88.9%; Pred. No. 4.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGAAAGTG 19  
37 GAGGTGCGGGTGAAAGTG 20

RESULT 10  
LOCUS CQ551412 60 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 21047 from Patent WO0210445.  
ACCESSION CQ551412  
VERSION CQ551412.1 GI:41517839  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shoshan,A., Wasserman,A., Mintz,B., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome  
JOURNAL Patent: WO 0210449-A 21047 07-FEB-2002;  
Compugen Inc. (US)  
FEATURES Location/Qualifiers  
source 1..60  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

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Query Match 72.0%; Score 14.4; DB 6; Length 60;  
Best Local Similarity 93.8%; Pred. No. 6.3e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGGTGCGGGTGAAAGT 18  
6 AGGTGCGGGTGAAAGT 21

Db

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RESULT 11
AU8144      100 bp      mRNA      linear      PRI 13-NOV-1998
LOCUS       Homo sapiens NIK gene, exon 6, 5'.
DEFINITION AJ008144
ACCESSION  AJ008144.1 GI:3873593
VERSION     NIK gene.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS    Aronson,F.C., Magnusson,P., Andersson,B., Karsten,S.L.,
            Shibasaki,Y., Lendon,C.L., Goate,A.M. and Brookes,A.J.
TITLE       The NIK protein kinase and C17orf1 genes: chromosomal mapping, gene
            structures and mutational screening in frontotemporal dementia and
            parkinsonism linked to chromosome 17
JOURNAL     Hum. Genet. 103 (3), 340-345 (1998)
PUBMED     9799091
REFERENCE   2 (bases 1 to 100)
AUTHORS    Brookes,A.
TITLE       Direct Submission
JOURNAL     Submitted (21-APR-1998) A. Brookes, Department of Genetics and
            Pathology, Biomedical Center, Box 589, 751 23 Uppsala, SWEDEN
FEATURES    source
            1..100
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            /db_xref="taxon:9606"
            /chromosome="17"
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Query Match      72.0%; Score 14.4; DB 8; Length 100;
Best Local Similarity 93.8%; Pred. No. 6.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 AGGTGCGGGTGAAGT 18
        |||||
        49 AGGTGCGGGTGAAGT 64

RESULT 12
ARI06307/c    30 bp      DNA      linear      PAT 14-FEB-2001
LOCUS       Sequence 11 from patent US 6107025.
DEFINITION  ARI06307
ACCESSION  ARI06307
VERSION     ARI06307.1 GI:12820837
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Caskey,C.Thomas., Nelson,D.L., Pieretti,M., Warren,S.T. and
            Oostra,B.A.
TITLE       Diagnosis of the fragile X syndrome
JOURNAL     Patent: US 6107025-A 11 22-AUG-2000;
            Location/Qualifiers
            1..30
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            /mol_type="unassigned DNA"

ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 30;
Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGTGCAGGTGAAGTGC 20
        |||||
        25 GAGTGCAGGTGAAGTGC 7

RESULT 13
ARI10116/c    30 bp      DNA      linear      PAT 14-FEB-2001
LOCUS       Sequence 7 from patent US 6114150.
DEFINITION  ARI10116
ACCESSION  ARI10116
VERSION     ARI10116.1 GI:12826392
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Weissman,S.M. and Baskaran,N.
TITLE       Amplification of nucleic acids
JOURNAL     Patent: US 6114150-A 7 05-SEP-2000;
            Location/Qualifiers
            1..30
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 30;
Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGTGCAGGTGAAGTGC 20
        |||||
        25 GAGTGCAGGTGAAGTGC 7

RESULT 14
ARI26277/c    30 bp      DNA      linear      PAT 16-MAY-2001
LOCUS       Sequence 11 from patent US 6180337.
DEFINITION  ARI26277
ACCESSION  ARI26277
VERSION     ARI26277.1 GI:14112870
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Caskey,C.Thomas., Nelson,D.L., Pieretti,M., Warren,S.T.,
            Oostra,B.A. and Fu,Y.-h.
TITLE       Diagnosis of the fragile X syndrome
JOURNAL     Patent: US 6180337-A 11 30-JAN-2001;
            Location/Qualifiers
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Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGTGCAGGTGAAGTGC 20
        |||||
        25 GAGTGCAGGTGAAGTGC 7

RESULT 15
BD075492      50 bp      DNA      linear      PAT 27-AUG-2002
LOCUS       Secretary and transmembrane polypeptide and nucleic acid encoding
            the same.
DEFINITION  BD075492
ACCESSION  BD075492
VERSION     BD075492.1 GI:22621095

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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGTGCAGGTGAAGTGC 20
        |||||
        25 GAGTGCAGGTGAAGTGC 7

RESULT 13
ARI10116/c    30 bp      DNA      linear      PAT 14-FEB-2001
LOCUS       Sequence 7 from patent US 6114150.
DEFINITION  ARI10116
ACCESSION  ARI10116
VERSION     ARI10116.1 GI:12826392
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Weissman,S.M. and Baskaran,N.
TITLE       Amplification of nucleic acids
JOURNAL     Patent: US 6114150-A 7 05-SEP-2000;
            Location/Qualifiers
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            /mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGTGCAGGTGAAGTGC 20
        |||||
        25 GAGTGCAGGTGAAGTGC 7

RESULT 14
ARI26277/c    30 bp      DNA      linear      PAT 16-MAY-2001
LOCUS       Sequence 11 from patent US 6180337.
DEFINITION  ARI26277
ACCESSION  ARI26277
VERSION     ARI26277.1 GI:14112870
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Caskey,C.Thomas., Nelson,D.L., Pieretti,M., Warren,S.T.,
            Oostra,B.A. and Fu,Y.-h.
TITLE       Diagnosis of the fragile X syndrome
JOURNAL     Patent: US 6180337-A 11 30-JAN-2001;
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ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 30;
Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGTGCAGGTGAAGTGC 20
        |||||
        25 GAGTGCAGGTGAAGTGC 7

RESULT 15
BD075492      50 bp      DNA      linear      PAT 27-AUG-2002
LOCUS       Secretary and transmembrane polypeptide and nucleic acid encoding
            the same.
DEFINITION  BD075492
ACCESSION  BD075492
VERSION     BD075492.1 GI:22621095

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KEYWORDS JP 2001516580-A/125.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.  
TITLE Secretary and transmembrane polypeptide and nucleic acid encoding the same  
JOURNAL Patent: JP 2001516580-A 125 02-OCT-2001;  
GENENTECH INC  
COMMENT OS Artificial Sequence  
PN JP 2001516580-A/125  
PD 02-OCT-2001  
PR 16-SEP-1998 JP 2000511867  
PR 17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059184 PR  
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17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR  
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR  
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR  
17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR  
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR  
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29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR  
29-OCT-1997 US 60/064103, 31-OCT-1997 US 60/063870 PR  
03-NOV-1997 US 60/064248, 07-NOV-1997 US 60/064809 PR  
12-NOV-1997 US 60/065186, 17-NOV-1997 US 60/065846 PR  
18-NOV-1997 US 60/065693, 21-NOV-1997 US 60/066120 PR  
21-NOV-1997 US 60/066364, 24-NOV-1997 US 60/066772 PR  
24-NOV-1997 US 60/066466, 24-NOV-1997 US 60/066770 PR  
25-NOV-1997 US 60/066511, 24-NOV-1997 US 60/066453 PR  
60/066840  
PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDLEY GODDARD, DIANE PENICA, PI  
JEAN CHEN,  
PI JEAN YUAN  
PC C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/00,  
PC C12N1/19  
PC C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, C12P21/08, PC  
C12R1:911,  
PC C12N15/00, C12N5/00  
CC Description of Artificial Sequence: Synthetic FH Key  
Location/Qualifiers  
FT source 1..50  
FEATURES  
source 1..50  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
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Query Match 71.0%; Score 14.2; DB 6; Length 50;  
Best Local Similarity 84.2%; Pred. No. 7, 9e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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DB 16 TGAAGGCGCGGTGGAAGTG 34

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OM nucleic - nucleic search, using sw model

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Title: US-09-296-264-9  
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Scoring table: IDENTITY\_NUC  
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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 768474

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	100	6	CF648803 3530.1.59
C 2	14.8	74.0	49	10	C2470063 C05523-5P
C 3	14.8	74.0	100	1	A1198185 A1198185
C 4	14.4	72.0	75	9	BH7902276 BH7902276
C 5	14.2	71.0	61	2	BF507253 BF507253
C 6	14.2	71.0	73	2	BE130245 BE130245
C 7	14.2	71.0	76	10	BX205183 BX205183
C 8	14.2	71.0	78	10	BX997035 BX997035
C 9	14.2	71.0	82	1	AA646813 AA646813
C 10	14.2	71.0	84	10	CG567843 CG567843
C 11	14.2	71.0	86	2	BG402252 BG402252
C 12	14.2	71.0	89	8	DT019117 DT019117
C 13	14.2	71.0	98	8	CV973314 CV973314
C 14	14.2	71.0	98	10	C2467313 C2467313
C 15	14.2	71.0	98	10	C2467324 C2467324
C 16	14.2	71.0	99	1	A1559239 A1559239
C 17	13.8	69.0	50	1	AU102737 AU102737
C 18	13.8	69.0	81	10	CG511332 CG511332
C 19	13.8	69.0	84	10	CG637376 CG637376
C 20	13.8	69.0	98	10	CL279855 CL279855
C 21	13.6	68.0	56	5	BU348446 BU348446
C 22	13.6	68.0	60	9	AZ982649 AZ982649

23	13.6	68.0	61	1	AA659447	AA659447 nu24D08.s
24	13.6	68.0	69	11	DR17P21S	AL740955 Danio rer
C 25	13.6	68.0	73	10	BX185949	BX185949 Danio rer
C 26	13.6	68.0	88	1	AA500773	AA500773 yq01b07.t
C 27	13.6	68.0	91	6	CA964627	CA964627 CCLX05a18
C 28	13.6	68.0	92	8	H55398	H55398 CHR220317 C
C 29	13.6	68.0	96	8	Z20250	Z20250 HSAABRW1 P
C 30	13.6	67.0	77	7	CN850437	CN850437 000918AAR
C 31	13.2	66.0	39	9	BH902151	BH902151 SALX.0913
C 32	13.2	66.0	61	6	CA772274	CA772274 i094a11.Y
C 33	13.2	66.0	61	10	CG715138	CG715138 1119040B0
C 34	13.2	66.0	63	7	CV573829	CV573829 oc40G01.Y
C 35	13.2	66.0	68	6	CB365695	CB365695 ZF001-P00
C 36	13.2	66.0	70	10	CG400347	CG400347 01S0611-1
C 37	13.2	66.0	72	9	AO248436	AO248436 T7M22-Sp6
C 38	13.2	66.0	73	2	BG879136	BG879136 iB70h10.Y
C 39	13.2	66.0	76	1	A1221944	A1221944 g01a03.x
C 40	13.2	66.0	76	10	C2442725	C2442725 IBB14G5.F
C 41	13.2	66.0	77	10	BX955021	BX955021 Reverse.s
C 42	13.2	66.0	77	10	CG575957	CG575957 OST210254
C 43	13.2	66.0	78	10	CL211282	CL211282 M051B01 G
C 44	13.2	66.0	84	1	AV848064	AV848064 AV848064
C 45	13.2	66.0	87	4	AK190815	AK190815 Mus muscu

#### ALIGNMENTS

RESULT 1  
LOCUS CF648803 100 bp mRNA linear EST 02-OCT-2003  
DEFINITION 3530.1.59.1 P10.x.2 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION CF648803  
VERSION CF648803.1 GI:37422195  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 100)  
Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)  
CONTACT: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

FEATURES  
source  
1..100  
/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="taxon:B73"  
/db\_xref="taxon:4577"  
/tissue\_type="multiple"  
/dev\_stage="varies by tissue"  
/lab\_host="DH108"  
/clone\_lib="3530 - Full length cDNA library created by Invitrogen from multiple tissues"  
/note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SORT 6.1; Site:1: BCARV, Site:2: NCRI; Maize Gene Discovery Project constructed with Invitrogen to produce a normalized, full length library in a pSPORT vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes."

Details of the vector and sequencing primers are available at ZMDB in the EST library description tables. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZMDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 100;  
Best Local Similarity 89.5%; Pred. No. 1.8e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAGTG 19  
Db 30 TGAGTGGCGGTGGAGGG 12

RESULT 2  
LOCUS CZ470063/c 49 bp DNA linear GSS 29-APR-2005  
DEFINITION c05523-3prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 5' end of piggyBac, genomic survey sequence.

ACCESSION CZ470063.1 GI:62964076  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
AUTHORS 1 (bases 1 to 49)  
TITLE  
JOURNAL  
COMMENT

Contact: Roger A Hoskins  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
Tel: 510 486 4015  
Fax: 510 486 6798  
Email: Rhooskins@lbl.gov  
Sequence recovery method was inverse PCR.  
Sequence orientation is forward strand relative to 5' end of piggyBac element.  
The piggyBac insertion position is 46 in the 49 bases. This insertion position refers to the first base of the 4 base TTA

FEATURES  
source  
target recognition sequence.  
Class: transposon insertion site.  
Location/Qualifiers

1. 49  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strain="isogenic w- strain"  
/db\_xref="taxon:7227"  
/note="Vector: piggyBac PB (Genbank accession number AY515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hep70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

## ORIGIN

Query Match 74.0%; Score 14.8; DB 10; Length 49;  
Best Local Similarity 88.9%; Pred. No. 4.9e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGTGGCGGTGGAGTG 19  
Db 33 GAGTGGAGGTGGAAGTG 16

RESULT 3  
LOCUS A1198185 100 bp mRNA linear EST 02-DEC-1998  
DEFINITION q151f03.x1 NCI CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:160029 3', mRNA sequence.

ACCESSION A1198185  
VERSION A1198185.1 GI:3750791  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index  
JOURNAL  
COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lemon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNL at:  
[www-bio.11nl.gov/bdrp/image/image.html](http://www-bio.11nl.gov/bdrp/image/image.html)  
Insert length: 1236 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 82.  
Location/Qualifiers  
1. 100  
/organism="Homo sapiens"  
/mol\_type="mRNA"

**ORIGIN**

Oy	1 TGAGGTGCGGGTGAAGT	18
Oy	6 TGAGGTCCGGGTGNACT	23

LOCUS	DEFINITION	75 bp DNA	linear	GSS	02-APR-2002
BH790276	SAK_056721.50.40.x Arabidopsis thaliana genomic clone SAK_056721.50.40.x, genomic survey sequence.				

ACCESSION	BH790276	GI:19868374
VERSION	BH790276.1	
KEYWORDS	GSS.	
SOURCE	Arabidopsis thaliana (thale cress)	
ORGANISM	Arabidopsis thaliana	
REFERENCE	<p>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons            rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsis.            1 (bases 1 to 75)</p>	

REFERENCE	1 (bases 1 to 75)
AUTHORS	Alonso, J.M., Leisae, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
TITLE	A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL	Unpublished (2001)
COMMENT	Contact: Joseph R. Ecker

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: [ecker@salk.edu](mailto:ecker@salk.edu)

This is single pass sequence recovered from the left border of DNA.

**Class: TDNA tagged.**

### FEATURES

#### Location/Qualifiers

```

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_056721.50.40.x"
/clone_1db="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna\_protocols.html"

```

ORIGIN	72.0%;	Score 14.4;	DB 9;	Length 75;
Query Match				

Qy 4 GGTCCGGGTGGAAGTC 19  
|||  
Db 45 GGTCCGGGTGGAAGTC 60

RESULT 5	LOCUS	DEFINITION	FEATURES
BF507253	BF507253	5923P-29 Pooled green leaf and root tissue Sorghum bicolor cDNA clone 5923P-29, mRNA sequence.	61 bp mRNA linear EST 07-DEC-2000

ACCESSION	BF507253
VERSION	BF507253.1
KEYWORDS	GI:11590551
SOURCE	EST
ORGANISM	Sorghum bicolor (sorghum)
	Sorghum bicolor

REFERENCE	1 (bases 1 to 61)
AUTHORS	Chapins,K.L., Klein,R.R., Klein,P.E., Morishige,D.T. and Mullet,J.E
TITLE	Mapping Genes on an Integrated Sorghum Genetic and Physical Map
JOURNAL	Using cDNA Selection Technology
COMMENT	Unpublished (2001)
	Contact: Kevin Childs

Department of Biochemistry and Biophysics  
Texas A&M University  
College Station, TX 77843, USA  
Tel: 979 845 0832  
Fax: 979 862 4718  
Email: kchills@unix.tamu.edu.

FEATURES	Location/Qualifiers
Source	1. .61

```

/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4556"
/clone="S923P-29"
/tissue_type="green leaf and root tissue"
/clone_id="Pooled green leaf and root tissue"
/note="Vector: pBluescript II (SK), Site_1: EcoRI, Site_2
EcoRI"

```

## ORIGIN

Query Match	71.0%;	Score 14.2;	DB 2;	Length 61;
Best Local Similarity	84.2%;	Pred. No. 9.1e+04;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

**Dy**      1 TGAGGTCGGGTGAAGTG 19  
         |||||  
**Db**      13 TGTGGTGGGTGTGAAGTG 31

RESULT 6	
BE130245	
LOCUS	
DEFINITION	
BE130245	73 bp
L48-385T3	ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-385 5'	
mRNA sequence.	

ACCESSION	BE130245	
VERSION	BE130245.1	GI:8577608
KEYWORDS	EST.	
SOURCE	Mesembryanthemum crystallinum (common iceplant)	
ORGANISM	Mesembryanthemum crystallinum	

REFERENCE

1 (bases 1 to 73)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alizaceae; Mesembryanthemum.

AUTHORS	TITLE
Cushman, J.C.	An expressed sequence tag database for the common ice plant <i>Mesembryanthemum crystallinum</i>

JOURNAL  
COMMENT

Unpublished (1997)  
Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcushman@unr.edu  
PCR Primers  
FORWARD: T7  
BACKWARD: T3  
Plate: L48-4 row: H column: 1  
Seq primer: T3  
High quality sequence stop: 73  
POLYA=No.

## FEATURES

## source

Location/Qualifiers  
1..73  
/organism="Mesembryanthemum crystallinum"  
/mol\_type="mRNA"  
/db\_xref="taxon:3544"  
/clone="L48-385"  
/issue\_type="Leaf, 48 h 0.4M NaCl"  
/dev\_stage="Six week old"  
/clone\_lib="Ice plant lambda Uni-Zap XR expression library, 48 hours NaCl treatment"  
/note="Vector: lambda Uni-Zap XR, Bluescript SK-, Site\_1: EcoRI, Site\_2: XhoI"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 2; Length 73;  
Best Local Similarity 84.2%; Pred. No. 9.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGTC 19  
|||||  
42 TGAAGTGGCGGTGGAATTG 60

Db

RESULT 7 76 bp DNA linear GSS 29-JAN-2003  
BX205183  
LOCUS BX205183  
DEFINITION Danio rerio genomic clone DKEX-223N20, genomic survey sequence.  
ACCESSION BX205183  
VERSION BX205183.1 GI:28037069  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

REFERENCE  
AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.  
TITLE Direct Submission  
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished

COMMENT  
This sequence was generated from the S66 end of BAC 223N20. 223N20 is part of the Daniokey BAC library created by R. Plasterik and N.V. Keygene. Further details:  
[http://www.sanger.ac.uk/projects/D\\_rerio/](http://www.sanger.ac.uk/projects/D_rerio/).

## FEATURES

## source

1..76  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-223N20"  
/issue\_type="Testis"  
/note="Vector pindigobAC-536"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 76;  
Best Local Similarity 84.2%; Pred. No. 9.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGTGGCGGTGGAAGTC 20  
|||||  
10 GAGCGCGAGAGGAAGTC 28

Db

RESULT 8 78 bp DNA linear GSS 05-JUL-2004  
BX997035  
LOCUS BX997035  
DEFINITION Forward strand read from insert in 3'HPT insertion targeting and chromosome engineering clone MHP294C05, genomic survey sequence.  
ACCESSION BX997035  
VERSION BX997035.1 GI:49728493  
KEYWORDS GSS; genome survey sequence; MICEP.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 78)

## REFERENCE

AUTHORS Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICEP>

## FEATURES

Location/Qualifiers  
1..78  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHP294C05"  
/clone\_lib="MHP"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 78;  
Best Local Similarity 84.2%; Pred. No. 9.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGTC 19  
|||||  
60 TGGGTGACGGGTGGAAGTC 78

Db

RESULT 9 82 bp mRNA linear EST 28-OCT-1997  
AA646813  
LOCUS AA646813  
DEFINITION vnt37b09.r1 StrataGene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1023353 5' similar to SW:ANXA\_RABIT P33477 ANNEXIN XI ;, mRNA sequence.  
ACCESSION AA646813  
VERSION AA646813.1 GI:2573242  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 82)

## REFERENCE

AUTHORS Maier, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
TITLE The WashU-HMIT Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Maria M/Mouse EST Project  
WashU-HMIT Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu



This clone is available royalty-free through LNL; contact the  
IMAG Consortium (info@image.lnl.gov) for further information.  
MGI:574129

Possible reversed clone: similarity on wrong strand  
Seq primer: -28ml3 rev1 RT from Amerisham  
High quality sequence stop: 1.

## FEATURES

## source

1..82  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1023353"  
/sex="females"  
/issue\_type="whole skin"  
/dev\_stage="11 weeks old"  
/lab\_host="SOLR (kanamycin resistant)"  
/clone\_lib="Stratagene mouse skin (#937313)"  
/note="Organ: skin; Vector: pBluescript SK-; Site 1:  
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dt: whole skin from 11 week old C57BL/6 female mice.  
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'  
adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor  
sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

## ORIGIN

Query Match 71.0%; Score 14.2; DB 1; Length 82;  
Best Local Similarity 84.2%; Pred. No. 9.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGGTGCGGTGGAAGTG 19  
|||||  
41 TGAGGAGCCGCTGGAAGTG 23

RESULT 10  
CG567843  
LOCUS

DEFINITION OS1194423 Mus musculus 129SV/Ev Mus musculus cDNA clone OST194423,  
mRNA sequence.  
CG567843  
ACCESSION CG567843.1 GI:37354430  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jai, C.,  
Key, B.W., Jr., Kipp, P., Kohlhaut, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.T., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C., and Sande, A.T.  
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
14610273

COMMENT  
Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: material@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

## FEATURES

## source

1..84  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129SV/Ev"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 84;  
Best Local Similarity 84.2%; Pred. No. 9.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGTGGAAGTG 20  
|||||  
1 GAGGTGCGGTGGAAGTG 19

RESULT 11  
BG402252  
LOCUS

DEFINITION BG402252 86 bp mRNA linear EST 12-MAR-2001  
602465822F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4593941 5',  
mRNA sequence.  
BG402252 GI:13295700

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 86)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: ILGM1334 row: 1 column: 06  
High quality sequence stop: 42.

## FEATURES

## source

1..86  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4593941"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="NIH\_MGC\_75"  
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggcgccggccgc); Site 2: SfiI (ggccatcggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGGCGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.65  
kb (range 0.5-4.0 kb). 15/15 clones contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 71.0%; Score 14.2; DB 2; Length 86;  
Best Local Similarity 84.2%; Pred. No. 9.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGGTGCGGTGGAAGTG 19  
|||||  
45 TGAGGTGATGTGGAAGTG 63

RESULT 12

DT019117 89 bp mRNA linear EST 05-AUG-2005  
 LOCUS DT019117  
 DEFINITION VV1033A04.588074 CabSau Flower Stage 12 (FLOU0012) Vitis vinifera  
 accession VV1033A04 5, mRNA sequence.  
 DT019117  
 VERSION DT019117.1 GI:71870062  
 KEYWORDS EST.  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; Vitaceae; Vitis.  
 1 (bases 1 to 89)  
 Iocco, P., Hua, C., Davies, C. and Thomas, M. R.  
 REFERENCES  
 AUTHORS Iocco, P., Hua, C., Davies, C. and Thomas, M. R.  
 TITLE Expressed sequence tags from the grapevine cultivar Cabernet  
 Sauvignon  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Cushman JC  
 Department of Biochemistry  
 University of Nevada  
 MS200, Reno, NV 89557-0014, USA  
 Tel: 775-784-1918  
 Fax: 775-784-1650  
 Email: jcushman@unr.edu  
 PCR Primers  
 FORWARD: T7 20mer (forward)  
 BACKWARD: SP6 18mer  
 Plate: 033 row: A column: 04  
 Seq primer: T7 20mer (forward)  
 High quality sequence stop: 89.  
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 /note="Organ: Inflorescence including flowers; Vector:  
 pZL; A cDNA library from immature inflorescences at stage  
 12 of the modified E-L system. Tissue collected from  
 field grown plants. A description of the modified E-L  
 system can be found in the paper by B. G. Coombe  
 'Adoption of a system for identifying grapevine growth  
 stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

ORIGIN  
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 13 GCGGTGCAAGTGCAGTGC 31  
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 accession CV973314  
 VERSION CV973314.1 GI:56134217  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticaceae; Triticum.  
 1 (bases 1 to 98)  
 Sprunck, S., Baumann, U., Edwards, K., Langridge, P. and Dresselhaus, T.  
 REFERENCES  
 AUTHORS The transcript composition of egg cells changes significantly

JOURNAL  
 PUBMED  
 15703054  
 COMMENT Contact: Sprunck S  
 Developmental Biology and Biotechnology  
 University of Hamburg, Biocenter Klein Flottbek  
 Ohnhorststrasse 18, D-22609 Hamburg, Germany  
 Email: sprunck@botanik.uni-hamburg.de  
 Sequenced as part of the BBSRC Investigating Gene Function program;  
 Wilson I., Bewick R., Shepherd S., Barker G., Parker J., Owen P.,  
 Edwards D., Coghill J., Holdsworth M., Lenton J., Shewry P.,  
 Edwards K. A BBSRC-funded wheat EST resource for the academic  
 community. Unpublished.  
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 genomic survey sequence.  
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 VERSION CZ467313.1 GI:62961326  
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 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 98)  
 Thibault, S. T., Singer, M. A., Miyazaki, W. Y., Mlaseh, B., Dompe, N. A.,  
 Singh, C. M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H. L.,  
 Ryner, L., Cheung, L. M., Chong, A., Erickson, C., Fisher, W. W.,  
 Greer, K., Hartouni, S. R., Howie, E., Jankula, J., Joo, D., Killpack, K.,  
 Laufer, A., Mazzotta, D., Smith, R. D., Stevens, L. M., Stuber, C.,  
 Tan, L. R., Ventura, R., Woo, A., Zakrjsek, I., Zhao, L., Chen, F.,  
 Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M. L. and Margolis, J.  
 A complementary transposon tool kit for Drosophila melanogaster  
 using P and piggyBac  
 Nat. Genet. 36 (3), 283-287 (2004)  
 14981521  
 JOURNAL  
 PUBMED  
 14981521  
 COMMENT Contact: Roger A Hoskins  
 Berkeley Drosophila Genome Project  
 Lawrence Berkeley National Laboratory  
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
 Tel: 510 486 4015  
 Fax: 510 486 6798  
 Email: Rhooskins@lbl.gov  
 Sequence recovery method was inverse PCR.  
 Sequence orientation is forward strand relative to 5' end of  
 piggyBac element.  
 The piggyBac insertion position is 1 in the 98 bases. This  
 insertion position refers to the first base of the 4 base TTA  
 target recognition sequence.  
 Class: transposon insertion site.

**FEATURES**  
**source**

Location/Qualifiers  
1. .98

organism="Drosophila melanogaster"  
mol\_type="genomic DNA"  
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/note="Vector: piggyBac PB (genbank accession number AY51516) : An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp90:piGyBac transposase from a single ammitation element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 370C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammitation) or the appearance of w+ male progeny (X chromosome ammitation). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

## ORIGIN

Query Match	71.0%;	Score 14.2;	DB 10;	Length 98;
Best Local Similarity	84.2%;	Pred. No. 9.1e+04;		
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Db      24 GAACTGGGAGTGAAGTGC 42

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## RESULT 15

LOCUS	CZ467324	98 bp	DNA	linear	GSS 29-APR-2005
DEFINITION	c01645-3prime Exelixis piggyBac PB insertions Drosophila				

### DEFINITION

## KEYWORDS

ORGANISM *Drosophila melanogaster*

## ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota, Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE AUTHORS

**AUTHORS**  
Thibault, S. T., Singer, M. A., Miyazaki, W. Y., Mliah, B., Dome, N. A., Singh, C. M., Buchholz, R., Demsey, M., Fawcett, R., Francis-Lang, H. L., Ryner, L., Cheung, L. M., Chong, A., Erickson, C., Fisher, W. W., Greer, K., Hartzoni, S. R., Howie, E., Jakula, L., Joe, D., Klipack, K., Laufer, A., Mazzotta, J., Smith, R. D., Stevens, L. M., Stuber, C., Tan, L. R., Ventura, R., Woo, A., Zakratski, I., Zhao, L., Chen, F., Swimmer, C., Koczynski, C., Duyk, G., Winberg, M. L., and Margolis, J.

**TITLE**  
A complementary transposon tool kit for *Drosophila melanogaster* using P and piggyBac

**JOURNAL**  
Nat. Genet. 36 (3), 283-287 (2004)

**PUBLISHED**  
14981521

**COMMENT**

Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
Tel: 510 486 4015

Tel: 510 486 4015  
 Fax: 510 486 6798  
 Email: [RHoskins@lbl.gov](mailto:RHoskins@lbl.gov)

Sequence recovery method was inverse PCR. Sequence orientation is forward strand relative to 5' end of

piggyBac element.

The piggyBac insertion position is 1 in the 98 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.

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Class: transposon insertion site
Location/Qualifiers
1. .98
FEATURES
source
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`organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/name="Vector: piggyBac PB (Genbank accession AY515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70::piggyBac transposase from a single ammitition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammitition) or the appearance of w+ male progeny (X chromosome ammitition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."`

## ORIGIN

Query Match	71.0%;	Score 14.2;	DB 10;	Length 98;
Best Local Similarity	84.2%;	Pred. No. 9.1e+04;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

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Job time : 1575 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds  
(without alignments)  
739.111 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20  
Sequence: 1 tgaagtcgcggcggaagtcgc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 2	15	75.0	24	2	US-08-529-190B-10	Sequence 10, Appl
C 3	14.8	74.0	25	3	US-09-396-196G-56226	Sequence 56226, A
C 4	14.8	74.0	25	3	US-09-396-196G-56227	Sequence 56227, A
C 5	14.2	71.0	21	6	PCT-US93-12600-10	Sequence 10, Appl
C 6	14.2	71.0	30	3	US-07-705-490-11	Sequence 11, Appl
C 7	14.2	71.0	30	3	US-08-758-662-7	Sequence 7, Appl
C 8	14.2	71.0	30	3	US-07-751-891B-11	Sequence 11, Appl
C 9	14.2	71.0	50	3	US-09-907-794A-151	Sequence 151, App
C 10	14.2	71.0	50	3	US-09-905-125A-151	Sequence 151, App
C 11	14.2	71.0	50	3	US-09-902-775A-151	Sequence 151, App
C 12	14.2	71.0	50	3	US-09-906-700-151	Sequence 151, App
C 13	14.2	71.0	50	3	US-09-903-603A-151	Sequence 151, App
C 14	14.2	71.0	50	3	US-09-904-920A-151	Sequence 151, App
C 15	14.2	71.0	50	3	US-09-909-064-151	Sequence 151, App
C 16	14.2	71.0	50	3	US-09-905-381A-151	Sequence 151, App
C 17	14.2	71.0	50	3	US-09-906-618-151	Sequence 151, App
C 18	14.2	71.0	50	3	US-09-906-646-151	Sequence 151, App
C 19	14.2	71.0	50	3	US-09-904-462-151	Sequence 151, App
C 20	14.2	71.0	50	3	US-09-902-736A-151	Sequence 151, App
C 21	14.2	71.0	50	3	US-09-906-722A-151	Sequence 151, App
C 22	14	70.0	24	2	US-08-529-190B-4	Sequence 4, Appl
C 23	14	70.0	24	2	US-08-529-190B-13	Sequence 13, Appl
C 24	14	70.0	24	2	US-08-529-190B-16	Sequence 16, Appl

C 25	13.8	69.0	27	3	US-09-435-327A-22	Sequence 22, Appl
C 26	13.8	69.0	48	2	US-07-917-034A-20	Sequence 20, Appl
C 27	13.6	68.0	65	3	US-09-744-931-57	Sequence 57, Appl
C 28	13.6	68.0	65	3	US-09-744-931-58	Sequence 58, Appl
C 29	13.4	67.0	47	3	US-09-422-978-2497	Sequence 2497, Ap
C 30	13.4	67.0	97	2	US-08-399-412A-79	Sequence 79, Appl
C 31	13.2	66.0	24	3	US-10-167-528-1	Sequence 1, Appl
C 32	13.2	66.0	25	3	US-09-733-042-4	Sequence 4, Appl
C 33	13.2	66.0	25	3	US-09-396-196G-67637	Sequence 67637, A
C 34	13.2	66.0	30	3	US-08-506-296B-34	Sequence 34, Appl
C 35	13.2	66.0	30	3	US-09-119-507B-10	Sequence 10, Appl
C 36	13.2	66.0	30	3	US-09-119-507B-38	Sequence 38, Appl
C 37	13.2	66.0	30	3	US-09-119-507B-39	Sequence 39, Appl
C 38	13.2	66.0	30	3	US-08-897-556A-10	Sequence 10, Appl
C 39	13.2	66.0	30	3	US-08-897-556A-38	Sequence 38, Appl
C 40	13.2	66.0	30	3	US-08-897-556A-39	Sequence 39, Appl
C 41	13.2	66.0	30	3	US-09-547-693-10	Sequence 10, Appl
C 42	13.2	66.0	30	3	US-09-547-693-38	Sequence 38, Appl
C 43	13.2	66.0	30	3	US-09-547-693-39	Sequence 39, Appl
C 44	13.2	66.0	51	2	US-08-285-936-44	Sequence 44, Appl
C 45	13.2	66.0	51	2	US-08-285-936-45	Sequence 45, Appl

## ALIGNMENTS

RESULT 1  
US-08-529-190B-7/c  
; Sequence 7, Application US/08529190B  
; Patent No. 5833991  
; GENERAL INFORMATION:  
; APPLICANT: Masucci, Maria G.  
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES  
; TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Banner & Witcoff, Ltd.  
; STREET: One Financial Center  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Wordperfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,190B  
; FILING DATE: 15-SEP-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE9501324-9  
; FILING DATE: 10-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US08/522,595  
; FILING DATE: 01-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Ph.D., Kathleen A  
; REGISTRATION NUMBER: 34,380  
; REFERENCE/DOCKET NUMBER: 3255/53015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-9110  
; TELEFAX: 617-345-9111  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 bases  
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RESULT 2  
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; Patent No. 5833991  
; GENERAL INFORMATION:  
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; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES  
; TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: One Financial Center  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02111  
; COMPUTER READABLE FORM:  
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; APPLICATION NUMBER: US/08/529,190B  
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; FILING DATE: 10-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US08/522,595  
; FILING DATE: 01-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Ph.D., Kathleen A  
; REGISTRATION NUMBER: 34,380  
; REFERENCE/DOCKET NUMBER: 3255/53015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-9100  
; TELEFAX: 617-345-9111  
; INFORMATION FOR SEQ ID NO: 10:  
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; LENGTH: 24 bases  
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; TOPOLOGY: linear  
US-08-529-1908-10

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US-09-396-1966-56226  
; Sequence 56226, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; ZIP: 60601

; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56226  
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; TYPE: DNA  
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US-09-396-1966-56226

Query Match 74.0%; Score 14.8; DB 3; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.3e+03;  
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RESULT 4  
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; Sequence 56227, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
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; ORGANISM: mus musculus  
US-09-396-1966-56227

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 5  
PCT-US93-12600-10/c  
; Sequence 10, Application PC/TUS9312600  
; GENERAL INFORMATION:  
; APPLICANT: Denner, Larry A.  
; APPLICANT: Rege, Ajay A.  
; APPLICANT: Dixon, Richard A.F.  
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Shore &  
; ADDRESSEE: Milamow, Ltd.  
; STREET: 180 North Stearns, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
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OPERATING SYSTEM: PC-DOS/MS-DOS  
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CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12600  
FILING DATE: 28-DEC-1993  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/999,706  
FILING DATE: December 31, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)616-5400  
TELEFAX: (312)616-5460  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US93-12600-10

Query Match 71.0%; Score 14.2; DB 6; Length 21;  
Best Local Similarity 84.2%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGTGGCGGTGAAGTGC 20  
Db 19 GATGTGGGCTGGAAGTGC 1

RESULT 6  
US-07-705-490-11/c  
Sequence 11, Application US/07705490  
Patent No. 6107025  
GENERAL INFORMATION:  
APPLICANT: Caskey, C. T.  
APPLICANT: Nelson, David L.  
APPLICANT: Pieretti, Maura  
APPLICANT: Warren, Stephen T.  
APPLICANT: Oostra, Ben A.  
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Thomas D. Paul  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/705,490  
FILING DATE: 19910708  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5350  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325  
TELEFAX: 762829  
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-07-705-490-11

Query Match 71.0%; Score 14.2; DB 3; Length 30;  
Best Local Similarity 84.2%; Pred. No. 2.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGTGGCGGTGAAGTGC 20  
Db 25 GAGCTGGGTGGAAGTGC 7

RESULT 7  
US-08-758-662-7/c  
Sequence 7, Application US/08758662  
Patent No. 6114150  
GENERAL INFORMATION:  
APPLICANT: Weissman, Sherman  
APPLICANT: Baskaran, Namadev  
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 701 Fifth Avenue, 6300 Columbia Center  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,662  
FILING DATE: 29-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6114150endurg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 390036.402C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-758-662-7

Query Match 71.0%; Score 14.2; DB 3; Length 30;  
Best Local Similarity 84.2%; Pred. No. 2.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGTGGCGGTGAAGTGC 20  
Db 25 GAGCTGGGTGGAAGTGC 7

RESULT 8  
US-07-751-891B-11/c  
Sequence 11, Application US/07751891B  
Patent No. 6180337  
GENERAL INFORMATION:  
APPLICANT: Caskey, C. T.

```

; Nelson, David L.
; pieretti, Maurea
; Warren, Stephen T.
; Oestre, Ben A.
; Fu, Ying-hui
;
; TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas D. Paul
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA: US/07/751,891B
; APPLICATION NUMBER: US/07/751,891B
; FILING DATE: 29-Aug-1991
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5350
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; TELEX: 762829
;
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-07-751-891B-11

Query Match      71.0%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  GAGGTGCGGTGGAAGTGC 20
Db      25  GAGCTGTGTGTGAAGTGC 7

RESULT 9
US-09-907-794A-151
; Sequence 151, Application US/09907794A
; Patent No. 6635468
;
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
```

```

; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
;
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-907-794A-151

Query Match      71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  TGAGTGGCGGTGGAAGTGC 19
Db      16  TGAGGCGCGGTGGAAGTGC 34

RESULT 10
US-09-905-125A-151
; Sequence 151, Application US/09905125A
; Patent No. 6664376
;
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
```



APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/905,125A  
CURRENT FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 151  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-905-125A-151  
Query Match 71.0%; Score 14.2; DB 3; Length 50;

Best Local Similarity 84.2%; Pred. No. 2.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TGAGGTGCGGTGGAATG 19  
Db 16 TGAGGGCGGTGGAATG 34  
RESULT 11  
US-09-902-775A-151  
Sequence 151, Application US/09902775A  
Patent No. 6686451  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,775A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20

```

; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-902-775A-151

Query Match
Best Local Similarity 84.2%; Score 14.2; DB 3; Length 50;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGGTGGCGGTGGAAGTG 19
Db 16 TGAAGGCGCGGTGAGAGTG 34

RESULT 12
US-09-906-700-151
; Sequence 151, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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```

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-906-700-151

Query Match
Best Local Similarity 84.2%; Score 14.2; DB 3; Length 50;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGGTGGCGGTGGAAGTG 19
Db 16 TGAAGGCGCGGTGAGAGTG 34

RESULT 13
US-09-903-603A-151
; Sequence 151, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
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; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/22089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-903-603A-151

Query Match      71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TGAGGTGGCGGTGAAGTG 19
      ||| ||||| ||||| |||
Db      16 TGAAGGCGCGGTGAAGTG 34

RESULT 14
US-09-904-920A-151
; Sequence 151. Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
```

```

; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-904-920A-151

Query Match      71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TGAGGTGGCGGTGAAGTG 19
      ||| ||||| ||||| |||
Db      16 TGAAGGCGCGGTGAAGTG 34

RESULT 15
US-09-909-064-151
; Sequence 151. Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
```

APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,064  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
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PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 151  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-909-064-151

Query Match 71.0%; Score 14.2; DB 3; Length 50;  
Best Local Similarity 84.2%; Pred. No. 2.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TGAAGTCCGGGTGGAAGTG 19  
||| ||||| ||||| |||||  
DB 16 TGAAGGCGCGGTGAGAGTG 34

Search completed: December 24, 2005, 18:36:29  
Job time : 48.1 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using ew model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-9  
Perfect score: 20  
Sequence: 1 tgaagtcgcgggtggaagtcgc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-9
2	15.2	76.0	25	8	US-10-719-900-855558
3	15.2	76.0	60	3	US-09-908-975-22618
4	14.8	74.0	25	5	US-10-098-263B-45504
5	14.8	74.0	25	9	US-10-809-189-56226
6	14.8	74.0	25	9	US-10-809-189-56227
7	14.4	72.0	25	5	US-10-215-112-8648
8	14.4	72.0	25	5	US-10-098-263B-86887
9	14.4	72.0	25	8	US-10-719-900-932959
10	14.4	72.0	60	3	US-09-908-975-21047
11	14.2	71.0	25	10	US-11-036-317-61324
12	14.2	71.0	25	10	US-11-036-317-319797
13	14.2	71.0	25	10	US-11-036-317-597647
14	14.2	71.0	30	5	US-10-073-353-7
15	14.2	71.0	50	3	US-09-909-320-151
16	14.2	71.0	50	3	US-09-909-088B-151
17	14.2	71.0	50	3	US-09-905-291A-151
18	14.2	71.0	50	3	US-09-902-853-151
19	14.2	71.0	50	3	US-09-907-824-151
20	14.2	71.0	50	3	US-09-907-841-151
21	14.2	71.0	50	3	US-09-904-011-151
22	14.2	71.0	50	3	US-09-903-640-151
23	14.2	71.0	50	3	US-09-908-093-151

24	14.2	71.0	50	3	US-09-906-742-151	Sequence 151, App
25	14.2	71.0	50	3	US-09-906-838-151	Sequence 151, App
26	14.2	71.0	50	3	US-09-907-613-151	Sequence 151, App
27	14.2	71.0	50	3	US-09-907-942-151	Sequence 151, App
28	14.2	71.0	50	3	US-09-904-859-151	Sequence 151, App
29	14.2	71.0	50	3	US-09-909-204-151	Sequence 151, App
30	14.2	71.0	50	3	US-09-904-820-151	Sequence 151, App
31	14.2	71.0	50	3	US-09-904-786-151	Sequence 151, App
32	14.2	71.0	50	3	US-09-906-646-151	Sequence 151, App
33	14.2	71.0	50	3	US-09-906-700-151	Sequence 151, App
34	14.2	71.0	50	3	US-09-903-786-151	Sequence 151, App
35	14.2	71.0	50	3	US-09-902-903-151	Sequence 151, App
36	14.2	71.0	50	3	US-09-903-749A-151	Sequence 151, App
37	14.2	71.0	50	3	US-09-904-119-151	Sequence 151, App
38	14.2	71.0	50	3	US-09-904-956-151	Sequence 151, App
39	14.2	71.0	50	3	US-09-902-736-151	Sequence 151, App
40	14.2	71.0	50	3	US-09-907-794-151	Sequence 151, App
41	14.2	71.0	50	3	US-09-903-943-151	Sequence 151, App
42	14.2	71.0	50	3	US-09-904-462-151	Sequence 151, App
43	14.2	71.0	50	3	US-09-907-925-151	Sequence 151, App
44	14.2	71.0	50	3	US-09-902-692-151	Sequence 151, App
45	14.2	71.0	50	3	US-09-903-520-151	Sequence 151, App

#### ALIGNMENTS

```

RESULT 1
US-09-296-264-9
; Sequence 9, Application US/09296264
; Publication No. US2003008374A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: NEUROPEPTIDE ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; FILE REFERENCE: 033396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-9

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TGAGTGCAGGAGTGC 20
Db      1  TGAGTGCAGGAGTGC 20

RESULT 2
US-10-719-900-855558
; Sequence 855558, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

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SEQ ID NO 855558  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-855558

Query Match 76.0%; Score 15.2; DB 8; Length 25;  
Best Local Similarity 85.0%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGAAGTGC 20  
|||||  
Db 1 TGAGTGGCGGTGAAGTGC 20

RESULT 3  
US-09-908-975-22618  
Sequence 22618, Application US/09908975  
Publication NO. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
APPLICANT: RAIGER, Shimon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 22618  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-22618

US-09-908-975-22618

Query Match 76.0%; Score 15.2; DB 3; Length 60;  
Best Local Similarity 85.0%; Pred. No. 3.5e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGAAGTGC 20  
|||||  
Db 25 TGAGTGGCGGTGAAGTGC 44

RESULT 4  
US-10-098-263B-45504/C  
Sequence 45504, Application US/10098263B  
Publication NO. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 45504  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-098-263B-45504

Query Match 74.0%; Score 14.8; DB 5; Length 25;  
Best Local Similarity 88.9%; Pred. No. 5.6e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGAAGT 18  
|||||  
Db 24 TGAGTGGCGGTGAAGT 7

RESULT 5  
US-10-809-189-56226  
Sequence 56226, Application US/10809189  
Publication NO. US20050048531A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 56226  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-809-189-56226

Query Match 74.0%; Score 14.8; DB 9; Length 25;  
Best Local Similarity 88.9%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGAAGT 18  
|||||  
Db 7 TGAGTGGCGGTGAAGT 24

RESULT 6  
US-10-809-189-56227  
Sequence 56227, Application US/10809189  
Publication NO. US20050048531A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 56227  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-809-189-56227

Query Match 74.0%; Score 14.8; DB 9; Length 25;  
Best Local Similarity 88.9%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TGAGTGGCGGTGAAGT 18  
|||||  
Db 4 TGAGTGGCGGTGAAGT 21

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RESULT 7
US-10-215-112-8648/c
; Sequence 8648, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 8648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-8648

Query Match          72.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGGTGCGGTGGAAG 17
      |||||
Db      24 GAGGTGCGGTGGAAG 9

RESULT 8
US-10-098-263B-86887
; Sequence 86887, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 86887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-86887

Query Match          72.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GTGCGGTGGAAGTGC 20
      |||||
Db      4 GTGCGGTGGAAGTGC 19

RESULT 9
US-10-719-900-932959/c
; Sequence 932959, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
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; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 932959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-932959

Query Match          72.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TGAGGTGCGGTGGA 16
      |||||
Db      16 TGAGGTGCGGTGGA 1

RESULT 10
US-09-908-975-21047
; Sequence 21047, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21047
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-21047

Query Match          72.0%; Score 14.4; DB 3; Length 60;
Best Local Similarity 93.8%; Pred. No. 7.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 AGGTGCGGTGGAAGT 18
      |||||
Db      6 AGGTGCGGTGGAAGT 21

RESULT 11
US-11-036-317-61324
; Sequence 61324, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-61324
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Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGTG 19  
DB 1 TGACGTGCTGTGTGGAAG 19

RESULT 12  
US-11-036-317-319797  
Sequence 319797, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 319797  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-319797

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGTG 19  
DB 7 TGAGTGGCGGTGGAAGTG 25

RESULT 13  
US-11-036-317-597647  
Sequence 597647, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 597647  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-597647

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGGTGGCGGTGGAAGTG 20  
DB 6 GAGGTGGCGGTGGAAGTG 24

RESULT 14  
US-10-073-353-7/C  
Sequence 7, Application US/10073353

Publication No. US20020168658A1  
GENERAL INFORMATION:  
APPLICANT: Sherman M. Weisman  
APPLICANT: Namadev Baskaran  
TITLE OF INVENTION: Amplification of Nucleic Acids  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan, Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Ave., NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/073,353  
FILING DATE: 03-May-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/758,662  
FILING DATE: 1996-12-07  
APPLICATION NUMBER: US 08/758,662 (CPA)  
FILING DATE: 1999-02-17  
APPLICATION NUMBER: US 09/585,437  
FILING DATE: 2000-06-02  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5007-03-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-073-353-7  
Query Match 71.0%; Score 14.2; DB 5; Length 30;  
Best Local Similarity 84.2%; Pred. No. 1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGGTGGCGGTGGAAGTG 20  
DB 25 GAGCTGTGTGTGGAAGTG 7

RESULT 15  
US-09-909-320-151  
Sequence 151, Application US/09909320  
Patent No. US20020132240A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerilsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.



APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,320  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 151  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide probe  
US-09-909-320-151  
Query Match 71.0%; Score 14.2; DB 3; Length 50;  
Best Local Similarity 84.2%; Pred. No. 9.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TGAGGTGGGGTGAAGTG 19  
Db 16 TGAAGGGGGGTGAAGTG 34

Search completed: December 25, 2005, 04:14:24  
Job time : 338.6 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds  
(without alignments)  
1953.383 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20

Sequence: 1 gtgcgcagcgtgagccacaga 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

1858228

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pro:\*  
9: gb\_ro:\*  
10: gb\_bts:\*  
11: gb\_gy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hlg:\*  
15: gb\_pli:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211667
2	17.6	88.0	21	6	ARS31240 Sequence
3	17.6	88.0	21	6	AX097265 Sequence
4	14.2	71.0	60	6	ARS61935 Sequence
5	13.8	69.0	27	6	AX188785 Sequence
6	13.8	69.0	50	6	CO009079 Sequence
7	13.8	69.0	65	6	CO512692 Sequence
8	13.8	69.0	72	4	AY604639
9	13.6	68.0	27	6	AY8650
10	13.6	68.0	51	6	AX162818 Sequence
11	13.6	68.0	65	6	CO532435 Sequence
12	13.6	68.0	65	6	CO532930 Sequence
13	13.4	67.0	30	6	AX611417 Sequence
14	13.4	67.0	50	6	CO008762 Sequence
15	13.2	66.0	27	6	AX002713 Sequence
16	13.2	66.0	33	6	AR127237 Sequence
17	13.2	66.0	33	6	AR127238 Sequence
18	13.2	66.0	33	6	BD130578

c	19	13.2	66.0	33	6	BD130579	BD130579 Controlle
c	20	13.2	66.0	35	6	AX358674	AX358674 Sequence
c	21	13.2	66.0	35	6	AX358675	AX358675 Sequence
c	22	13.2	66.0	44	6	AR143578	AR143578 Sequence
c	23	13.2	66.0	44	6	AR168947	AR168947 Sequence
c	24	13.2	66.0	44	6	AR232695	AR232695 Sequence
c	25	13.2	66.0	44	6	AR262637	AR262637 Sequence
c	26	13.2	66.0	44	6	AR316574	AR316574 Sequence
c	27	13.2	66.0	65	6	CO534393	CO534393 Sequence
c	28	13.2	66.0	83	6	BD040906	BD040906 Sequence
c	29	13.2	66.0	83	6	AX905373	AX905373 Sequence
c	30	13.2	66.0	90	8	HSEXT2	X99574 H. sapiens e
c	31	12.8	64.0	22	6	E11187	E11187 Probe. 9/19
c	32	12.8	64.0	24	6	BD131726	BD131726 Method fo
c	33	12.8	64.0	24	6	AR606669	AR606669 Sequence
c	34	12.8	64.0	24	6	AX019309	AX019309 Sequence
c	35	12.8	64.0	25	6	AR065111	AR065111 Sequence
c	36	12.8	64.0	25	6	E09880	E09880 Primer. 9/1
c	37	12.8	64.0	30	8	HUMPLTP12	U37819 Human phosp
c	38	12.8	64.0	35	6	AX756529	AX756529 Sequence
c	39	12.8	64.0	48	6	A97298	A97298 Sequence. 15
c	40	12.8	64.0	51	6	CO002980	CO002980 Sequence
c	41	12.8	64.0	53	6	E11189	E11189 Probe. 9/19
c	42	12.8	64.0	62	6	AR127979	AR127979 Sequence
c	43	12.8	64.0	62	6	AR408324	AR408324 Sequence
c	44	12.8	64.0	68	8	AY805392	AY805392 Homo sapi
c	45	12.8	64.0	70	6	E03982	E03982 Probe for d

#### ALIGNMENTS

RESULT 1  
BD211667  
LOCUS  
DEFINITION  
BD211667 20 bp DNA linear PAT 17-JUL-2003  
using the same for controlling cell proliferation.

ACCESSION  
BD211667  
VERSION  
BD211667.1 GI:33021437  
KEYWORDS  
JP 2002512793-A/10.  
SOURCE  
Homo sapiens  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo

REFERENCE  
1 (bases 1 to 20)  
Wright,J.A., Young,A.H. and Lee,Y.S.  
TITLE  
Antisense oligonucleotide sequence of neuropilin and method of  
using the same for controlling cell proliferation  
JOURNAL  
GENESENSE TECHNOLOGIES INC  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002512793-A/10  
PD 08-MAY-2002  
PF 23-APR-1999 JP 2000545999  
PR 23-APR-1998 US 60/082791  
PI JIM A WRIGHT,ALPING H YOUNG,YOON S LEE  
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC  
Antisense oligonucleotide sequence of neuropilin and method of  
using the same for controlling cell proliferation  
CC same for controlling cell proliferation  
FH Key location/Qualifiers  
FT source 1..20 location/Qualifiers  
FT 1..20 location/Qualifiers

FEATURES  
source  
1..20 location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

#### ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAGA 20  
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Db 1 GTGCCGACGTGGACCCAGA 20

RESULT 2  
ARS31240/c  
LOCUS ARS31240 21 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 2443 from patent US 6727063.  
ACCESSION ARS31240  
VERSION ARS31240.1 GI:53919677  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 21)  
Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.O. and  
McCarthy,J.J.  
TITLE Single nucleotide polymorphisms in genes  
JOURNAL Patent: US 6727063-A 2443 27-APR-2004;  
Millennium Pharmaceuticals, Inc. and Whitehead Institute for  
Biomedical Research; Cambridge, MA  
FEATURES  
source 1..21  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 88.0%; Score 17.6; DB 6; Length 21;  
Best Local Similarity 94.4%; Pred. No. 4.1e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCCA 18  
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Db 18 GTGCCGAYGTGGACCCCA 1

RESULT 3  
AX097265/c  
LOCUS AX097265 21 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 2443 from Patent WO0118250.  
ACCESSION AX097265  
VERSION AX097265.1 GI:13513682  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Carchinh;  
Homnidae; Homo.  
REFERENCE  
AUTHORS 1  
Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.O. and  
McCarthy,J.J.  
TITLE Single nucleotide polymorphisms in genes  
JOURNAL Patent: WO 0118250-A 2443 15-MAR-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium  
Pharmaceuticals, Inc. (US)  
FEATURES  
source 1..21  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 88.0%; Score 17.6; DB 6; Length 21;  
Best Local Similarity 94.4%; Pred. No. 4.1e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCCA 18  
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Db 18 GTGCCGAYGTGGACCCCA 1

RESULT 4  
ARS61935/c  
LOCUS ARS61935 60 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 162 from patent US 6759198.  
ACCESSION ARS61935  
VERSION ARS61935.1 GI:53975586  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 60)  
Kris,R.M. and Felder,S.  
TITLE High throughput assay system  
JOURNAL Patent: US 6759198-A 162 06-JUL-2004;  
High Throughput Genomics, Inc.; Tucson, AZ  
FEATURES  
source 1..60  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 60;  
Best Local Similarity 84.2%; Pred. No. 2.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAG 19  
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Db 48 GTGCTTACGTGGACCTCAG 30

RESULT 5  
AX188785  
LOCUS AX188785 27 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 32 from Patent WO0148228.  
ACCESSION AX188785  
VERSION AX188785.1 GI:15142326  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS 1  
Chater,K.F., Bruton,C.J., O'Rourke,S.J. and Wietzorrek,A.W.  
TITLE Methods and materials relating to gene expression  
JOURNAL Patent: WO 0148228-A 32 05-JUL-2001;  
Plant Bioscience Limited (GB)  
FEATURES  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer"

ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 27;  
Best Local Similarity 88.2%; Pred. No. 3.7e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGACCCAG 19  
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Db 3 GCCGACGCGGACCCCG 19

RESULT 6  
CQ009079/c  
LOCUS CQ009079 50 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 7719 from Patent WO0147944.  
ACCESSION CQ009079  
VERSION CQ009079.1 GI:41015805  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.

REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acid containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0147944-A 7719 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
Source 1..50  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
25..26  
misc\_feature  
/note="Nucleotide deleted between bases 25 and 26"  
Accession number CG43931874"

ORIGIN  
Query Match 69.0%; Score 13.8; DB 6; Length 50;  
Best Local Similarity 88.2%; Pred. No. 3.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGAGCCAG 19  
|||  
Db 26 GCCCAGTGGAGCCAG 10  
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RESULT 7  
LOCUS CQ532692 65 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 2327 from Patent WO0210449.  
ACCESSION CQ532692  
VERSION CQ532692.1 GI:41498956  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1  
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, J. and Paigler, S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcritome  
JOURNAL Patent: WO 0210449-A 2327 07-FEB-2002;  
Compugen Inc. (US)  
FEATURES Location/Qualifiers  
Source 1..65  
/organism="Rattus norvegicus"  
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/db\_xref="taxon:10116"

ORIGIN  
Query Match 69.0%; Score 13.8; DB 6; Length 65;  
Best Local Similarity 88.2%; Pred. No. 3.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGAGCCAG 19  
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Db 23 GCACGACGTGGAGCCAG 39  
|||

RESULT 8  
LOCUS AY604639 72 bp mRNA linear MAM 09-JUN-2004  
DEFINITION Sus scrofa clone 8413-11 T-cell receptor delta chain CDR3 region (TCRD) mRNA, partial cds.  
ACCESSION AY604639  
VERSION AY604639.1 GI:48249576  
KEYWORDS  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;

Sus.  
1 (bases 1 to 72)  
AUTHORS Holtmeier, W., Geisel, W., Bernert, K., Butler, J.E., Sinkora, M., Renakova, Z., Sinkora, J. and Caspar, W.F.  
TITLE Prenatal development of the porcine TCR delta repertoire: Dominant expression of an invariant T cell receptor Vdelta3-Jdelta3 chain  
JOURNAL Eur. J. Immunol. (2004) In press  
REFERENCE 2 (bases 1 to 72)  
AUTHORS Holtmeier, W., Geisel, W., Bernert, K., Butler, J.E., Sinkora, M., Renakova, Z., Sinkora, J. and Caspar, W.F.  
TITLE Direct Submission  
JOURNAL Submitted (22-APR-2004) Medizinische Klinik II, Department of Gastroenterology, Johann Wolfgang Goethe-Universitaet, Theodor-Stern-Kai 7, Frankfurt am Main 60590, Germany  
FEATURES Location/Qualifiers  
Source 1..72  
/organism="Sus scrofa"  
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ORIGIN  
Query Match 69.0%; Score 13.8; DB 4; Length 72;  
Best Local Similarity 88.2%; Pred. No. 3.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGACGTGGAGCCAGA 20  
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Db 45 CCGACGTGGAGCCAGA 29  
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RESULT 9  
LOCUS A98650 27 bp DNA linear PAT 26-JAN-2000  
DEFINITION Sequence 6 from Patent WO9910500.  
ACCESSION A98650  
VERSION A98650.1 GI:6781694  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Schlichter, U. and Steinbiss, H.  
TITLE NUCLEIC ACID MOLECULES CODING FOR A CYSTEINE PROTEINASE OF PLANT ORIGIN AND THEIR REGULATING REGIONS  
JOURNAL Patent: WO 9910500-A 6 04-MAR-1999;  
MAX PLANCK GESLELSCHAFT (DE); SCHLICHTER URSULA (DE)  
FEATURES Location/Qualifiers  
Source 1..27  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 27;  
Best Local Similarity 80.0%; Pred. No. 4.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCAGA 20  
|||  
Db 6 GTGTGGACCTGGAGCCAGA 25  
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RESULT 10  
AX162818/c  
LOCUS AX162818 51 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6146 from Patent WO0140521.  
ACCESSION AX162818  
VERSION AX162818.1 GI:14544149  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0140521-A 6146 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="2 of 2 allelic variants (6145 is other entry)  
Accession number CG44914955"  
misc\_feature  
ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 51;  
Best Local Similarity 80.0%; Pred. No. 4.6e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GTGCCGACGTGGAGCCAGCA 20  
DB 45 GTTCAGACGTGGGTCGACAGA 26  
RESULT 11  
CQ532435  
LOCUS CQ532435 65 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 2070 from Patent WO0210449.  
ACCESSION CQ532435  
VERSION CQ532435.1 GI:41498699  
KEYWORDS  
SOURCE  
ORGANISM Rattus norvegicus (Norway rat)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE  
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcriptome  
JOURNAL Patent: WO 0210449-A 2070 07-FEB-2002;  
Comugen Inc. (US)  
FEATURES  
source  
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/organism="Rattus norvegicus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10116"  
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Query Match 68.0%; Score 13.6; DB 6; Length 65;  
Best Local Similarity 80.0%; Pred. No. 4.6e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GTGCCGACGTGGAGCCAGCA 20  
DB 5 GTCCAGACGTGGAGCCAGCA 24

RESULT 12  
CQ532930/c  
LOCUS CQ532930 65 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 2565 from Patent WO0210449.  
ACCESSION CQ532930  
VERSION CQ532930.1 GI:41499194  
KEYWORDS  
SOURCE  
ORGANISM Rattus norvegicus (Norway rat)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE  
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcriptome  
JOURNAL Patent: WO 0210449-A 2565 07-FEB-2002;  
Comugen Inc. (US)  
FEATURES  
source  
1..65  
/organism="Rattus norvegicus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10116"  
ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 65;  
Best Local Similarity 80.0%; Pred. No. 4.6e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GTGCCGACGTGGAGCCAGCA 20  
DB 20 GTGCCGACGTGGAGCCAGCA 1  
RESULT 13  
AX611417/c  
LOCUS AX611417 30 bp DNA linear PAT 17-FEB-2003  
DEFINITION Sequence 2442 from Patent WO02072882.  
ACCESSION AX611417  
VERSION AX611417.1 GI:28406846  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
AUTHORS Cullen, P. and Seedorf, U.  
TITLE Coronary chip  
JOURNAL Patent: WO 02072882-A 2442 19-SEP-2002;  
OGHAM GmbH (DE)  
FEATURES  
source  
1..30  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 67.0%; Score 13.4; DB 6; Length 30;  
Best Local Similarity 93.3%; Pred. No. 5.9e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 TGCCGACGTGGAGCC 16  
DB 18 TGCCGACGTGGAGCC 4  
RESULT 14  
CQ008762/c  
LOCUS CQ008762 50 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 7402 from Patent WO0147944.  
ACCESSION CQ008762  
VERSION CQ008762.1 GI:41015477

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS 1 Shimkova, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
JOURNAL methods of use thereof  
Patent: WO 0147944-A 7402 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES  
source Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
25..26  
/note="Nucleotide deleted between bases 25 and 26  
Accession number cg43922182"

ORIGIN  
Query Match 67.0%; Score 13.4; DB 6; Length 50;  
Best Local Similarity 93.3%; Pred. No. 5.8e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAC 15  
DB 29 GTGCCGACGTGGAC 15

RESULT 15  
AX002713/c 27 bp DNA linear PAT 21-AUG-2000  
LOCUS AX002713  
DEFINITION Sequence 5 from Patent WO9900490.  
ACCESSION AX002713  
VERSION AX002713.1 GI:3885040

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 other sequences; artificial sequences.

REFERENCE  
AUTHORS 1 Weinberg, M.A.  
TITLE Attenuated human immunodeficiency virus vaccine  
JOURNAL Parent: WO 9800490-A 5 07-JAN-1999;  
WEINBERG MARK A (CA); SIR MORTIMER B DAVIS JEWISH GE (CA)  
FEATURES  
source Location/Qualifiers  
1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 27;  
Best Local Similarity 83.3%; Pred. No. 7.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCGACGTGGAGCCAG 20  
DB 26 GCCGACGTGGAGCCAG 9

Search completed: December 24, 2005, 14:06:15  
Job time : 584 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds  
(without alignments)  
777.677 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20

Sequence: 1 gtccgcagctgagaccacaga 20

Scoring table: IDENTITY\_NUC

Searched: 4596997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N Geneseq\_21:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2002as:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002as:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003as:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31440 Human neu
2	20	100.0	20	9	ADA74692 GTT3610 a
3	18	90.0	21	4	AA97678 Human gen
4	15.2	76.0	25	9	AC190367 Human mic
5	14.2	71.0	25	9	ACK25958 Human mic
6	14.2	71.0	60	8	AB272759 Human mic
7	13.8	69.0	25	9	ACK26420 Human mic
8	13.8	69.0	25	9	ACT182748 Human mic
9	13.8	69.0	27	4	AA507631 Streptoco
10	13.8	69.0	28	2	AA83785 Pmel rest
11	13.8	69.0	50	4	AA134511 Human SNP
12	13.8	69.0	55	12	ADN00075 Human FCE
13	13.8	69.0	65	6	ABN29579 Rat splic
14	13.6	68.0	25	9	ACT190366 Human mic
15	13.6	68.0	27	2	AAK23277 H. vulgar
16	13.6	68.0	51	4	AA179205 Human s11
17	13.6	68.0	65	6	ABN29817 Rat splic
18	13.6	68.0	65	6	ABN29322 Rat splic
19	13.4	67.0	25	9	ACT35533 Human mic

C	20	13.4	67.0	50	4	AA134194 Human SNP
C	21	13.2	66.0	20	10	AB298158 Human CD2
C	22	13.2	66.0	20	11	ABD31189 Human CD2
C	23	13.2	66.0	20	12	ADU60023 Oligonuci
C	24	13.2	66.0	20	12	AD045513 Human o1i
C	25	13.2	66.0	21	13	ADU43138 Knock-dow
C	26	13.2	66.0	21	13	ADU45352 Knock-dow
C	27	13.2	66.0	25	9	ACT125240 Human mic
C	28	13.2	66.0	25	9	ACK09387 Human mic
C	29	13.2	66.0	27	2	AAK03341 PCR prime
C	30	13.2	66.0	33	2	AAK89941 Sequence
C	31	13.2	66.0	33	2	AAK89942 Sequence
C	32	13.2	66.0	35	6	ABL32002 Dihydroxy
C	33	13.2	66.0	44	2	AAT38282 Murine 10
C	34	13.2	66.0	44	3	AAA51915 Reverse p
C	35	13.2	66.0	44	4	AAK03383 3' primer
C	36	13.2	66.0	44	4	AAK077055 Murine 10
C	37	13.2	66.0	44	4	AAK92152 Mouse 103
C	38	13.2	66.0	44	4	AAK23475 3' Oligon
C	39	13.2	66.0	44	4	AA170278 Mouse 103
C	40	13.2	66.0	44	4	AAK82626 Murine TH
C	41	13.2	66.0	44	6	AB553332 Mouse 103
C	42	13.2	66.0	44	8	ABQ77055 Murine 10
C	43	13.2	66.0	44	9	ADB37507 Mouse Th-
C	44	13.2	66.0	44	11	ADM68648 Mouse try
C	45	13.2	66.0	50	14	ADM98969 Human her
C	45	13.2	66.0	51	10	ADP92437 PCR prime

## ALIGNMENTS

RESULT 1	AAZ31440	AAZ31440 standard; DNA; 20 BP.
ID	AAZ31440;	
AC	AAZ31440;	
XX	07-FEB-2000	(first entry)
DT	Human neuropilin mRNA specific antisense oligo GTT3610.	
DE	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;	
XX	papilloma; diabetic retinopathy; antisense; ss.	
KW	Synthetic.	
XX	Homo sapiens.	
OS	MO9955855-A2.	
XX	04-NOV-1999.	
PD	23-APR-1999;	99WO-CA000324.
XX	23-APR-1998;	98US-0082791P.
PF	(GENE-) GENESENSE TECHNOLOGIES INC.	
XX	Wright JA, Young AH, Lee YS;	
PA	WPI; 2000-023357/02.	
XX	Antisense oligonucleotides that inhibit neuropilin expression, useful for	
XX	treating cancer.	
FT	Claim 4; Page 16; 57pp; English.	
PS	Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit	
XX	human neuropilin expression. The antisense oligonucleotides can be used	
CC	to inhibit the growth or metastasis of a mammalian tumor and inhibit	
CC	neovascularisation. The oligonucleotides may be used to treat various	
CC	forms of cancers or tumors, such as sarcomas, melanomas, adenomas,	
CC	carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of	
CC	the mouth, throat, larynx and lung, genitourinary cancers such as	

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
 CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
 CC cancer, head and neck cancers, and nervous system cancers, as well as  
 CC benign lesions such as papillomas. The methods may be used to treat  
 CC neovascularisation disorders such as diabetic retinopathy, and  
 CC retinopathy of prematurity and age related macular degeneration  
 XX  
 SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCGAGA 20  
 |||||  
 DB 1 GTGCCGACGTGGAGCCGAGA 20

RESULT 2  
 ADA74692

ID ADA74692 standard; DNA; 20 BP.

AC ADA74692;

DT 20-NOV-2003 (first entry)

DE GT1610 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
 KW cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;  
 KW GT1610; antisense; human; ss.

OS Homo sapiens.

PN US2003083274-A1.

PD 01-MAY-2003.

PF 22-APR-1999; 99US-00296264.

PR 23-APR-1998; 98US-0082791P.

PA (WRIGHT) WRIGHT J A.

PA (YOUNG) YOUNG A H.

PA (LEBY/) LEE Y S.

PI Wright JA, Young AH, Lee YS;

DR WPI; 2003-576622/54.

PT New antisense oligonucleotide that inhibits neuropilin expression, useful  
 PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
 PT mammalian tumor.

PS Claim 1, Page 5; 27pp; English.

CC The invention relates to a novel antisense oligonucleotide that inhibits  
 CC the expression of neuropilin, also known as VEGF165R (vascular  
 CC endothelial growth factor receptor). The oligonucleotide of the invention  
 CC demonstrates cytostatic activity and may be useful for inhibiting the  
 CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in  
 CC mammals. Furthermore, the oligonucleotide may be utilised during gene  
 CC therapy. The current sequence is that of the GT1610 antisense  
 CC oligonucleotide of the invention which is targeted to human neuropilin  
 CC mRNA.

SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCGAGA 20

DB 1 GTGCCGACGTGGAGCCGAGA 20  
 |||||

RESULT 3

AA97678/c  
 ID AA97678 standard; DNA; 21 BP.

AC AA97678;

DT 18-NOV-2004 (revised)

DT 06-JUN-2001 (first entry)

DE Human gene single nucleotide polymorphism #2439.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
 KW polymorphism; vascular disease; coronary artery disease; forensics;  
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
 KW pulmonary embolism; paternity test; ds.

OS Homo sapiens.  
 OS Unidentified.

XX Key Location/Qualifiers

FT variation 11  
 FT /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism"

PN W0200118250-A2.

PD 15-MAR-2001.

PF 07-SEP-2000; 2000WO-US024503.

PR 10-SEP-1999; 99US-0153357P.

PR 26-JUL-2000; 2000US-0220947P.

PR 16-AUG-2000; 2000US-0225724P.

PA (MHED ) WHITEHEAD INST BIOMEDICAL RES.

PA (MILL-) MILLENNIUM PHARM INC.

PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JF;

DR WPI; 2001-226749/23.

PT Nucleic acids comprising single nucleotide polymorphisms, useful in  
 PT applications such as forensics, paternity testing, medicine, genetic  
 PT analysis and phenotype correlations to diseases such as diabetes and  
 PT atherosclerosis.

PS Example; Page 213; 242pp; English.

CC The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided  
 CC in the specification. In particular, the method can be used in the  
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and  
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
 CC useful in forensics, paternity testing, genetic analysis and phenotype  
 CC correlations to diseases. The present sequence is an example of one of  
 CC the human gene SNPs shown in the specification

CC Revised record issued on 18-NOV-2004 : The variation feature was  
 CC incorrectly given a capital V

SQ Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 4; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGACCCA 18  
|||  
Db 18 GTGCCGACGTGGACCCA 1

## RESULT 4

AC190367/c  
ID AC190367 standard; DNA; 25 BP.

AC AC190367;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 90358.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFY-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 90358; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridization to a DNA library,  
CC in analysis of genetic variation or in hybridization of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridizing at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridization. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridization, in Southern, Northern or dot-  
CC blot hybridization to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 9; Length 25;

Best Local Similarity 85.0%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGACCCA 20  
|||  
Db 1 GTGCCGACGTGGACCCA 20

Db 23 GTGCCGACGTGTACCGAGA 4

## RESULT 5

ACK25958/c  
ID ACK25958 standard; DNA; 25 BP.

AC ACK25958;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 125939.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFY-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 125939; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridization to a DNA library,  
CC in analysis of genetic variation or in hybridization of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridizing at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridization. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridization, in Southern, Northern or dot-  
CC blot hybridization to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 4 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 9; Length 25;

Best Local Similarity 84.2%; Pred. No. 4.9e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGACCCA 20  
|||  
Db 25 TGACGACGTGAGACCCA 7

RESULT 6  
AB272759/C  
ID AB272759 standard; DNA; 60 BP.  
XX  
AC AB272759;  
XX  
DT 09-APR-2003 (first entry)  
XX  
DE Linker oligonucleotide SEQ ID NO:162.  
XX  
KW High throughput assay system; nucleic acid detection; anchor; target;  
KM linker; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003002750-A2.  
XX  
PD 09-JAN-2003.  
XX  
PF 26-JUN-2002; 2002WO-US020039.  
XX  
PR 26-JUN-2001; 2001US-00888413.  
XX  
PA (HIGH-) HIGH THROUGHPUT GENOMICS INC.  
XX  
PI Krie RM, Felder S;  
XX  
DR WPI; 2003-201508/19.  
XX  
PT Detecting nucleic acid target in sample by using combination comprising  
PT multiple regions each of which has two different loci of anchors in  
PT association with a bifunctional linker that has portion specific for  
PT anchor.  
XX  
PS Example 30; Page 116; 129pp; English.  
XX  
XX The present invention describes a method for detecting a nucleic acid  
CC target (T) in a sample (S). The method involves: (a) contacting (S) which  
CC may comprise the target(s) with a nuclease protection fragment(s) (I)  
CC specific for and which binds to the target(s), exposing the (S) to a  
CC nuclease effective to digest remaining single stranded nucleic acid, and  
CC then contacting the resultant (S) with a combination (II) which  
CC comprises, before addition of (S), a surface comprising multiple  
CC spatially discrete regions, at least two of which are substantially  
CC identical, each region comprising at least two different loci of anchors,  
CC the anchors at each locus, each in association with a bifunctional linker  
CC which has a first portion that is specific for the anchor, and a second  
CC portion that comprises a probe which is specific for one of the (I),  
CC under conditions effective for the (I) to bind to the combination, where  
CC two or more of the anchors located at a first locus of a region are in  
CC association with different bifunctional linkers, having different target  
CC specificities; and (b) detecting the bound protection fragment(s), and  
CC where the regions are tubes, and the loci of anchors are arranged in a  
CC linear array in the tubes. Such an assay can be termed a multi array  
CC plate screen (MAPs) method or assay. When the probes are  
CC oligonucleotides, the MAPs can be used for diagnosing the presence of  
CC genetic variations or detects e.g. polymorphisms or specific mutations  
CC associated with disease such as cystic fibrosis or pathogenic organisms.  
CC When the probes are antigen binding molecules, the assays can be used for  
CC screening variant proteins or protein expression patterns. The assay can  
CC also be used for mapping expressed sequence tags (ESTs). AB272599 to  
CC AB272762, and AB256911, represent sequences used in the exemplification  
CC of the present invention  
XX  
SQ Sequence 60 BP; 16 A; 14 C; 19 G; 11 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 8; Length 60;  
Best Local Similarity 84.2%; Pred. No. 4.9e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCGACGTGGAGCCAG 19  
||||| ||||| |||||

DB 48 GTGCCTACGTGCACTCAG 30  
RESULT 7  
ACK26420  
ID ACK26420 standard; DNA; 25 BP.  
XX  
AC ACK26420;  
XX  
DT 14-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 126401.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KM genetic variation; diallelic marker; polymorphism; human;  
KM cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Miltmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 126401; 9pp; English.  
XX  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridization to a DNA library,  
CC in analysis of genetic variation or in hybridization of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridizing at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridization. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying diallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridization, in Southern, Northern or dot-  
CC blot hybridization to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 5 A; 9 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;  
Best Local Similarity 88.2%; Pred. No. 7.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGACGTGGAGCCAGA 20  
||||| ||||| |||||

DB 4 CGGACGTGAGCCAGCA 20

## RESULT 8

AC182748 standard; DNA; 25 BP.

AC182748;

14-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 82739.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

Miltmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 82739; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridization to a DNA library, in analysis of genetic variation or in hybridization of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridizing at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridization. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Sequence 25 BP; 5 A; 7 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;

Best Local Similarity 88.2%; Pred. No. 7.7e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 CCGAGCTGGGACCCAGA 20

7 CCGAGCTGGGACCCAGA 23

## RESULT 9

AAS07631 standard; DNA; 27 BP.

AAS07631;

11-SEP-2003 (revised)

23-OCT-2001 (first entry)

Streptococcus coelicolor mmyTOG promoter PCR primer CR344.

SCP1; ss; methylenomycin cluster; mmc; MmyR; Mmf; MmyTOG; MmfL;

MmR; MmyT; MmyO; MmyG; MmyJ; Mmz; heterologous gene expression;

PCR primer; CR344.

Streptomyces coelicolor.

WO200148228-A1.

05-JUL-2001.

20-DEC-2000; 2000WO-GB004972.

23-DEC-1999; 99GB-00030477.

(PLAN-) PLANT BIOSCIENCE LTD.

Chater KF, Bruton CJ, O'rouke SJ, Wietzorrek AW;

WPI; 2001-425675/45.

Novel expression cassette for expressing a nucleic acid of interest, derived from the regulatory region of methylenomycin gene cluster of SCP1 plasmid of Streptomyces coelicolor A3(2).

Example 11; Page 75; 142pp; English.

The sequence represents a PCR primer used to amplify the promoter mmyTOG from an expression cassette SCP1 (the regulatory region of the methylenomycin cluster (mmc) from Streptomyces coelicolor A3(2)), which encodes the MmyR, Mmf, MmfH, MmfL, MmR, MmyT, MmyO, MmyG, MmyJ and partial Mmr polypeptides) for use as a strong promoter for heterologous gene expression. The expression cassette is useful for expressing a nucleic acid of interest, substantially only when the host cell culture reaches high cell density at or close to the stationary phase of host cell culture. In particular the system is useful in regulating methylenomycin production. Reduced or no expression of the nucleic acid of interest is observed earlier in growth, avoiding toxic effects of some gene products on growth and the system does not require addition of an exogenous inducer. The methylenomycin cluster naturally present on a highly transmissible plasmid permits properly regulated expression in diverse Streptomyces host and the expression is driven by a strong promoter, leading to high yield of the desired end product. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 27 BP; 3 A; 12 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 4; Length 27;

Best Local Similarity 88.2%; Pred. No. 7.7e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GCCGACGCGGACCCG 19

3 GCCGACGCGGACCCG 19

## RESULT 10

AAX83785 standard; DNA; 28 BP.

AAX83785;

06-SEP-1999 (first entry)

```
DE PmeI restriction endonuclease PCR primer PmeI-IP1.
XX
XX PmeI: restriction endonuclease; modification methylase;
KM recombinant DNA technique; molecular cloning; gene characterization;
KM Pseudomonas mendocina; PCR primer; ss.
XX
OS Synthetic.
OS Pseudomonas mendocina.
XX
XX EP91835-A2.
XX
XX 28-JUL-1999.
XX
XX 24-NOV-1998; 98BP-00309629.
XX
XX 24-NOV-1997; 97US-00976703.
XX
XX (NEW) NEW ENGLAND BIOLABS INC.
XX
XX Chang Z, Morgan RD;
PI
XX WPI, 1999-397163/34.
XX
XX New restriction endonuclease useful in recombinant DNA techniques.
PT
XX Example 1; Page 9; 28pp; English.
XX
XX The present sequence represents a PCR primer for the 27 kD Pseudomonas
CC endonuclease PmeI restriction endonuclease protein. The PmeI restriction
CC endonuclease is used to cut DNA in the middle of the site GTTTAAC
CC between the third T and the first A, to produce blunt ends. The PmeI
CC restriction endonuclease is therefore useful in recombinant DNA
CC techniques such as molecular cloning and gene characterization
XX
XX Sequence 28 BP; 5 A; 7 C; 10 G; 6 T; 0 U; 0 Other;
SQ
Query Match 69.0%; Score 13.8; DB 2; Length 28;
Best Local Similarity 88.2%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TCCGACGTGGAGCCCA 18
DB 19 TCCGACGTGGAGCCCA 3
RESULT 11
AAL34511/c
ID AAL34511 standard; DNA; 50 BP.
XX
XX AAL34511;
AC
XX
DT 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #7719.
DE
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KM complement related protein; cytochrome; kinase; cytokine; interferon;
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM multifactorial disease; autoimmune disease; infection;
KM nervous system disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200147944-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 28-DEC-2000; 2000WO-US035498.
PF
XX
XX 28-DEC-1999; 99US-0173419P.
PR
```

```
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
PI
XX WPI, 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
XX Claim 1; Page 3620; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amyloses, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
XX Sequence 50 BP; 7 A; 15 C; 17 G; 11 T; 0 U; 0 Other;
SQ
Query Match 69.0%; Score 13.8; DB 4; Length 50;
Best Local Similarity 88.2%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 GCCGACGTGGAGCCAG 19
DB 26 GCCGACGTGGAGCCAG 10
RESULT 12
ADN00075
ID ADN00075 standard; DNA; 55 BP.
XX
XX ADN00075;
AC
XX
DT 15-JUL-2004 (first entry)
XX
XX Human FCER2 (CD23) single nucleotide polymorphism-containing DNA 24.
DE
XX
XX variation; drug sensitivity; chronic obstructive pulmonary disease; COPD;
KM asthma; depression; corticosteroid; beta-agonist; human; SNP;
KM single nucleotide polymorphism; ds; FCER2; CD23.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH variation 26
FT /*tag= a
FT /label= Single nucleotide polymorphism (SNP)
XX
XX WO2004033650-A2.
PN
XX
XX 22-APR-2004.
PD
XX
XX 08-OCT-2003; 2003WO-US031917.
PF
XX
XX 08-OCT-2002; 2002US-0416969P.
PR
XX
XX (BGM) BRIGHAM & WOMEN'S HOSPITAL INC.
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XX XX Weles ST, Tantistira K;
XX XX WPI; 2004-364864/34.
XX XX
XX XX Use of sequence variations in candidate pathway genes for assessing
PT sensitivity to therapeutic agents, e.g. corticosteroids or beta-agonists,
PT in a subject with chronic obstructive pulmonary disease, asthma or
PT depression.
XX XX
XX XX Claim 54; SEQ ID NO 256; 212pp; English.
XX XX
XX XX The invention relates to a novel use for sequence variations in candidate
CC pathway genes for assessing sensitivity to a therapeutic agent in a
CC subject with chronic obstructive pulmonary disease (COPD), asthma or
CC depression. The sequence variations in candidate pathway genes of the
CC invention may be useful for assessing sensitivity to a therapeutic
CC agent, such as corticosteroids or beta-agonists, in a subject with COPD,
CC asthma or depression. The current sequence is that of a human FCER2
CC (CD23) SNP (single nucleotide polymorphism)-containing DNA of the
CC invention.
XX XX
XX XX Sequence 55 BP; 6 A; 11 C; 24 G; 12 T; 0 U; 2 Other;
SQ
XX XX
Query Match 69.0%; Score 13.8; DB 12; Length 55;
Best Local Similarity 78.9%; Pred. No. 7.6e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 2 TGCCGACGTGGAGCCAG 20
DB 18 TGCAGCGCGGAGCTCAGA 36
RESULT 13
ABN29579
ID ABN29579 standard; DNA; 65 BP.
XX XX
AC ABN29579;
XX XX
DT 15-JUL-2002 (first entry)
XX XX
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2327.
XX XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX XX
OS Rattus norvegicus.
XX XX
PN WO200210449-A2.
XX XX
PD 07-FEB-2002.
XX XX
PF 20-JUL-2001; 2001WO-1B001903.
XX XX
PR 28-JUL-2000; 2000US-0221607P.
XX XX
PR 02-MAY-2001; 2001US-0287724P.
XX XX
PA (COMP-) COMPUGEN INC.
XX XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX XX
XX WPI; 2002-257383/30.
XX XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX XX
XX Example 1; SEQ ID NO 2327; 47pp; English.
XX XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC )transcriptome comprises messenger RNAs transcribed from multiple
```

```
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX XX
XX XX Sequence 65 BP; 14 A; 14 C; 18 G; 19 T; 0 U; 0 Other;
SQ
XX XX
Query Match 69.0%; Score 13.8; DB 6; Length 65;
Best Local Similarity 88.2%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 GCCGACGTGGAGCCAG 19
DB 23 GCAGACGTGGAGCCAG 39
RESULT 14
ACT190366/c
ID ACT190366 standard; DNA; 25 BP.
XX XX
AC ACT190366;
XX XX
DT 14-OCT-2003 (first entry)
XX XX
DE Human microarray DNA oligonucleotide SEQ ID NO 90357.
XX XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX XX
OS Homo sapiens.
XX XX
PN US2003104410-A1.
XX XX
PD 05-JUN-2003.
XX XX
PF 15-MAR-2002; 2002US-00098263.
XX XX
PR 16-MAR-2001; 2001US-0276759P.
XX XX
PA (AFY-) AFFYMETRIX INC.
XX XX
PI Miltmann MP;
XX XX
XX WPI; 2003-567953/53.
XX XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX XX
XX Claim 1; SEQ ID NO 90357; 9pp; English.
XX XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
```

CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying allelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX  
SQ Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 9; Length 25;  
Best Local Similarity 80.0%; Pred. No. 9.6e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGAGCCGAGA 20  
DB 23 GTGCCGACGTGGAGCCGAGA 4

## RESULT 15

AAK23277 standard; DNA; 27 BP.

AAK23277;

11-JUN-1999 (first entry)

DE H. vulgare cysteine protease PCR primer GSPL.

XX Cysteine protease; barley; transgenic plant; disease resistance;  
KW prevention; treatment; infection; stress; temperature; drought; salt;  
KW wound; root-specific expression; antimicrobial; antistress;  
KW anti-wounding; PCR primer; ss.

XX Synthetic.

OS Hordeum vulgare.

XX WO9910500-A1.

PD 04-MAR-1999.

XX 21-AUG-1998; 98WO-EP005339.

XX 26-AUG-1997; 97DE-01037118.

PR 22-JAN-1998; 98DE-01002384.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Schlichter U, Steinbiss H, Antoniw J;

XX WPI; 1999-204668/17.

DR Nucleic acid encoding plant cysteine protease - that increases resistance  
PT to injury and infection.

XX Example 5; Page 71; 81pp; German.

XX This invention describes a novel Hordeum vulgare cysteine protease which  
CC is used to produce transgenic plants with (a) increased or reduced  
CC expression of protease or (b) increased resistance to disease  
CC (particularly prevention of infection) or other stress  
CC factors such as extreme temperatures, drought, salt or wounding. The

CC invention also describes a regulatory region which is used to provide  
CC root-specific expression of heterologous DNA following infection/injury  
CC of roots. The products of the invention have antimicrobial, antistress  
CC and anti-wounding activity in plants

XX Sequence 27 BP; 6 A; 6 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 2; Length 27;  
Best Local Similarity 80.0%; Pred. No. 9.6e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGAGCCGAGA 20  
DB 6 GTGTGACCTGCGAGCCGAGA 25

Search completed: December 24, 2005, 12:29:04  
Job time : 173.4 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds  
(without alignments)  
595.256 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20  
Sequence: 1 gtgcgcagctgtgcacccaga 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	74	9	BH215436 1006027A1
2	14.2	71.0	82	11	CR056878 Reverse s
3	13.8	69.0	57	10	CG718544 1119053B0
4	13.8	69.0	91	1	AA837667 cd73h03.s
5	13.6	68.0	49	10	CL520524 DA17C01.F
6	13.6	68.0	75	10	CG627915 OST338592
7	13.6	68.0	91	1	AA930982 y79f05.r
8	13.4	67.0	60	9	AZ776503 2M0010U11
9	13.2	66.0	49	10	CL520524 DA17C01.F
10	13.2	66.0	50	1	AU103727 AU103727
11	13.2	66.0	51	9	AZ438521 1M0228112
12	13.2	66.0	67	10	CG503103 OST49376
13	13.2	66.0	68	9	CG326401 XN749.Bay
14	13.2	66.0	75	10	BX287246 Arabidops
15	13.2	66.0	79	10	CL903354 RR8310.Ba
16	13.2	66.0	83	10	CM882832 BGA521.Ba
17	13.2	66.0	84	10	CM509348 BGA296.Ba
18	13.2	66.0	88	5	BQ756506 EBem09.SQ
19	13.2	66.0	89	9	CC325628 RRH312.Ba
20	13.2	66.0	93	9	CC325627 RRH312.Ba
21	13.2	66.0	95	9	AZ653293 1M0526G21
22	12.8	64.0	67	2	BG327801 602426812

23	12.8	64.0	67	10	CG506889	CG506889 OST56627
24	12.8	64.0	76	6	CD028849	CD028849 mgny005xc
25	12.8	64.0	77	10	CG733899	CG733899 111916G0
26	12.8	64.0	88	1	AU077180	AU077180 AU077180
27	12.8	64.0	89	1	AA094815	AA094815 cpl650..se
28	12.8	64.0	93	4	AK211710	AK211710 Mus muscu
29	12.6	63.0	25	8	CK001203	CK001203 iv39f11.b
30	12.6	63.0	39	1	AJ922836	AJ922836 AJ922836
31	12.6	63.0	44	10	CZ471572	CZ471572 d00396-3P
32	12.6	63.0	45	10	AG218255	AG218255 Drosoph11
33	12.6	63.0	50	1	AU106651	AU106651 AU106651
34	12.6	63.0	50	1	AU106652	AU106652 AU106652
35	12.6	63.0	50	1	AU106653	AU106653 AU106653
36	12.6	63.0	50	1	AU106654	AU106654 AU106654
37	12.6	63.0	50	1	AU106658	AU106658 AU106658
38	12.6	63.0	50	1	AU106659	AU106659 AU106659
39	12.6	63.0	50	1	AU106661	AU106661 AU106661
40	12.6	63.0	50	1	AU106662	AU106662 AU106662
41	12.6	63.0	50	1	AU106663	AU106663 AU106663
42	12.6	63.0	50	1	AU106664	AU106664 AU106664
43	12.6	63.0	50	1	AU106668	AU106668 AU106668
44	12.6	63.0	50	1	AU106670	AU106670 AU106670
45	12.6	63.0	50	1	AU106674	AU106674 AU106674

#### ALIGNMENTS

RESULT 1  
LOCUS BH215436  
DEFINITION 1006027A1.2SL.Y2 1006 - Rescuemu Grid G Zea mays genomic, genomic survey sequence.  
ACCESSION BH215436  
VERSION BH215436.1 GI:16806094  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 74)  
Maize genomic sequences found using engineered Rescuemu transposon  
REFERENCE  
AUTHORS Walbot V.  
TITLE Unpublished (2001)  
JOURNAL  
COMMENT  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1006027 row: 42  
Class: transposon-tagged.  
Location/Qualifiers  
1..74  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cullivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/label\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - Rescuemu Grid G"  
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmbd.iastate.edu' and follow the links for



## High quality sequence stop: 1.

FEATURES  
Location/Qualifiers

1..91

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1373621"

/sex="female"

/tissue\_type="ovary"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Ov2"

/note="Vector: PAMPI0; mRNA made from invasive ovarian tumor, cDNA made by oligo-dt priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

## ORIGIN

Query Match 69.0%; Score 13.8; DB 1; Length 91;

Best Local Similarity 88.2%; Pred. No. 7.3e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GCCGACGTGGAGCCGAC 19

DB 30 GACGGCGTGGAGCCGAC 46

RESULT 5  
CLUS20524/c

LOCUS CLUS20524 49 bp DNA linear GSS 02-APR-2004  
DEFINITION DA17C01 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines

Oryza sativa (japonica cultivar-group) genomic, genomic survey  
sequence.

ACCESSION CLUS20524.1 GI:46147324  
VERSION CLUS20524.1  
KEYWORDS GSS.

SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota: Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 49)

REFERENCE Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanel, P., Piegou, B., Broc, G., Regard, F., Bourgeois, E., Meynard, D., Perin, C., Ghesquiere, A., Delenry, M., Glaszmann, J. C. and Guiderdoni, B.

TITLE High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics

JOURNAL Plant J. (2004) In press

COMMENT Contact: Guiderdoni  
IMR PTA Biotrop program

CIRAD  
TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE  
Tel: 33467615629  
Fax: 33467615605

Email: emmanuel.guiderdon@cirad.fr  
Class: T-DNA tagged.

FEATURES  
Location/Qualifiers

1..49

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="genomic DNA"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone\_lib="Flanking Sequence Tag of Oryza sativa T-DNA insertion lines"

/note="PCR was performed on DNA of primary transformants of Oryza sativa plants. The DNA fragment(s) resulting of PCR were directly sequenced from the left border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display is available from June 2004 at <http://genoplante-info.infobiogen.fr/oryzasatline/>.

This sequence has been generated in the framework of the

French plant genomics program Genoplante  
(<http://www.genoplante.org> and  
<http://genoplante-info.infobiogen.fr>).

## ORIGIN

Query Match 68.0%; Score 13.6; DB 10; Length 49;

Best Local Similarity 80.0%; Pred. No. 9.2e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGAGCCGACA 20

DB 40 GGGCCGACGTGGAGCCGACA 21

RESULT 6  
CG627915

LOCUS CG627915 75 bp mRNA linear GSS 02-OCT-2003  
DEFINITION OSTR338592 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSTR338592,  
mRNA sequence.

ACCESSION CG627915  
VERSION CG627915.1 GI:37451764

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 75)

REFERENCE Zambrowicz, B. P., Abidin, A., Ramirez-Solis, R., Richter, L. J., Piggott, J., Beltrando, R. O., Buxton, E. C., Edwards, J., Finch, R. A., Fridlie, C. J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jia, C., Key, B. W., Jr., Klipp, P., Kohlhauf, B., Ma, Z., -Q., Markesich, D., Payne, R., Potter, D. G., Qian, N., Shaw, U., Schrick, J., Shi, Z., -Z., Sparks, M. J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A. T.

TITLE Mki kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

COMMENT Contact: Zambrowicz BP  
OmniBank

Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: [materials@lexgen.com](mailto:materials@lexgen.com)

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.  
Location/Qualifiers

1..75  
/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129Sv/Ev"

/db\_xref="taxon:10090"

/clone="OSTR338592"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 68.0%; Score 13.6; DB 10; Length 75;

Best Local Similarity 80.0%; Pred. No. 9.1e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGAGCCGACA 20

DB 42 GTGCCGACGTGGAGCCGACA 61

RESULT 7  
AA930982

LOCUS AA930982 91 bp mRNA linear EST 23-APR-1998  
DEFINITION VY79F05 r1 Stragene mouse macrophage (H937306) Mus musculus cDNA clone IMAGE:1312449 5' similar to gb:52839 60S RIBOSOMAL PROTEIN L17 (HUMAN);, mRNA sequence.

This sequence has been generated in the framework of the

ACCESSION	AA930982	GI:3079415
VERSION	AA930982.1	GI:3079415
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 91)	
	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucabada,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenger,K.B., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thaisang,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	
TITLE	The WashU-HHMI Mouse EST Project	
JOURNAL	Unpublished (1996)	
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watsn.wustl.edu This clone is available royalty-free through LINTL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:682745 Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 20. Location/Qualifiers	
FEATURES	1..91	
source	/organism="Mus musculus" /mol_type="mRNA" /db_xref="caxon:10090" /clone="IMAGE:1312449" /tissue_type="macrophage" /dev_stage="MEH1-3 cell line" /lab_host="SOLR (kanamycin resistant)" /clone_lib="Stratagene mouse macrophage (#937306)" /note="Organ: blood; Vector: plasmid; SK: Site 1; EcorI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. MEH1-3 cell line. Average insert size: 1.5 kb; Uni-CAP XR Vector: -5' adaptor sequence: 5' GAATTCGGACGACGAGA 3' -3' adaptor sequence: 5' CTCGAGTTTTCCTTTTTCCTTTT 3' "	
ORIGIN		
Query Match	68.0%; Score 13.6; DB 1; Length 91;	
Best Local Similarity	80.0%; Pred. No. 9.1e+04;	
Matches	16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 GTGCCGACGTGGACCCGAGA 20	
Db	21 GTGCAGACTTGTGCCCGAGA 40	
RESULT 8		
LOCUS	AZ776503 60 bp DNA linear GSS 16-FEB-2001	
DEFINITION	2M0010J1F Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGM0010J1 F, genomic survey sequence.	
ACCESSION	AZ776503	
VERSION	AZ776503.1 GI:12904143	
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	
	1 (bases 1 to 60)	
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	
REFERENCE	Mouse whole genome scaffolding with paired end reads from 10kb	
AUTHORS		
TITLE		

JOURNAL  
COMMENT

Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: rdunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0010 row: 5 column: 11  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 60.

FEATURES  
source

Location/Qualifiers

1..60

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGC2W0010J11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1fb="Mouse 10kb plasmid UGCLM library"  
/note="Vector: PWD42nv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2.2 (gil4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 67.0%; Score 13.4; DB 9; Length 60;  
Best Local Similarity 93.3%; Pred. No. 1.1e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCGGACGTGGGACC 16  
|||||  
DB 39 TGCGGACGTGGGACC 25

RESULT 9  
CLS20524 49 bp DNA GSS 02-APR-2004  
LOCUS  
DEFINITION  
DA17C01 Flanking Sequence Tag of Oryza sativa T-DNA insertion line  
Oryza sativa (japonica cultivar-group) genomic, genomic survey  
sequence.  
CLS20524  
CLS20524.1 GI:46147324  
GSS.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 49)  
Sallaud,C., Gay,C., Larmande,P., Bee,M., Piffanelli,P., Piegut,B.,  
Droc,G., Regad,F., Bougeois,E., Meynard,D., Perin,C.,  
Ghesquiere,A., Delenry,M., Glaszmann,J.C. and Guiderdoni,E.

REFERENCE  
AUTHORS

TITLE High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics

JOURNAL Plant J. (2004) In press

COMMENT Contact: Guiderdoni  
UMR PIA Biotrop program

CIRAD  
TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE  
Tel: 33467615629  
Fax: 33467615605  
Email: emmanuel.guiderdoni@cirad.fr  
Class: TDNA tagged.

FEATURES  
source location/Qualifiers  
1..49  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="Nippondare"  
/db\_xref="taxon:39947"  
/clone\_lib="Flanking Sequence Tag of Oryza sativa T-DNA insertion lines"  
/note="PCR was performed on DNA of primary transformants of Oryza sativa plants. The DNA fragment(s) resulting of PCR were directly sequenced from the left border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display is available from June 2004 at <http://genoplante-info.infobiogen.fr/oryzatagline/>. This sequence has been generated in the framework of the French plant genomics program Genoplante (<http://www.genoplante.org> and <http://genoplante-info.infobiogen.fr>."

ORIGIN  
Query Match 66.0%; Score 13.2; DB 10; Length 49;  
Best Local Similarity 83.3%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTGCCAGCTGGAGCCCA 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 25 GGCCCACTGGAGCCCA 42

RESULT 10  
LOCUS AU103727 50 bp mRNA linear EST 28-JAN-2004  
DEFINITION AU103727 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HEP06017, mRNA sequence.  
ACCESSION AU103727  
VERSION AU103727.1 GI:13553248  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
11375929  
Contact: Yutaka Suzuki  
Institute of Virology  
Department of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ms.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.  
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
location/Qualifiers

FEATURES

source 1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="HEP06017"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
Query Match 66.0%; Score 13.2; DB 1; Length 50;  
Best Local Similarity 83.3%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 GCCGACGTGGAGCCAGA 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 30 GCCAAGCTGGAGCTCAG 13

RESULT 11  
LOCUS A2438521/c 51 bp DNA linear GSS 03-OCT-2000  
DEFINITION IM022811R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
clone UGCGIM0228112 R, genomic survey sequence.  
ACCESSION A2438521  
VERSION A2438521.1 GI:10562534  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 51)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0228 row: 1 column: 12  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 51.  
location/Qualifiers  
1..51  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0228112"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0228 row: 1 column: 12  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 51.  
location/Qualifiers

FEATURES  
source

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 51;  
Best Local Similarity 83.3%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TGCCGACGTGGAGCCAG 19  
|||||  
Db 31 TGCCGACGTGGAGCCAG 14

# RESULT 12

CG503103

LOCUS OSTR9376 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSTR9376,  
DEFINITION mRNA sequence.  
ACCESSION CG503103 GI:37278741  
VERSION CG503103  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

# REFERENCE

AUTHORS Zambrowicz,B.P., Abujin,A., Ramirez-Solis,R., Richter,L.J.,  
Piggott,J., Baltranderio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jang,C.,  
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
Payne,R., Porter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
Zhu,Q., Person,C. and Sands,A.T.  
Wnk1 Kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

# TITLE

JOURNAL PubMed  
COMMENT Contact: Zambrowicz BP  
OmiBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

# FEATURES

source  
1..67  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST9376"  
/cell\_type="embryonic stem cell"  
/clone\_1ib="Mus musculus 129Sv/Ev"

# ORIGIN

Query Match 66.0%; Score 13.2; DB 10; Length 67;  
Best Local Similarity 83.3%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTCCGACGTGGAGCCCA 18  
|||||  
Db 29 GTCCGACGTGGAGCCCA 46

RESULT 13  
CC326401/c

LOCUS CC326401 68 bp mRNA linear GSS 16-MAY-2003  
DEFINITION XN749 BayGenomics Gene Trap library pGT2Lxf Mus musculus cDNA, mRNA  
sequence.  
ACCESSION CC326401  
VERSION CC326401.1 GI:30795572  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
1 (bases 1 to 68)  
BayGenomics.  
http://baygenomics.ucsf.edu/  
Unpublished (2001)  
Contact: BayGenomics  
Bay Area Functional Genomics Consortium (BayGenomics)  
Email: info@baygenomics.ucsf.edu  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from BayGenomics. Annotation  
information available from  
http://baygenomics.ucsf.edu/cgi-bin/Baysearch.py?OPTION=EXACTTYPE=CELL\_LINERKEY=XN749  
Class: Gene Trap.

AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1..68  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Ola"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/clone\_1ib="BayGenomics Gene Trap Library pGT2Lxf"  
/note="Vector: pGT2Lxf"

# ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 68;  
Best Local Similarity 83.3%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TGCCGACGTGGAGCCAG 19  
|||||  
Db 64 TGCTGCGTGGAGTCCAG 47

# RESULT 14

BX287246

LOCUS BX287246 75 bp DNA linear GSS 02-APR-2004  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-398F02-017892,  
genomic survey sequence.  
ACCESSION BX287246  
VERSION BX287246.1 GI:2886242  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (chale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicotyledons,  
rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsis.  
1  
Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.  
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
the identification of T-DNA insertion mutants in Arabidopsis  
thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
PUBMED 12874060  
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reis,B., Dekker,K. and  
Weisshaar,B.  
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
JOURNAL 14756321  
PUBMED

REFERENCE  
AUTHORS 3  
Strizhov,N., Li,Y., Rosso,M.G., Viehovever,P., Dekker,K.A. and  
Weishaar,B.  
TITLE High-throughput generation of sequence indexes from T-DNA  
mutagenized Arabidopsis thaliana lines  
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)  
PUBMED 14682050  
REFERENCE 4 (bases 1 to 75)  
AUTHORS Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.  
TITLE Direct Submission  
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer  
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion within the locus defined by BAC clone  
c166. Details on the protocols used for generation of the sequence  
are described in References 1-3. The sequences are generated at the  
MPI for Plant Breeding Research in the context of the GABI-Kat  
project. GABI-Kat is part of the German Plant Genomics program  
designated 'GABI'. Information on line availability can be found  
at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.  
Location/Qualifiers  
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/clone="GK-398P02-017892"  
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/ecotype="Col-0"  
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plants (T1) which were transformed with the T-DNA from  
vector PAC161 (Genbank accession number: AJ537514). The  
lines contain one or more T-DNA insertions. The DNA  
fragment(s) resulting from the PCR were directly sequenced  
to determine the genomic sequence flanking the insertion.  
T-DNA derived sequences were removed."

ORIGIN  
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Best Local Similarity 83.3%; Pred. No. 1.4e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Gy 1 GTGCCGACGTGGACCCA 18  
||| ||||| |||||  
Db 20 GTGCCACGTGGCCCCCA 37

RESULT 15  
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LOCUS RR2600 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA,  
DEFINITION mRNA sequence.  
ACCESSION CL903354  
VERSION CL903354.1 GI:51832700  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 79)  
BayGenomics.  
<http://baygenomics.ucsf.edu/>  
Unpublished (2001)  
Contact: BayGenomics  
Bay Area Functional Genomics Consortium (BayGenomics)  
Email: [info@baygenomics.ucsf.edu](mailto:info@baygenomics.ucsf.edu)  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from BayGenomics. Annotation  
information available from  
[http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL\\_LINE&KEY=RR2600](http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=RR2600)  
Class: Gene Trap.

FEATURES  
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/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Gy 2 TGCCGACGTGGACCCAG 19  
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Db 43 TGCTGGCGTGGACCCAG 26

Search completed: December 24, 2005, 18:28:41  
Job time : 1574 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds  
(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20

Sequence: 1 tgaggtcggtggaagtcgc 20

Scoring table: IDENTITY\_NUC

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications NA.New.\*

1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*  
10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15.2	76.0	25	US-11-121-849-398180	Sequence 398180,
2	13.8	69.0	25	US-11-121-849-319018	Sequence 319018,
3	13.8	69.0	25	US-11-121-849-444612	Sequence 444612,
4	13.8	69.0	25	US-11-121-849-446110	Sequence 446110,
5	13.2	66.0	25	US-11-121-849-219600	Sequence 219600,
6	13.2	66.0	25	US-11-121-849-361208	Sequence 361208,
7	13.2	66.0	25	US-11-121-849-382504	Sequence 382504,
8	13.2	66.0	25	US-11-121-849-430379	Sequence 430379,
9	13.2	66.0	25	US-11-121-849-44457	Sequence 44457,
10	12.8	64.0	25	US-11-121-849-462472	Sequence 462472,
11	12.8	64.0	25	US-11-121-849-509636	Sequence 509636,
12	12.8	64.0	25	US-11-121-849-509636	Sequence 509636,
13	12.8	64.0	25	US-11-121-849-509636	Sequence 509636,
14	12.6	63.0	21	US-10-770-726-31094	Sequence 31094, A
15	12.6	63.0	21	US-10-770-726-31095	Sequence 31095, A
16	12.6	63.0	25	US-11-121-849-71670	Sequence 71670, A
17	12.6	63.0	25	US-11-121-849-71671	Sequence 71671, A
18	12.6	63.0	25	US-11-121-849-71672	Sequence 71672, A
19	12.6	63.0	25	US-11-121-849-71673	Sequence 71673, A
20	12.6	63.0	25	US-11-121-849-72121	Sequence 72121, A
21	12.6	63.0	25	US-11-121-849-197732	Sequence 197732,
22	12.6	63.0	25	US-11-121-849-275097	Sequence 275097,
23	12.6	63.0	25	US-11-121-849-281195	Sequence 281195,

c 24	12.6	63.0	25	US-11-121-849-472861	Sequence 472861,
c 25	12.6	63.0	25	US-11-121-849-670747	Sequence 670747,
c 26	12.6	63.0	32	US-10-939-294A-17649	Sequence 17649, A
c 27	12.6	63.0	32	US-10-939-294A-19547	Sequence 19547, A
c 28	12.6	63.0	36	US-10-893-584-181	Sequence 181, App
c 29	12.4	62.0	25	US-11-121-849-178887	Sequence 178887,
c 30	12.4	62.0	25	US-11-121-849-454693	Sequence 454693,
c 31	12.4	62.0	25	US-11-121-849-454694	Sequence 454694,
c 32	12.4	62.0	25	US-11-121-849-626774	Sequence 626774,
c 33	12.4	62.0	32	US-10-939-294A-15650	Sequence 15650, A
c 34	12.4	62.0	36	US-10-845-413-415	Sequence 415, App
c 35	12.4	62.0	36	US-10-845-413-415	Sequence 415, App
c 36	12.2	61.0	21	US-10-770-726-23690	Sequence 23690, A
c 37	12.2	61.0	21	US-11-069-908-1485	Sequence 1485, App
c 38	12.2	61.0	21	US-11-069-908-1485	Sequence 1485, App
c 39	12.2	61.0	25	US-11-121-849-15659	Sequence 15659, A
c 40	12.2	61.0	25	US-11-121-849-21171	Sequence 21171, A
c 41	12.2	61.0	25	US-11-121-849-221805	Sequence 221805,
c 42	12.2	61.0	25	US-11-121-849-221806	Sequence 221806,
c 43	12.2	61.0	25	US-11-121-849-221973	Sequence 221973,
c 44	12.2	61.0	25	US-11-121-849-229969	Sequence 229969,
c 45	12.2	61.0	25	US-11-121-849-374133	Sequence 374133,

#### ALIGNMENTS

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RESULT 1
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; Sequence 398180, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 398180
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-398180

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TGAGGTGCGGTGGAAGTGC 20
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319018

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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-319018

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGTGCGGGTGAAGT 18
DB 1 GAGTGTGCGGGTGAAGT 17

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; Sequence 444612, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-444612

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGTGCGGGTGAAGT 18
DB 9 GAGTGTGCGGGTGAAGT 25

RESULT 4
US-11-121-849-446110
; Sequence 446110, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
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; SEQ ID NO 446110
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-446110

Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 9 GAGTGTGCGGGTGAAGT 25

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US-11-121-849-219600/c
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219600
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-219600

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGGTGCGGGTGAAGT 18
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US-11-121-849-361208
; Sequence 361208, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 361208
; LENGTH: 25
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; ORGANISM: Homo sapien
US-11-121-849-361208

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
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PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 382504  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-382504

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Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
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Db 8 TGAGTTCGGGTAGAAAT 25

RESULT 8  
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Sequence 430379, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

TITLE OF INVENTION: Microarrays  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121.849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
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LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-430379

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Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 24 TGAGTTCGGGTAGAAAT 7

RESULT 9  
US-11-121-849-541084/C  
Sequence 541084, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
TITLE OF INVENTION: Microarrays  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121.849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 541084  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-541084

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGTGGCGGTGGAAGT 19  
Db 25 GAGTTCGGGTAGAAAT 8

RESULT 10  
US-11-121-849-44457/C  
Sequence 44457, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

TITLE OF INVENTION: Microarrays  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121.849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 44457  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-44457

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGGTGGCGGTGGAAGT 18  
Db 17 AAGTCTGCTGGAAGT 2

RESULT 11  
US-11-121-849-462472  
Sequence 462472, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
TITLE OF INVENTION: Microarrays  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121.849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 462472  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-462472

Query Match 64.0%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGAGTGGCGGTGGA 16  
Db 5 TGAAGTCTGCTGGA 20

RESULT 12  
US-11-121-849-509636  
Sequence 509636, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
TITLE OF INVENTION: Microarrays

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FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 509636
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-509636

Query Match          64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 GGTGCGGGTGAAGTG 19
        |||||  |||  |||
Db      2 GGTGCGGAGAGAGTG 17

RESULT 13
US-11-123-115-60
; Sequence 60, Application US/11123115
; Publication No. US2005026657A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Tzu-Chih
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLY-UNSATURATED FATTY ACIDS BY OLEAGINOUS
; FILE REFERENCE: 4867-0102PUS2
; CURRENT APPLICATION NUMBER: US/11/123,115
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US 60/568,692
; PRIOR FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 60
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Mortierella alpine
; FEATURE:
; NAME/KEY: primer
; LOCATION: (1)..(59)
; OTHER INFORMATION: reverse primer of D12-desaturase gene
US-11-123-115-60

Query Match          64.0%; Score 12.8; DB 7; Length 59;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 GTGCGGGTGAAGTGC 20
        |||||  |||||  |||
Db      36 GTACGTGTGAAGTGC 51

RESULT 14
US-10-770-726-31094
; Sequence 31094, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 31094
; LENGTH: 21
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-31094

Query Match          63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 TGAGTGGCGGTGAAGTG 19
        |||||  |||||  |||
Db      3 TGAGTGCAGCTGGACATG 21

RESULT 15
US-10-770-726-31095
; Sequence 31095, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 31095
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-770-726-31095

Query Match          63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 57.9%; Pred. No. 4.6e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1 TGAGTGGCGGTGAAGTG 19
        |||||  |||||  |||
Db      1 TGAGGUGCAGCUGGACAU 19
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Search completed: December 25, 2005, 04:37:03  
Job time : 135.3 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds

(without alignments)  
739.111 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20

Sequence: 1 gtgcgcagctgggaccacaga 20

Scoring table: IDENTITY\_NUC

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/1/COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5/COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A/COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B/COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H/COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PC/US/COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP/COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE/COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.6	88.0	21	3	US-09-657-472-2443
C 2	14.2	71.0	60	3	US-09-888-413-162
C 3	13.8	69.0	28	2	US-08-976-703-10
C 4	13.6	68.0	25	3	US-09-396-196G-14669
C 5	13.2	66.0	25	3	US-09-396-196G-14668
C 6	13.2	66.0	25	3	US-09-396-196G-26712
C 7	13.2	66.0	33	3	US-09-237-712-41
C 8	13.2	66.0	33	3	US-09-237-712-42
C 9	13.2	66.0	44	3	US-08-829-525-34
C 10	13.2	66.0	44	3	US-08-609-583A-34
C 11	13.2	66.0	44	3	US-08-937-399-34
C 12	13.2	66.0	44	3	US-09-560-639-27
C 13	13.2	66.0	44	3	US-09-310-367-34
C 14	13.2	66.0	44	3	US-09-032-337-34
C 15	13.2	66.0	44	3	US-09-464-231-34
C 16	13.2	66.0	24	3	US-09-513-999C-21236
C 17	12.8	64.0	25	2	US-08-590-674-1
C 18	12.8	64.0	48	3	US-08-509-595B-11
C 19	12.8	64.0	62	2	US-08-658-665-153
C 20	12.8	64.0	62	3	US-08-796-101-129
C 21	12.8	64.0	62	3	US-09-085-273-153
C 22	12.8	64.0	62	3	US-09-916-963-153
C 23	12.8	64.0	20	3	US-08-777-708C-14
C 24	12.6	63.0	20	3	US-08-777-708C-14

C 25	12.6	63.0	20	3	US-09-397-168-92	Sequence 92, Appl
C 26	12.6	63.0	21	2	US-08-480-473B-61	Sequence 61, Appl
C 27	12.6	63.0	21	3	US-08-915-213-61	Sequence 61, Appl
C 28	12.6	63.0	21	3	US-09-235-217-61	Sequence 61, Appl
C 29	12.6	63.0	25	3	US-09-396-196G-98183	Sequence 98183, A
C 30	12.6	63.0	25	3	US-09-396-196G-118801	Sequence 118801, A
C 31	12.6	63.0	25	3	US-09-396-196G-127604	Sequence 127604, A
C 32	12.6	63.0	45	3	US-09-199-737-46	Sequence 46, Appl
C 33	12.6	63.0	45	3	US-09-088-333A-46	Sequence 46, Appl
C 34	12.6	63.0	50	3	US-10-131-827-1442	Sequence 1442, Ap
C 35	12.4	62.0	25	3	US-09-396-196G-13858	Sequence 13858, A
C 36	12.2	61.0	20	3	US-09-561-497-65	Sequence 65, Appl
C 37	12.2	61.0	20	3	US-09-561-497-66	Sequence 66, Appl
C 38	12.2	61.0	23	3	US-08-852-001-29	Sequence 29, Appl
C 39	12.2	61.0	25	3	US-09-396-196G-55452	Sequence 55452, A
C 40	12.2	61.0	34	2	US-08-852-806-11	Sequence 11, Appl
C 41	12.2	61.0	34	3	US-09-163-669-11	Sequence 11, Appl
C 42	12.2	61.0	57	2	US-08-149-097D-25	Sequence 25, Appl
C 43	12.2	61.0	92	3	US-08-973-965-4	Sequence 4, Appl
C 44	12.2	61.0	93	3	US-08-973-965-5	Sequence 5, Appl
C 45	12.2	61.0	93	3	US-08-973-965-38	Sequence 38, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-657-472-2443/C
; Sequence 2443, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolz, Stacey
; APPLICANT: Daley, George O.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2443
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-2443

Query Match      88.0%; Score 17.6; DB 3; Length 21;
Best Local Similarity 94.4%; Pred. No. 36;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTGCCGAGTGGACCA 18
Db      18 GTGCCGAGTGGACCA 1

RESULT 2
US-09-888-413-162/C
; Sequence 162, Application US/09888413
; Patent No. 6759198
; GENERAL INFORMATION:
; APPLICANT: KRIS, RICHARD M.
; APPLICANT: FIELDER, STEPHEN
; TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
; FILE REFERENCE: NEOGEN-1 P4
```

; CURRENT APPLICATION NUMBER: US/09/888,413  
; CURRENT FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: 09/337,325  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/218,166  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 09/109,076  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/068,291  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 162  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-888-413-162  
Query Match 71.0%; Score 14.2; DB 3; Length 60;  
Best Local Similarity 84.2%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GTCCGACGTGGAGCCAG 19  
Db 48 GTGCTACTGTGCACCTCAG 30  
RESULT 3  
US-08-976-703-10/c  
; Sequence 10, Application US/08976703  
; Patent No. 5945288  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, ZHIYU  
; APPLICANT: MORGAN, RICHARD D.  
; TITLE OF INVENTION: METHOD FOR CLONING AND  
; TITLE OF INVENTION: PRODUCING THE PmeI RESTRICTION ENDONUCLEASE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: New England Biolabs, Inc.  
; STREET: 32 Tozer Road  
; CITY: Beverly  
; STATE: MA  
; COUNTRY: US  
; ZIP: 01915  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/976,703  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Gregory D  
; REGISTRATION NUMBER: 30901  
; REFERENCE/DOCKET NUMBER: NEB-132  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 978-927-5054  
; TELEFAX: 978-927-1705  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA  
US-08-976-703-10  
Query Match 69.0%; Score 13.8; DB 2; Length 28;  
Best Local Similarity 88.2%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 TGCCGACGTGGAGCCCA 18  
Db 19 TGCCGACGTGGATCCA 3  
RESULT 4  
US-09-396-196G-14669/c  
; Sequence 14669, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14669  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-14669  
Query Match 68.0%; Score 13.6; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.8e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 GTCCGACGTGGAGCCAGA 20  
Db 24 GAGCCGACATGAGACCCAGA 5  
RESULT 5  
US-09-396-196G-14668/c  
; Sequence 14668, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14668  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-14668  
Query Match 66.0%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 GCCGACGTGGAGCCAGA 20

Db 24 GCCGACATAGAACCCAGA 7

## RESULT 6

US-09-396-196G-26712/c  
; Sequence 26712, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26712  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-26712

## Query Match

Best Local Similarity 66.0%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCCAG 19

Db 20 TGCGCATGTAGACCCAG 3

## RESULT 7

US-09-237-712-41  
; Sequence 41, Application US/09237712  
; Patent No. 6180391  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, WILLIAM C.  
; TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS  
; TITLE OF INVENTION: GENES IN E. COLI  
; FILE REFERENCE: A-518  
; CURRENT APPLICATION NUMBER: US/09/237,712  
; CURRENT FILING DATE: 1999-01-26  
; EARLIER APPLICATION NUMBER: 60/072,794  
; EARLIER FILING DATE: 1998-01-28  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: oligonucleotide  
US-09-237-712-41

## Query Match

Best Local Similarity 66.0%; Score 13.2; DB 3; Length 33;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCCAG 19

Db 12 TGCTAGCTGGGCTCTAG 29

## RESULT 8

US-09-237-712-42/c  
; Sequence 42, Application US/09237712  
; Patent No. 6180391  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, WILLIAM C.  
; TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS  
; TITLE OF INVENTION: GENES IN E. COLI

## FILE REFERENCE: A-518

; CURRENT APPLICATION NUMBER: US/09/237,712  
; CURRENT FILING DATE: 1999-01-26  
; EARLIER APPLICATION NUMBER: 60/072,794  
; EARLIER FILING DATE: 1998-01-28  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: oligonucleotide  
US-09-237-712-42

## Query Match

Best Local Similarity 66.0%; Score 13.2; DB 3; Length 33;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCCAG 19

Db 26 TGCTAGCTGGGCTCTAG 9

## RESULT 9

US-08-829-525-34/c  
; Sequence 34, Application US/0829525  
; Patent No. 6084083  
; GENERAL INFORMATION:  
; APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/829,525  
; FILING DATE: 28-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/609,583  
; FILING DATE: 01-MAR-1996  
; APPLICATION NUMBER: US 08/487,748  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/398,633  
; FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:  
; NAME: Cortuzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-081  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-829-525-34

## Query Match

Best Local Similarity 66.0%; Score 13.2; DB 3; Length 44;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGAGCTGGGACCCA 18  
||| ||| ||| ||| ||| |||  
DB 33 GTGCAGACTTGGGATCCA 16

## RESULT 10

US-08-609-583A-34/C  
; Sequence 34, Application US/08609583A  
; Patent No. 6204371

; GENERAL INFORMATION:

; APPLICANT: Levinson, Douglas A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/609,583A

; FILING DATE: 01-MAR-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,748

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/398,633

; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7853-048

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

; TELEFAX: 212-869-8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 44 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; US-08-609-583A-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;

Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGAGCTGGGACCCA 18  
||| ||| ||| ||| ||| |||  
DB 33 GTGCAGACTTGGGATCCA 16

## RESULT 11

US-08-937-399-34/C

; Sequence 34, Application US/08937399

; Patent No. 6288218

; GENERAL INFORMATION:

; APPLICANT: Levinson, Douglas A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,399

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/609,583

FILING DATE: 01-MAR-1996

APPLICATION NUMBER: US 08/487,748

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/398,633

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-048

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-937-399-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;

Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGAGCTGGGACCCA 18  
||| ||| ||| ||| ||| |||  
DB 33 GTGCAGACTTGGGATCCA 16

## RESULT 12

US-09-560-639-27/C

; Sequence 27, Application US/09560639

; Patent No. 6323334

; GENERAL INFORMATION:

; APPLICANT: Kingsbury, G.

; APPLICANT: Leiby, K.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TREATMENT OF IMMUNE DISORDERS

; FILE REFERENCE: 7853-158

; CURRENT APPLICATION NUMBER: US/09/560,639

; CURRENT FILING DATE: 2000-04-28

; EARLIER APPLICATION NUMBER: 60/155,862

; EARLIER FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 27

; LENGTH: 44

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 3' oligonucleotide

US-09-560-639-27

Query Match 66.0%; Score 13.2; DB 3; Length 44;



Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGGACCCA 18  
Db 33 GTGCAGACTTGGGATCCA 16

## RESULT 13

US-09-310-367-34/C  
; Sequence 34, Application US/09310367  
; Patent No. 6414117  
; GENERAL INFORMATION:  
; APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/310,367  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/829,525  
; FILING DATE: 28-MAR-1997  
; APPLICATION NUMBER: US 08/609,583  
; FILING DATE: 01-MAR-1996  
; APPLICATION NUMBER: US 08/487,748  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/398,633  
; FILING DATE: 03-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-081  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; US-09-310-367-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGGACCCA 18  
Db 33 GTGCAGACTTGGGATCCA 16

RESULT 14  
US-09-032-337-34/C  
; Sequence 34, Application US/09032337  
; Patent No. 6455685  
; GENERAL INFORMATION:

APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,337  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/609,583  
; FILING DATE: 01-MAR-1996  
; APPLICATION NUMBER: US 08/487,748  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/398,633  
; FILING DATE: 03-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; US-09-032-337-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGGACCCA 18  
Db 33 GTGCAGACTTGGGATCCA 16

RESULT 15  
US-09-464-231-34/C  
; Sequence 34, Application US/09464231  
; Patent No. 6562343  
; GENERAL INFORMATION:  
; APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/464,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-464-231-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCGACGTGGGACCA 18
Db 33 GTGCGACTTGGGATCCA 16
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Search completed: December 24, 2005, 18:36:30  
Job time : 49.1 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 : Search time 337.6 Seconds  
(without alignment)  
489.892 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20

Sequence: 1 gtgcgcacgtgaccaccaga 20

Scoring table: IDENTITY\_NUC

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA Main:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-10
2	15.4	77.0	25	10	US-11-036-317-797309
3	15.2	76.0	25	5	US-10-098-263B-90358
4	14.8	74.0	25	8	US-10-719-900-32172
5	14.8	74.0	25	8	US-10-098-263B-125937
6	14.2	71.0	25	5	US-10-098-263B-125939
7	14.2	71.0	25	8	US-10-719-900-149619
8	14.2	71.0	25	8	US-10-719-900-460924
9	14.2	71.0	25	8	US-10-719-900-908051
10	14.2	71.0	25	10	US-11-036-317-153174
11	14.2	71.0	60	3	US-09-888-413-162
12	14.2	71.0	60	8	US-10-865-853-162
13	13.8	69.0	25	5	US-10-098-263B-82739
14	13.8	69.0	25	5	US-10-098-263B-126401
15	13.8	69.0	25	10	US-11-036-317-664199
16	13.8	69.0	25	10	US-11-036-317-797308
17	13.8	69.0	27	7	US-10-168-663-32
18	13.8	69.0	55	7	US-10-681-818-256
19	13.8	69.0	65	3	US-09-908-975-2227
20	13.6	68.0	25	5	US-10-098-263B-90357
21	13.6	68.0	25	7	US-10-719-956-29463
22	13.6	68.0	25	7	US-10-719-956-648937
23	13.6	68.0	25	7	US-10-719-956-648938

24	13.6	68.0	25	7	US-10-719-956-649365	Sequence 649365,
25	13.6	68.0	25	7	US-10-719-956-649366	Sequence 649366,
26	13.6	68.0	25	7	US-10-719-956-649367	Sequence 649367,
27	13.6	68.0	25	8	US-10-719-900-702543	Sequence 702543,
28	13.6	68.0	25	8	US-10-719-900-656352	Sequence 856352,
29	13.6	68.0	25	8	US-10-719-900-943473	Sequence 943473,
30	13.6	68.0	25	8	US-10-719-900-981074	Sequence 981074,
31	13.6	68.0	25	9	US-10-809-189-14669	Sequence 14669, A
32	13.6	68.0	25	9	US-10-956-157-271970	Sequence 271970,
33	13.6	68.0	25	9	US-10-956-157-29487	Sequence 29487,
34	13.6	68.0	25	10	US-11-036-317-728659	Sequence 728659,
35	13.6	68.0	25	10	US-11-036-317-842622	Sequence 842622,
36	13.6	68.0	65	3	US-09-908-975-2070	Sequence 2070, Ap
37	13.6	68.0	65	3	US-09-908-975-2565	Sequence 2565, Ap
38	13.4	67.0	25	5	US-10-098-263B-35524	Sequence 35524, A
39	13.4	67.0	25	8	US-10-719-900-156716	Sequence 156716,
40	13.4	67.0	25	10	US-11-036-317-467428	Sequence 467428,
41	13.4	67.0	25	10	US-11-036-317-797017	Sequence 797017,
42	13.2	66.0	25	5	US-10-098-263B-25231	Sequence 25231, A
43	13.2	66.0	25	5	US-10-098-263B-109368	Sequence 109368,
44	13.2	66.0	25	7	US-10-719-956-181453	Sequence 181453,
45	13.2	66.0	25	7	US-10-719-956-181454	Sequence 181454,

#### ALIGNMENTS

```

RESULT 1
US-09-296-264-10
Sequence 10, Application US/09296264
Publication No. US20030083274A1
GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Alping H.
TITLE OF INVENTION: NEUROPEPTIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
FILE REFERENCE: 032396-043
CURRENT APPLICATION NUMBER: US/09/296,264
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Human
US-09-296-264-10

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GTGCCGACGTGGACCCAGA 20
Db 1 GTGCCGACGTGGACCCAGA 20

RESULT 2
US-11-036-317-797309
Sequence 797309, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174

```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 797309
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-797309
```

```
Query Match          77.0%; Score 15.4; DB 10; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 CCGACGTGGAGCCCA 20
        |||||||
DB      4 CCCAGCTGGAGCCCA 20
```

```
RESULT 3
US-10-098-263B-90358/c
; Sequence 90358, Application US/10098263B
; Publication No. US20030104410A1
```

```
/ GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90358
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-90358
```

```
Query Match          76.0%; Score 15.2; DB 5; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 GTGCCGAGCTGGAGCCCA 20
        |||||||
DB      23 GTGCCGAGCTGGAGCCCA 4
```

```
RESULT 4
US-10-719-900-32172
; Sequence 32172, Application US/10719900
; Publication No. US20050026164A1
```

```
/ GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 32172
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-32172
```

```
Query Match          74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GCCGACGTGGAGCCCA 20
        |||||||
DB      6 GCCGAGTAGAGCCCA 23
```

```
RESULT 5
US-10-719-900-799047
; Sequence 799047, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
```

```
/ APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 799047
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-799047
```

```
Query Match          74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GTGCCGAGCTGGAGCCCA 18
        |||||||
DB      7 GTGCTACTTGGAGCCCA 24
```

```
RESULT 6
US-10-098-263B-125939/c
; Sequence 125939, Application US/10098263B
; Publication No. US20030104410A1
```

```
/ GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 125939
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-125939
```

```
Query Match          71.0%; Score 14.2; DB 5; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 TGCCGAGCTGGAGCCCA 20
        |||||||
DB      25 TGACGACGTAGAGCCCA 7
```

```
RESULT 7
US-10-719-900-149619/c
; Sequence 149619, Application US/10719900
; Publication No. US20050026164A1
```

```
/ GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

SEQ ID NO 149619  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-149619

Query Match 71.0%; Score 14.2; DB 8; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCGACGTGGAGCCGAG 19  
DB 22 GTGCTGATGTGGATCCAG 4

RESULT 8  
US-10-719-900-460924/c  
Sequence 460924, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 460924  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-460924

Query Match 71.0%; Score 14.2; DB 8; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCGACGTGGAGCCGAG 19  
DB 21 GAGCCGATGTGGAGCCGAG 3

RESULT 9  
US-10-719-900-908051  
Sequence 908051, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 908051  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-908051

Query Match 71.0%; Score 14.2; DB 8; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCCGACGTGGAGCCGAG 20  
DB 1 TGTGACTTGGAGCCGAG 19

RESULT 10

US-11-036-317-153174/c  
Sequence 153174, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 153174  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-153174

Query Match 71.0%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCCGACGTGGAGCCGAG 20  
DB 20 TACCGACGTGAGACCTGGA 2

RESULT 11

US-09-888-413-162/c  
Sequence 162, Application US/09888413  
Publication No. US20050096232A1  
GENERAL INFORMATION:  
APPLICANT: KRIS, RICHARD M.  
APPLICANT: FELDER, STEPHEN  
TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM  
FILE REFERENCE: NEOGEN-1 P4  
CURRENT APPLICATION NUMBER: US/09/888,413  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: 09/337,325  
PRIOR FILING DATE: 1999-06-21  
PRIOR APPLICATION NUMBER: 09/218,166  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 09/109,076  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/068,291  
PRIOR FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 165  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 162  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-888-413-162

Query Match 71.0%; Score 14.2; DB 3; Length 60;  
Best Local Similarity 84.2%; Pred. No. 3.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCGACGTGGAGCCGAG 19  
DB 48 GTGCTTACGTGGACCTCAG 30

RESULT 12  
US-10-865-853-162/c  
Sequence 162, Application US/10865853  
Publication No. US20050026193A1

```
/ GENERAL INFORMATION:
/ APPLICANT: KRIS, RICHARD M.
/ APPLICANT: FELDER, STEPHEN
/ TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
/ FILE REFERENCE: NEOGEN-1 P4
/ CURRENT APPLICATION NUMBER: US/10/865,853
/ CURRENT FILING DATE: 2004-06-14
/ PRIOR APPLICATION NUMBER: US/09/888,413
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 09/337,325
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/218,166
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: 09/109,076
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/068,291
/ PRIOR FILING DATE: 1997-12-19
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 162
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: linker oligonucleotide
US-10-865-853-162
```

```
Query Match      71.0%; Score 14.2; DB 8; Length 60;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 GTGCCGACGTGGGACCCAG 19
         ||||| ||||| |||||
DB      48 GTCCCTACGTGGCACTCAG 30
```

```
RESULT 13
US-10-098-263B-82739
/ Sequence 82739, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 82739
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-82739
```

```
Query Match      69.0%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 CCGACGTGGGACCCAGA 20
         ||||| ||||| |||||
DB      7 CCGACGTGGGACCCAGA 23
```

```
RESULT 14
US-10-098-263B-126401
/ Sequence 126401, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
```

```
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 126401
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-126401
```

```
Query Match      69.0%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 CCGACGTGGGACCCAGA 20
         ||||| ||||| |||||
DB      4 CCGACGTGGGACCCAGA 20
```

```
RESULT 15
US-11-036-317-664199
/ Sequence 664199, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 664199
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-664199
```

```
Query Match      69.0%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 TGCCGACGTGGGACCCA 18
         ||||| ||||| |||||
DB      6 TGCTGCCGTGGGACCCA 22
```

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Search completed: December 25, 2005, 04:14:24
Job time : 337.6 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds  
(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-10  
Perfect score: 20  
Sequence: 1 gtgcgcgacgtgagaccaga 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications NA\_New:\*  
1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	88.0	21	6	US-10-831-997-2443 Sequence 2443, Ap
2	14.4	72.0	25	7	US-11-121-849-262718 Sequence 262718, A
3	13.8	69.0	25	7	US-11-121-849-464323 Sequence 464323, A
4	13.8	69.0	25	7	US-11-121-849-543962 Sequence 543962, A
5	13.6	68.0	25	7	US-11-121-849-25423 Sequence 25423, A
6	13.6	68.0	25	7	US-11-121-849-58450 Sequence 58450, A
7	13.6	68.0	25	7	US-11-121-849-295520 Sequence 295520, A
8	13.4	67.0	25	7	US-11-121-849-437066 Sequence 437066, A
9	13.2	66.0	25	7	US-11-121-849-642465 Sequence 642465, A
10	12.8	64.0	25	7	US-11-121-849-214760 Sequence 214760, A
11	12.8	64.0	25	7	US-11-121-849-228144 Sequence 228144, A
12	12.6	63.0	25	7	US-11-121-849-7040 Sequence 7040, Ap
13	12.6	63.0	25	7	US-11-121-849-40743 Sequence 40743, A
14	12.6	63.0	25	7	US-11-121-849-245344 Sequence 245344, A
15	12.6	63.0	25	7	US-11-121-849-245345 Sequence 245345, A
16	12.6	63.0	25	7	US-11-121-849-536316 Sequence 536316, A
17	12.6	63.0	25	7	US-11-121-849-577016 Sequence 577016, A
18	12.6	63.0	25	7	US-11-121-849-609410 Sequence 609410, A
19	12.6	63.0	25	7	US-11-121-849-623806 Sequence 623806, A
20	12.6	63.0	25	7	US-11-121-849-657376 Sequence 657376, A
21	12.4	62.0	20	6	US-10-949-720-209 Sequence 209, App
22	12.4	62.0	20	7	US-11-006-031-71 Sequence 71, App1
23	12.4	62.0	25	7	US-11-121-849-38318 Sequence 38318, A

C	24	12.4	62.0	25	7	US-11-121-849-98520	Sequence 98520, A
C	25	12.4	62.0	25	7	US-11-121-849-449264	Sequence 449264, A
C	26	12.4	62.0	25	7	US-11-121-849-543564	Sequence 543564, A
C	27	12.4	62.0	25	7	US-11-121-849-636232	Sequence 636232, A
C	28	12.4	62.0	30	6	US-10-857-780-1665	Sequence 1665, Ap
C	29	12.2	61.0	25	7	US-11-121-849-25334	Sequence 25334, A
C	30	12.2	61.0	25	7	US-11-121-849-43541	Sequence 43541, A
C	31	12.2	61.0	25	7	US-11-121-849-507286	Sequence 507286, A
C	32	12.2	61.0	25	7	US-11-121-849-211363	Sequence 211363, A
C	33	12.2	61.0	25	7	US-11-121-849-231409	Sequence 231409, A
C	34	12.2	61.0	25	7	US-11-121-849-232670	Sequence 232670, A
C	35	12.2	61.0	25	7	US-11-121-849-239731	Sequence 239731, A
C	36	12.2	61.0	25	7	US-11-121-849-299167	Sequence 299167, A
C	37	12.2	61.0	25	7	US-11-121-849-388073	Sequence 388073, A
C	38	12.2	61.0	25	7	US-11-121-849-471473	Sequence 471473, A
C	39	12.2	61.0	25	7	US-11-121-849-471822	Sequence 471822, A
C	40	12.2	61.0	25	7	US-11-121-849-517468	Sequence 517468, A
C	41	12.2	61.0	32	6	US-10-939-2944-15292	Sequence 15292, A
C	42	12	60.0	25	7	US-11-121-849-13433	Sequence 13433, A
C	43	12	60.0	25	7	US-11-121-849-13434	Sequence 13434, A
C	44	12	60.0	25	7	US-11-121-849-33500	Sequence 33500, A
C	45	12	60.0	25	7	US-11-121-849-80232	Sequence 80232, A

## ALIGNMENTS

```
RESULT 1
US-10-831-997-2443/c
; Sequence 2443, Application US/10831997
; Publication No. US20050244834A1
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Boyle, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OR INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/10/831,997
; PRIOR APPLICATION NUMBER: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/657,472
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2443
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-831-997-2443

Query Match      88.0%; Score 17.6; DB 6; Length 21;
Best Local Similarity 94.4%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTGCCGACGTGGACCCA 18
Db      18 GTGCCGACGTGGACCCA 1

RESULT 2
US-11-121-849-262718/c
; Sequence 262718, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
```

```

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 262718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-262718

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGGACC 16
Db 19 GTGCCGACCTGGGACC 4

RESULT 3
US-11-121-849-464323/c
; Sequence 464323, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 464323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-464323

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGGACC 19
Db 17 GCCGACGTGGTCCAG 1

RESULT 4
US-11-121-849-543962/c
; Sequence 543962, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 543962
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-543962

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGGACC 17
Db 20 GTGCCGACGTGGGACC 4

RESULT 5
US-11-121-849-25423
; Sequence 25423, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 25423
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-25423

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGGACCAGA 20
Db 4 GTGCCGTGTGGGCCACAGA 23

RESULT 6
US-11-121-849-58450/c
; Sequence 58450, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 58450
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-58450

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGGACCAGA 20
Db 22 GTGCCCAAGTGGGCCACAGA 3

RESULT 7
US-11-121-849-295520
```



```
; Sequence 295520, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 295520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-295520

Query Match      68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGAGCCAGCA 20
    |||||
Db 2 GTGCCGACATGTGCACACAGA 21

RESULT 8
US-11-121-849-437066
; Sequence 437066, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 437066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-437066

Query Match      67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCC 16
    |||||
Db 1 TGCCGACGTGGAGCC 15

RESULT 9
US-11-121-849-642465
; Sequence 642465, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 642465
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-642465

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCCAG 19
    |||||
Db 6 TCCTCATGTGGAGCCAG 23

RESULT 10
US-11-121-849-214760
; Sequence 214760, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 214760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-214760

Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCC 17
    |||||
Db 2 TGCCGCGGTGGAGCC 17

RESULT 11
US-11-121-849-228144
; Sequence 228144, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 228144
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-228144

Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCGACGTGGAGCCAG 19
    |||||
Db 10 CCGACATGGAGCCCTG 25
```

```
RESULT 12
US-11-121-849-7040
; Sequence 7040, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 7040
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-7040

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAG 19
Db 6 GTGCCTAAGTAGATCCAG 24

RESULT 13
US-11-121-849-40743
; Sequence 40743, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 40743
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-40743

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCCCGACGTGGACCCAGA 20
Db 7 TCCCAACCGTAGACACAGA 25

RESULT 14
US-11-121-849-245344
; Sequence 245344, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
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; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 245344
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-245344

Query Match
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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAG 19
Db 5 GAGCTGGCGTTGGACCCAG 23

RESULT 15
US-11-121-849-245345
; Sequence 245345, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 245345
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-245345

Query Match
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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 GAGCTGGCGTTGGACCCAG 19
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Search completed: December 25, 2005, 04:37:04  
Job time : 136.3 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds  
(without alignments)  
1953.383 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20

Sequence: 1 gacccccagggcactcatg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_scs:\*  
11: gb\_ey:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	BD211668	BD211668 Antisense
2	17.6	88.0	21	AX153915	AX153915 Sequence
3	16	80.0	20	BD211677	BD211677 Antisense
4	15.2	76.0	44	108796	108796 Sequence 18
5	15.2	76.0	51	CQ001874	CQ001874 Sequence
6	15.2	76.0	60	CQ537667	CQ537667 Sequence
7	14.4	72.0	39	AR302389	AR302389 Sequence
8	14.2	71.0	51	CQ001873	CQ001873 Sequence
9	14.2	71.0	51	CQ001875	CQ001875 Sequence
10	14.2	71.0	60	CQ562289	CQ562289 Sequence
11	13.8	69.0	51	CQ001876	CQ001876 Sequence
12	13.8	69.0	100	CQ667191	CQ667191 Sequence
13	13.6	68.0	51	CQ002646	CQ002646 Sequence
14	13.6	68.0	59	AR073712	AR073712 Sequence
15	13.6	68.0	60	CQ542906	CQ542906 Sequence
16	13.6	68.0	61	AX085810	AX085810 Sequence
17	13.6	68.0	93	E29108	E29108 Expression
18	13.4	67.0	47	AR288463	AR288463 Sequence

19	13.4	67.0	78	6	BD177575	BD177575 Anti-1gE
20	13.4	67.0	78	6	AR652888	AR652888 Sequence
21	13.4	67.0	78	6	AX404028	AX404028 Sequence
22	13.2	66.0	24	6	AR104159	AR104159 Sequence
23	13.2	66.0	39	6	CQ888497	CQ888497 Sequence
24	13.2	66.0	50	6	CQ002645	CQ002645 Sequence
25	13.2	66.0	51	6	AX117457	AX117457 Sequence
26	13.2	66.0	51	6	AX158478	AX158478 Sequence
27	13.2	66.0	51	8	AB013762	AB013762 Macaca as
28	13.2	66.0	51	8	AB013763	AB013763 Macaca as
29	13.2	66.0	51	8	AB013764	AB013764 Macaca fa
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32	13.2	66.0	75	6	AR128284	AR128284 Sequence
33	13	65.0	50	6	CQ005220	CQ005220 Sequence
34	12.8	64.0	20	6	CQ747755	CQ747755 Sequence
35	12.8	64.0	20	6	AR582069	AR582069 Sequence
36	12.8	64.0	25	6	AR525293	AR525293 Sequence
37	12.8	64.0	25	6	AX937336	AX937336 Sequence
38	12.8	64.0	60	8	HUMHPABA	M3197 Human haplo
39	12.8	64.0	66	6	E03396	E03396 DNA encodin
40	12.8	64.0	69	6	I66412	I66412 Sequence 10
41	12.8	64.0	71	6	CS136211	CS136211 Sequence
42	12.8	64.0	71	6	AX955894	AX955894 Sequence
43	12.8	64.0	87	6	AX135351	AX135351 Sequence
44	12.8	64.0	88	6	CO183413	CO183413 Sequence
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#### ALIGNMENTS

RESULT 1  
BD211668  
LOCUS BD211668 20 bp DNA linear PAT 17-JUN-2003  
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION BD211668.1 GI:33021438  
VERSION JP 2002512793-A/11.  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 20)

AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.  
TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

JOURNAL Patent: JP 2002512793-A 11 08-MAY-2002;  
GENENSENSE TECHNOLOGIES INC

COMMENT OS Homo sapiens (human)  
PN JP 2002512793-A/11  
PD 08-MAY-2002

PF 23-APR-1998 JP 2000545999  
PR 23-APR-1998 US 60/082791

PT JIM A WRIGHT, AIPING H YOUNG, YOON S LEE  
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC

Antisense oligonucleotide sequence of neuropilin and method of using the

CC same for controlling cell proliferation  
FH key Location/Qualifiers

FT source 1..20 Location/Qualifiers

FEATURES 1..20 Location/Qualifiers

source /organism="Homo sapiens (human)"

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
AX153915/c  
LOCUS AX153915 21 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 13 from Patent WO0138576.  
ACCESSION AX153915 GI:14535529  
VERSION AX153915.1 GI:14535529  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.  
TITLE Human single nucleotide polymorphisms  
JOURNAL Patent: WO 0138576-A 13 31-MAY-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
FEATURES  
source 1..21  
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ORIGIN

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Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
BD211677  
LOCUS BD211677 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of  
using the same for controlling cell proliferation.  
ACCESSION BD211677.1 GI:33021447  
VERSION BD211677  
KEYWORDS JP 2002512793-A/20.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 20)  
REFERENCE Wright, J.A., Young, A.H. and Lee, Y.S.  
AUTHORS Antisense oligonucleotide sequence of neuropilin and method of  
TITLE using the same for controlling cell proliferation  
JOURNAL Patent: JP 2002512793-A 20 08-MAY-2002;  
GENESENSE TECHNOLOGIES INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002512793-A/20  
PD 08-MAY-2002  
PF 23-APR-1999 JP 2000545999  
PR 23-APR-1998 US 60/082791  
PT JIM A WRIGHT, AIPING H YOUNG, YOON S LEE  
PC C12N15/09, A61K31/711, A61K48/00, A61P35/00, C12N15/00 CC  
Antisense oligonucleotide sequence of neuropilin and method of  
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source 1..20  
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QY 5 CCCCAGGCATCATGG 20  
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Db 1 CCCCAGGCATCATGG 16

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DEFINITION Sequence 18 from Patent WO 8804690.  
ACCESSION I08796  
VERSION I08796.1 GI:588501  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Bollen, A.J., Gheysen, D., Jacobs, P., Pierard, L. and Collen, D.J.  
JOURNAL Patent: WO 8804690-A 18 30-JUN-1988;  
FEATURES  
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RESULT 5  
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LOCUS CQ001874 51 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 514 from Patent WO0147944.  
ACCESSION CQ001874  
VERSION CQ001874.1 GI:4108506  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1  
REFERENCE Shinkens, R.A. and Leach, M.  
AUTHORS Nucleic acids containing single nucleotide polymorphisms and  
TITLE methods of use thereof  
JOURNAL Patent: WO 0147944-A 514 05-JUL-2001;  
Curegen Corporation (US)  
COMMENT OS Homo sapiens (human)  
PN JP 2002512793-A/20  
PD 08-MAY-2002  
PF 23-APR-1999 JP 2000545999  
PR 23-APR-1998 US 60/082791  
PT JIM A WRIGHT, AIPING H YOUNG, YOON S LEE  
PC C12N15/09, A61K31/711, A61K48/00, A61P35/00, C12N15/00 CC  
Antisense oligonucleotide sequence of neuropilin and method of  
using the  
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RESULT 6  
LOCUS COS37667/c 60 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 7302 from Patent WO0210449.  
ACCESSION COS37667  
VERSION COS37667.1 GI:41503931  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcritpome  
JOURNAL Patent: WO 0210449-A 7302 07-FEB-2002;  
CompuGen Inc. (US)  
FEATURES  
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/organism="Homo sapiens"  
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LOCUS AR302389/c 39 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 16 from patent US 6541224.  
ACCESSION AR302389  
VERSION AR302389.1 GI:31690644  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.  
TITLE Tumor necrosis factor delta polypeptides  
JOURNAL Patent: US 6541224-A 16 01-APR-2003;  
Human Genome Sciences, Inc.; Rockville, MD  
FEATURES  
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Db 32 CCCAGGCGACTCATGG 17

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DEFINITION Sequence 513 from Patent WO0147944.

ACCESSION CQ001873  
VERSION CQ001873.1 GI:41008505  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0147944-A 513 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES  
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Db 30 AGCCTCAGGCGAGTCATGG 48

RESULT 9  
LOCUS CQ001875 51 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 515 from Patent WO0147944.  
ACCESSION CQ001875  
VERSION CQ001875.1 GI:41008507  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0147944-A 515 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES  
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Best Local Similarity 84.2%; Pred. No. 6e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCCCGAGGCACTCATGG 20  
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Db 6 AGCCTCAGGCGAGTCATGG 24

RESULT 10  
LOCUS CQ562289/c 60 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 31924 from Patent WO0210449.  
ACCESSION CQ562289  
VERSION CQ562289.1 GI:41528716  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
REFERENCE 1  
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
JOURNAL variants that populate a transcriptome  
Patent: WO 0210449-A 31924 07-FEB-2002;  
COMPUGEN Inc. (US)  
FEATURES Location/Qualifiers  
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DEFINITION Sequence 516 from Patent WO0147944.  
ACCESSION CQ001876  
VERSION CQ001876.1 GI:41008508  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
REFERENCE 1  
AUTHORS Shinkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
JOURNAL methods of use thereof  
Patent: WO 0147944-A 516 05-JUL-2001;  
CURAGEN Corporation (US)  
FEATURES Location/Qualifiers  
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DB 2 CCTCAGGCGCATCATG 18  
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RESULT 12  
LOCUS CQ667191/c 100 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 12117 from Patent WO02070737.  
ACCESSION CQ667191  
VERSION CQ667191.1 GI:42152617  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1  
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.  
TITLE Compositions and methods relating to osteoarthritis  
JOURNAL Patent: WO 02070737-A 12117 12-SEP-2002;  
Chondrogene Inc. (CA)  
FEATURES Location/Qualifiers  
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QY 1 GACCCCGAGGCACATCA 17  
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RESULT 13  
LOCUS CQ002646/c 51 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 1286 from Patent WO0147944.  
ACCESSION CQ002646  
VERSION CQ002646.1 GI:41009278  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
REFERENCE 1  
AUTHORS Shinkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
JOURNAL methods of use thereof  
Patent: WO 0147944-A 1286 05-JUL-2001;  
CURAGEN Corporation (US)  
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Query Match 68.0%; Score 13.6; DB 6; Length 51;  
Best Local Similarity 80.0%; Pred. No. 1.2e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GACCCCGAGGCACATCATG 20  
| | | | | | | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | | | | | | |  
DB 41 GTCTCCAGGCACATCATG 22  
| | | | | | | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | | | | | | |  
RESULT 14  
LOCUS AR073712 59 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 5 from patent US 5952190.  
ACCESSION AR073712  
VERSION AR073712.1 GI:10000472  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 59)  
AUTHORS Joenje,H. and Jo Ten Poe,J.R.  
TITLE CDNA for farnoni anemia complementation group A  
JOURNAL Patent: US 5952190-A 5 14-SEP-1999;  
FEATURES Location/Qualifiers  
source 1..59

ORIGIN /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 59;  
Best Local Similarity 80.0%; Pred. No. 1.1e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCATGG 20  
Db 27 GACCGACATGGCGCATCATGG 46

RESULT 15

LOCUS COS42906/c 60 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 12541 from Patent WO0210449.  
ACCESSION COS42906  
VERSION COS42906.1 GI:41509170  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.

REFERENCE 1  
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
JOURNAL variants that populate a transcriptome  
Patent: WO 0210449-A 12541 07-FEB-2002;  
Compugen Inc. (US)

FEATURES  
source location/Qualifiers  
1..60  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 60;  
Best Local Similarity 80.0%; Pred. No. 1.1e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCATGG 20  
Db 29 GACCTCCAGGCGCATCAAGG 10

Search completed: December 24, 2005, 14:06:18  
Job time : 585 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds  
(without alignments)  
777.677 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20

Sequence: 1 gacccccagggcactcatg 20

Scoring table: IDENTITY\_NUC

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 21:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001s:\*  
5: geneseqn2002as:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31441
2	18.4	92.0	20	4	ADA74693
3	16.4	82.0	21	4	AAH62112
4	16	80.0	20	3	AAZ31450
5	16	80.0	20	9	ADA74702
6	15.2	76.0	39	12	ADP04390
7	15.2	76.0	51	4	AAI27305
8	15.2	76.0	60	6	ABN34554
9	14.4	72.0	20	12	ADN97884
10	14.4	72.0	20	12	ADN40820
11	14.4	72.0	25	13	ADU06785
12	14.4	72.0	39	6	ABK88692
13	14.4	72.0	39	6	ABK13410
14	14.4	72.0	39	10	ADP72622
15	14.4	72.0	74	13	ADU06792
16	14.2	71.0	51	4	AAI27305
17	14.2	71.0	51	4	AAI27307
18	14.2	71.0	60	6	ABN59176
19	14	70.0	20	12	ADN97873

20	14	70.0	20	12	ADN40809	Adh40809 Human for
21	13.8	69.0	51	4	AAI27308	AAI27308 Human SNP
22	13.8	69.0	80	12	ADN95272	Adm95272 Rat antic
23	13.6	68.0	25	9	ACI97315	Act97315 Human mic
24	13.6	68.0	25	9	ACK08854	ACK08854 Human mic
25	13.6	68.0	41	11	ADM11706	Adm11706 Amplifica
26	13.6	68.0	41	11	ADM11708	Adm11708 Amplifica
27	13.6	68.0	51	4	AAI28078	AAI28078 Human SNP
28	13.6	68.0	59	2	AAV18190	AAV18190 Primer fo
29	13.6	68.0	60	6	ABN39793	Abn39793 Human spl
30	13.6	68.0	61	4	AAI75272	AAI75272 Human ppa
31	13.6	68.0	93	2	AAZ27697	AAZ27697 Intron fir
32	13.4	67.0	20	14	ADY54617	Ady54617 Mouse Myb
33	13.4	67.0	30	14	ABZ80496	Abz80496 PCR prime
34	13.4	67.0	36	10	ABZ80496	Abz80496 Igb cytoC
35	13.4	67.0	40	10	ACA55295	Acas55295 Baculovir
36	13.4	67.0	40	10	ACA55254	Acas55254 Human IGE
37	13.4	67.0	40	10	ACA55251	Acas55251 Human IGE
38	13.2	66.0	24	2	AAK90284	Aax90284 Macrophag
39	13.2	66.0	25	10	ABZ84504	Abz84504 Toxicolog
40	13.2	66.0	31	2	AAK07235	Aax07235 PCR prime
41	13.2	66.0	38	3	AAK82076	Aac82076 p53 PCR p
42	13.2	66.0	39	13	ADT07017	Adt07017 Rabbit pa
43	13.2	66.0	40	10	ADP15475	Adp15475 Human alb
44	13.2	66.0	40	10	ADH21445	Adh21445 Human TR6
45	13.2	66.0	43	10	ADP15481	Adp15481 Human alb

## ALIGNMENTS

RESULT 1	
AAZ31441	
ID	AAZ31441 standard; DNA, 20 BP.
AC	
AAZ31441;	
XX	
DT	07-FEB-2000 (first entry)
XX	
DE	Human neuropilin mRNA specific antisense oligo GTT3611.
XX	
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;
KW	papilloma; diabetic retinopathy; antisense; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	W0955855-A2.
XX	
PD	04-NOV-1999.
XX	
PF	23-APR-1999; 99WO-CA000324.
XX	
PR	23-APR-1998; 98US-0082791P.
XX	
PA	(GENE-) GENESENSE TECHNOLOGIES INC.
XX	
PI	Wright JA, Young AH, Lee YS;
XX	
DR	WPI; 2000-023357/02.
XX	
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for
PT	treating cancer.
XX	
PS	Claim 4; Page 16; 57pp; English.
XX	
CC	Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit
CC	human neuropilin expression. The antisense oligonucleotides can be used
CC	to inhibit the growth of a mammalian tumor and inhibit
CC	neovascularisation. The oligonucleotides may be used to treat various
CC	forms of cancers or tumors, such as sarcomas, melanomas, adenomas,
CC	carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of
CC	the mouth, throat, larynx and lung, genitourinary cancers such as

```
CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration
XX
SQ Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GACCCCGAGGCACTCATGG 20
Db 1 GACCCCGAGGCACTCATGG 20

RESULT 2
ADA74693
ID ADA74693 standard; DNA; 20 BP.
AC ADA74693;
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX GT13611 antisense oligonucleotide targeted to human neuropilin mRNA.
DE
XX neurophilin; VEGF165R; vascular endothelial growth factor receptor;
XX cyclostatic; growth; tumour metastasis; angiogenesis; gene therapy;
XX GT13611; antisense; human; ss.
XX
XX Homo sapiens.
OS
XX US2003083274-A1.
XX
XX 01-MAY-2003.
XX
XX 22-APR-1999; 99US-00296264.
XX
XX 23-APR-1998; 98US-0082791P.
XX
XX (WRIG/) WRIGHT J A.
XX (YOUNG/) YOUNG A H.
XX (LEBY/) LEE Y S.
XX
XX Wright JA, Young AH, Lee YS;
XX
XX WPI; 2003-576622/54.
XX
XX New antisense oligonucleotide that inhibits neuropilin expression, useful
XX for inhibiting growth of mammalian tumor or inhibiting metastasis of a
XX mammalian tumor.
XX
XX Claim 1; Page 5; 27p; English.
XX
XX The invention relates to a novel antisense oligonucleotide that inhibits
XX the expression of neuropilin, also known as VEGF165R (vascular
XX endothelial growth factor receptor). The oligonucleotide of the invention
XX demonstrates cytostatic activity and may be useful for inhibiting the
XX growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
XX mammals. Furthermore, the oligonucleotide may be utilised during gene
XX therapy. The current sequence is that of the GT13611 antisense
XX oligonucleotide of the invention which is targeted to human neuropilin
XX mRNA.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      92.0%; Score 18.4; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GACCCCGAGGCACTCATGG 20
```

```
Db 1 GACCCCGAGGCACTCATGG 20

RESULT 3
AAH62112/c
ID AAH62112 standard; DNA; 21 BP.
XX
XX AAH62112;
AC
XX
XX 09-SEP-2004 (revised)
DT 12-SEP-2001 (first entry)
XX
XX
XX Neuropilin 1 (NRP1) polymorphism containing DNA fragment #13.
XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
XX heart disease; paternity testing; forensic science; ds.
XX
XX Homo sapiens.
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH variation 11
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX MO200138576-A2.
XX
XX 31-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-US031639.
XX
XX 24-NOV-1999; 99US-0167334P.
XX
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
XX
XX WPI; 2001-367705/38.
XX
XX New nucleic acid segments of the human genome, particularly from genes
XX including polymorphic sites, for phenotype correlation, forensics,
XX paternity testing, medicine and genetic analysis.
XX
XX Claim 1; Page 29; 80pp; English.
XX
XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
XX contain single nucleotide polymorphisms (SNPs). A method is included in
XX the invention for analysing a nucleic acid sample, which consists of
XX determining the base occupying any one of the polymorphic sites given in
XX the SNP containing sequences. The nucleotide sequences can be used in the
XX diagnosis or monitoring of diseases, such as cancer, inflammation, heart
XX diseases, diseases of the cardiovascular system, and infection by
XX microorganisms. The oligonucleotides are also useful in the manufacture
XX of a medicament for the treatment or prophylaxis of the diseases, and as
XX a pharmaceutical. SNP containing oligonucleotides are useful in
XX applications such as phenotype correlation, forensics, paternity testing,
XX medicine and genetic analysis
XX
XX Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
SQ Sequence 21 BP; 3 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match      82.0%; Score 16.4; DB 4; Length 21;
Best Local Similarity 94.4%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 CCCCCAGGCACTCATGG 20
Db 21 CCCCCAGGCGCTCATGG 4

RESULT 4
```

AAZ31450  
ID AAZ31450 standard; DNA; 20 BP.  
XX  
AC AAZ31450;  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Human neuropilin mRNA specific antisense oligo GT13621.  
XX  
KM Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;  
KM papilloma; diabetic retinopathy; antisense; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
PM WO9555855-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 23-APR-1999; 99WO-CA000324.  
XX  
PR 23-APR-1998; 98US-0082791P.  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
PI Wright JA, Young AH, Lee YS;  
XX  
DR WPI; 2000-023357/02.  
XX  
PT Antisense oligonucleotides that inhibit neuropilin expression, useful for  
XX treating cancer.  
XX  
PS Claim 4; Page 16; 57pp; English.  
XX  
CC Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit  
CC human neuropilin expression. The antisense oligonucleotides can be used  
CC to inhibit the growth or metastasis of a mammalian tumor and inhibit  
CC neovascularisation. The oligonucleotides may be used to treat various  
CC forms of cancers or tumors, such as sarcomas, melanomas, adenomas, of  
CC carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of  
CC the mouth, throat, larynx and lung, genitourinary cancers such as  
CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
CC cancer, head and neck cancers, and nervous system cancers, as well as  
CC benign lesions such as papillomas. The methods may be used to treat  
CC neovascularisation disorders such as diabetic retinopathy, and  
CC retinopathy of prematurity and age related macular degeneration  
CC  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 80.0%; Score 16; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 5 CCCAGGGGCACTCATGG 20  
DB 1 CCCAGGGGCACTCATGG 16  
XX  
RESULT 5  
ADA74702  
ID ADA74702 standard; DNA; 20 BP.  
XX  
AC ADA74702;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE GT13621 antisense oligonucleotide targeted to human neuropilin mRNA.  
XX  
KM neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
KM cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;  
KM GT13621; antisense; human; ss.  
XX

OS Homo sapiens.  
XX  
PM US2003083274-A1.  
XX  
PD 01-MAY-2003.  
XX  
PF 22-APR-1999; 99US-00296264.  
XX  
PR 23-APR-1998; 98US-0082791P.  
XX  
PA (WRIGHT) WRIGHT J A.  
PA (YOUNG) YOUNG A H.  
PA (LEEY) LEE Y S.  
XX  
PI Wright JA, Young AH, Lee YS;  
XX  
DR WPI; 2003-576622/54.  
XX  
PF New antisense oligonucleotide that inhibits neuropilin expression, useful  
XX for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
XX mammalian tumor.  
XX  
PS Claim 1; Page 5; 27pp; English.  
XX  
CC The invention relates to a novel antisense oligonucleotide that inhibits  
CC the expression of neuropilin, also known as VEGF165R (vascular  
CC endothelial growth factor receptor). The oligonucleotide of the invention  
CC demonstrates cytostatic activity and may be useful for inhibiting the  
CC growth or metastasis of a mammalian tumor and to inhibit angiogenesis in  
CC mammals. Furthermore, the oligonucleotide may be utilized during gene  
CC therapy. The current sequence is that of the GT13621 antisense  
CC oligonucleotide of the invention which is targeted to human neuropilin  
CC mRNA.  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 80.0%; Score 16; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 5 CCCAGGGGCACTCATGG 20  
DB 1 CCCAGGGGCACTCATGG 16  
XX  
RESULT 6  
ADP04390/C  
ID ADP04390 standard; DNA; 39 BP.  
XX  
AC ADP04390;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE PCR primer 1 used to amplify human SRC-1 (PPARdelta coactivator) cDNA.  
XX  
KM transcriptional regulation;  
KM peroxisome proliferator activated receptor delta; PPARdelta;  
KM retinoid X receptor; RXR; cytosolic; antiarteriosclerotic; anti-lipemic;  
KM osteopontin; osteoporosis; colon cancer; arteriosclerosis; PCR; primer;  
KM ss; human; coactivator; SRC-1.  
XX  
OS Homo sapiens.  
XX  
PM JP2004141120-A.  
XX  
PD 20-MAY-2004.  
XX  
PF 28-OCT-2002; 2002JP-00312619.  
XX  
PR 28-OCT-2002; 2002JP-00312619.  
XX  
PA (FUJII) FUJISAWA PHARM CO LTD.  
XX

DR WPI, 2004-382695/36.  
XX Measuring influence of test compound on transcriptional-regulation  
PT activity of peroxisome proliferator activated receptor (PPAR delta), and  
PT comprises contacting test compound with cell expressing PPAR delta, and  
PT measuring signal.  
PS Example 1; SEQ ID NO 9; 30pp; Japanese.  
XX  
CC The invention relates to a novel method of measuring the influence of a  
CC test compound on the transcriptional-regulatory activity of peroxisome  
CC proliferator activated receptor delta (PPARdelta). The method comprises  
CC contacting the test compound with a cell expressing PPARdelta or a  
CC protein functionally equivalent to PPARdelta, retinoid X receptor (RXR)  
CC or a protein functionally equivalent to RXR and a protein which acts as a  
CC co-activator of PPARdelta. Subsequently, the signal generated by the cell  
CC is measured. The method of the invention has cytosstatic,  
CC antiarteriosclerotic, antihypaemic and osteopathic applications and may  
CC be useful for evaluating the influence of a test compound on the  
CC transcriptional-regulatory activity of PPARdelta and for screening a  
CC compound which controls the transcriptional-regulatory activity of  
CC PPARdelta. The PPARdelta regulator may be useful for treating diseases  
CC including osteoporosis, colon cancer and arteriosclerosis. The current  
CC sequence is that of the PCR primer 1 of the invention which was used to  
CC amplify human SRC-1 (PPARdelta coactivator) cDNA.  
XX  
SQ Sequence 39 BP; 8 A; 10 C; 11 G; 10 T; 0 U; 0 Other;  
Query Match 76.0%; Score 15.2; DB 12; Length 39;  
Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GACCCCGAGGCGCATCATGG 20  
DB 32 GTCCCGAGGCGCATCATGG 13  
RESULT 7  
AAL27306  
ID AAL27306 standard; DNA; 51 BP.  
XX  
AC AAL27306;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #514.  
XX  
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US035498.  
XX  
PR 28-DEC-1999; 99US-0173419P.  
XX  
PT 27-DEC-2000; 2000US-00173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkete RA, Leach M;  
XX  
DR WPI, 2001-465210/50.  
XX

PT Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
PS Claim 1; Page 1536; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amyloses, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosis and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
XX  
SQ Sequence 51 BP; 10 A; 18 C; 11 G; 12 T; 0 U; 0 Other;  
Query Match 76.0%; Score 15.2; DB 4; Length 51;  
Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GACCCCGAGGCGCATCATGG 20  
DB 26 GAGCCTCAGGCGCATCATGG 45  
RESULT 8  
ABN34554/C  
ID ABN34554 standard; DNA; 60 BP.  
XX  
AC ABN34554;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO: 7302.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
XX Homo sapiens.  
XX  
OS WO200210449-A2.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB001903.  
XX  
PR 28-JUL-2000; 2000US-0221607P.  
XX  
PT 02-MAY-2001; 2001US-0287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
DR WPI, 2002-257383/30.  
XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
PS Example 1; SEQ ID NO 7302; 47pp; English.  
XX  
XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-

CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 60 BP; 17 A; 14 C; 19 G; 10 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 6; Length 60;  
Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GACCCCGAGGCACTCATG 20  
Db 46 GAGCCTCAGGCGACTCATG 27

RESULT 9  
ADN97884  
ID ADN97884 standard; DNA; 20 BP.  
XX  
AC ADN97884;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Monkey foxhead box O1A sequence inhibitory oligo #3.  
XX  
KM ss; cytosaratic; antidiabetic; foxhead box O1A inhibitor;  
KM forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KM diabetes; H-ras gene; antisense; gene expression; primer.  
XX  
OS Synthetic.  
XX  
PN WO2004031350-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 25-SEP-2003; 2003WO-US030352.  
XX  
PR 26-SEP-2002; 2002US-00260203.  
XX  
PA (AMGE-) AMGEN INC.  
PA (ISIS-) ISIS PHARM INC.  
PI Dobie KM, Bhanot S, Veniant-Elisson M, Lindberg RA, Shutter JR;  
XX  
DR WPI; 2004-330164/30.  
XX  
PT New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.  
XX  
PS Example 25; SEQ ID NO 174; 146bp; English.  
XX  
CC The invention relates to a compound 8-80 nucleobases in length targeted  
CC to a nucleic acid molecule encoding forkhead box O1A, where the compound  
CC is at least 70% complementary to a nucleic acid molecule encoding

CC forkhead box O1A and modulates expression of forkhead box O1A by at least  
CC 10%. The compound is useful for treating an animal having a disease or  
CC condition associated with forkhead box O1A, e.g. a hyperproliferative  
CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This  
CC sequence corresponds to an oligonucleotide targeted to the monkey foxhead  
CC box O1A genes in order to inhibit gene expression.  
XX  
SQ Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 12; Length 20;  
Best Local Similarity 93.8%; Pred. No. 5.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 CCCCCAGGCACTCAT 18  
Db 1 CCGCCAGGCACTCAT 16

RESULT 10  
ADN40820  
ID ADN40820 standard; DNA; 20 BP.  
XX  
AC ADN40820;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Monkey forkhead box O1A DNA antisense oligonucleotide #3.  
XX  
KM Monkey; forkhead box O1A; ss; antisense oligonucleotide;  
KM phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;  
KM 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;  
KM type 2 diabetes; cytosaratic; antidiabetic.  
XX  
OS Primates.  
XX  
PN US2004097459-A1.  
XX  
PD 20-MAY-2004.  
XX  
PF 25-SEP-2003; 2003US-00671074.  
XX  
PR 26-SEP-2002; 2002US-00260203.  
XX  
PA (DOBI/) DOBIE K W.  
PA (BHAN/) BHANOT S.  
PA (VENI/) VENIANT-ELISSON M.  
PA (LIND/) LINDBERG R A.  
PA (SHUT/) SHUTTER J R.  
PI Dobie KM, Bhanot S, Veniant-Elisson M, Lindberg RA, Shutter JR;  
XX  
DR WPI; 2004-389194/36.  
XX  
PT New compounds, particularly antisense oligonucleotides, targeted to a  
PT nucleic acid molecule encoding forkhead box O1A, useful for treating  
PT cancer, or type 2 diabetes.  
XX  
PS Example 25; SEQ ID NO 174; 80bp; English.  
XX

CC The invention relates to a compound targeted to a nucleic acid molecule  
CC encoding the human forkhead box O1A polypeptide. The compound is an  
CC antisense oligonucleotide that specifically hybridises with the nucleic  
CC acid and inhibits expression of the polypeptide. The antisense  
CC oligonucleotide comprises at least one modified internucleoside linkage  
CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,  
CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified  
CC nucleobase comprising a 5-methylcytosine. The antisense compounds are  
CC useful for modulating the expression of the human forkhead box O1A  
CC polypeptide and in preparation of a composition for treating  
CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,  
CC and type 2 diabetes. This sequence represents an antisense  
CC oligonucleotide targeted to DNA encoding the monkey forkhead O1A  
CC polypeptide of the invention.

XX Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;  
SQ Best Local Similarity 72.0%; Score 14.4; DB 12; Length 20;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Query Match  
Best Local Similarity 93.8%; Pred. No. 5.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 CCCCAGGGGCACTCAT 18  
Db 1 CCGCCAGGGCACTCAT 16  
RESULT 11  
ID ADU06785 standard; DNA; 25 BP.  
AC ADU06785;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Mouse GPR4 cDNA probe.  
XX  
KW ss; antiinflammatory; GPR4 signal transduction inhibitor;  
KW neutrophil inflammation disease; signal transduction; GPR4; probe.  
XX  
OS Mus musculus.  
XX  
PN WO2004093912-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 23-APR-2004; 2004WO-JP005930.  
XX  
PR 23-APR-2003; 2003JP-00118432.  
PR 26-FEB-2004; 2004JP-00052191.  
XX  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
XX  
PI Saki M, Nonaka H, Miyaji H, Takahashi C, Manabe H, Hiura N;  
PI Miki I, Abe Y, Sasaki K, Kobatake C, Ichikawa S, Goto A, Suda T;  
XX  
DR WPI; 2004-795424/78.  
XX  
PT Agent comprises nitrogen-containing tricyclic compound, as active  
PT ingredient capable of inhibiting signal transduction function of protein,  
PT useful for treating or preventing neutrophil inflammation disease.  
XX  
PS Example 6; SEQ ID NO 19; 293bp; Japanese.  
XX  
CC The invention relates to a preventive and/or therapeutic agent (P1) of  
CC neutrophil inflammation disease, comprises nitrogen-containing tricyclic  
CC compound, as an active ingredient that is capable of inhibiting signal  
CC transduction function of a protein. (P1) comprises a fully defined  
CC sequence of 362 (S1) amino acids as given in the specification, an  
CC antibody that recognizes (S1) or two fully defined sequence having 365  
CC (S2) amino acids as given in the specification, in which one or more  
CC amino acids are deleted, substituted or added, an oligonucleotide (ON)  
CC complementary to 15-60 continuous bases of a fully defined sequence of  
CC 2932 (S3), 1098 (S4) or 1098 (S5) nucleotides as given in the  
CC specification or its derivative or an oligonucleotide sequence that  
CC hybridizes with (S3)-(S5) under stringent conditions, an antibody (P2)  
CC that specifically recognizes (S1) or (S2), or nitrogen-containing  
CC tricyclic compound of formula (I) or (II) or its quaternary ammonium  
CC salt, as an active ingredient that is capable of inhibiting signal  
CC transduction function of a protein. (P1) is useful for preventing and/or  
CC treating neutrophil inflammation disease. (P2) is useful for producing  
CC (P1). (P1) enables to inhibit GPR4 signal transduction. This sequence  
CC corresponds to a probe for the cDNA encoding the mouse GPR4 signal  
CC transduction protein of the invention. The sequence corresponds to  
CC nucleotides 577-601 of the mouse GPR4 cDNA.  
XX  
SQ Sequence 25 BP; 2 A; 10 C; 5 G; 8 T; 0 U; 0 Other;

Query Match  
Best Local Similarity 72.0%; Score 14.4; DB 13; Length 25;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 CCCCAGGGGCACTCATG 19  
Db 6 CCCCAGGGGCACTCATG 21  
RESULT 12  
ID ABK8692/C  
XX ABK8692 standard; DNA; 39 BP.  
XX  
AC ABK8692;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Human transmembrane activator and CAML-interactor (TACI), PCR primer #2.  
XX  
KW Human; tumour necrosis factor; TNF delta; pulmonary system disorder;  
KW immunoglobulin production; B-cell proliferation; immune system disorder;  
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;  
KW microbial infection; parasitic infection; bone disease; atherosclerosis;  
KW cardiovascular disorder; neurodegenerative disease; wound healing;  
KW graft versus host disease; haematopoietic cell disorder; nephritis;  
KW transmembrane activator and CAML-interactor; TACI; TNF epsilon; PCR;  
KW primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002064829-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 14-JUN-2001; 2001US-00879919.  
XX  
PR 14-MAR-1996; 96US-0016812P.  
PR 12-MAR-1997; 97US-00815783.  
PR 15-JUN-2000; 2000US-0211537P.  
PR 23-OCT-2000; 2000US-0241952P.  
PR 13-DEC-2000; 2000US-0254875P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 23-MAR-2001; 2001US-0277978P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Yu G, Ni J, Gentz RL, Dillon PJ;  
XX  
DR WPI; 2002-556722/59.  
XX  
PT Novel human multimeric tumor necrosis factor delta or epsilon protein  
PT useful for treating disease or disorder of immune system such as  
PT autoimmune disease, immunodeficiency, or cancer of immune system.  
XX  
PS Example 29; Page 115; 143bp; English.  
XX  
CC The present invention relates to the isolation of human tumour necrosis  
CC factor (TNF) delta and TNF epsilon proteins, and the polynucleotide  
CC sequences encoding them. The proteins are useful for modulating  
CC immunoglobulin production or for modulating proliferation of B-cells. The  
CC sequences of the invention are useful for treating diseases or disorders  
CC of the immune system. Such disorders include autoimmune diseases (e.g.  
CC systemic lupus erythematosus (SLE), acquired immunodeficiency syndrome  
CC (AIDS)), cancers of the immune system (e.g. chronic lymphocytic leukaemia  
CC (CLL), multiple myeloma, non-Hodgkin's lymphoma or Hodgkin's disease),  
CC lymphoproliferative disorders, microbial infections (e.g. viral,  
CC bacterial), parasitic infections, nephritis, bone disease (e.g.  
CC osteoporosis), atherosclerosis, pain, cardiovascular disorders (e.g.  
CC myocardial infarction, stroke), neurodegenerative diseases (e.g.  
CC Alzheimer's disease, Parkinson's disease), graft versus host disease,  
CC wound healing, haematopoietic cell disorders (e.g. anaemia), inflammatory  
CC disorders (e.g. asthma), diseases or disorders associated with various

CC mucous membranes of the body (e.g. mucositis), and disorders of the  
 CC pulmonary system. The proteins are also useful as a vaccine adjuvant that  
 CC enhances immune responsiveness to specific antigens. The present sequence  
 CC represents a PCR primer used to amplify human transmembrane activator and  
 CC CAML-interactor (TACI) cDNA in the examples of the present invention  
 XX

SQ Sequence 39 BP; 8 A; 11 C; 13 G; 7 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 6; Length 39;  
 Best Local Similarity 93.8%; Pred. No. 5.7e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 CCCAGGCGCCTCATGG 20  
 |||||  
 Db 32 CCCAGGCGCCTCATGG 17

RESULT 13  
 ABK13410/c  
 ID ABK13410 standard; DNA; 39 BP.

XX AC ABK13410;  
 XX DT 09-APR-2002 (first entry)

XX DE Tumour necrosis factor (TNF) receptor TACI, 5' PCR primer #2.

XX KM Tumour necrosis factor; TNF; cytostatic; arteriosclerosis; analgesic;  
 KM cerebroprotective; neurotropic; hepatotropic;  
 KM immunoglobulin production; B cell proliferation; immunosuppressive; HIV;  
 KM human immunodeficiency virus; autoimmune disease; immunodeficiency;  
 KM Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;  
 KM common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;  
 KM acquired immunodeficiency virus; cancer; multiple myeloma; CLL;  
 KM chronic lymphocytic leukaemia; lymphoproliferative disorder;  
 KM bacterial infection; viral infection; osteoporosis; atherosclerosis;  
 KM pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;  
 KM neurodegenerative disease; inflammation; liver disease; cirrhosis;  
 KM cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;  
 KM ulcerative colitis; angiogenesis; septic shock; wound healing; PCR;  
 KM primer; ss; tumour necrosis factor receptor; TACI.

XX OS Homo sapiens.

XX PN W020019658-A2.

XX PD 20-DEC-2001.

XX PF 14-JUN-2001; 2001WO-US019026.

XX PR 15-JUN-2000; 2000US-0211537P.  
 PR 23-OCT-2000; 2000US-0241952P.  
 PR 13-DEC-2000; 2000US-0254875P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 23-MAR-2001; 2001US-0277978P.  
 PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;

XX DR WPI; 2002-130727/17.

XX PT Novel multimeric human tumor necrosis factor delta or epsilon protein  
 PT useful for treating cancer, immune system disorders, infection,  
 PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and  
 PT psoriasis.

XX PS Example 29; Page 295; 344pp; English.

XX CC The invention describes a multimeric human tumour necrosis factor (TNF)  
 CC delta or epsilon protein (I). (I) or a composition containing them (II)  
 CC are useful for modulating immunoglobulin production or proliferation of B

CC cells. (I) or (II) is useful: for treating a disease or disorder of the  
 CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,  
 CC systemic lupus erythematosus or common variable immunodeficiency (CVID));  
 CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);  
 CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's  
 CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in  
 CC the diagnosis and treatment or prevention of cancer, lymphoproliferative  
 CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,  
 CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,  
 CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.  
 CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,  
 CC glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting  
 CC angiogenesis and wound healing; as a diagnostic research reagent; as an  
 CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon  
 CC receptor; in apoptosis of transformed cell lines; mediation of cell  
 CC activation and proliferation; and as an immunogen to produce (II). (II)  
 CC is useful to purify, detect and target (I), for measuring levels of (I)  
 CC in biological samples, for immunophenotyping samples, and to treat,  
 CC inhibit or prevent diseases and disorders associated with aberrant  
 CC expression and/or activity of (I). This sequence represents a 5' PCR  
 CC primer used to isolate the TNF receptor superfamily member TACI, required  
 CC in an assay to establish if tumour necrosis factor epsilon (TNF-epsilon)  
 CC binds the receptor described in the method of the invention

SQ Sequence 39 BP; 8 A; 11 C; 13 G; 7 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 6; Length 39;  
 Best Local Similarity 93.8%; Pred. No. 5.7e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 CCCAGGCGCCTCATGG 20  
 |||||  
 Db 32 CCCAGGCGCCTCATGG 17

RESULT 14

ID ADF72622/c

XX AC ADF72622;

XX DT 12-FEB-2004 (first entry)

XX DE Human tumour necrosis factor (TNF)-related PCR primer #2.

XX KM Human; tumour necrosis factor; TNF; PCR; ss; septic shock; inflammation;  
 KM cancer; cerebral malaria; HIV; bone resorption; rheumatoid arthritis;  
 KM cachexia; Grave's disease; diabetes; hepatitis; asthma;  
 KM cardiovascular disorder; infection; allergy; Alzheimer's disease;  
 KM Parkinson's disease; nephritis; primer.

XX OS Homo sapiens.

XX PN US2003166864-A1.

XX PD 04-SEP-2003.

XX PF 11-OCT-2002; 2002US-00268951.

XX PR 14-MAR-1996; 96US-0016812P.  
 PR 12-MAR-1997; 97US-00815783.  
 PR 15-JUN-2000; 2000US-0211537P.  
 PR 23-OCT-2000; 2000US-0241952P.  
 PR 13-DEC-2000; 2000US-0254875P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 23-MAR-2001; 2001US-0277978P.  
 PR 25-MAY-2001; 2001US-0293499P.

XX PR 14-JUN-2001; 2001US-0087991P.  
 PR 12-OCT-2001; 2001US-0328401P.  
 PR 26-FEB-2002; 2002US-00082260.

XX PA (YUGG/) YU G.  
 PA (NIJUT/) NI J.

PA (GENTZ/) GENTZ R.  
 XX  
 PI Yu G, Ni J, Gentz R;  
 XX  
 DR WPI: 2003-898107/82.  
 XX  
 PR New human tumor necrosis factor (TNF) delta and epsilon, useful for  
 PT diagnosing, preventing or treating dysfunctions or diseases associated  
 PT with aberrant activity of TNF delta or epsilon, e.g. septic shock,  
 PT inflammation or cancer.  
 XX  
 PS Example 30; SEQ ID NO 16; 155bp; English.  
 XX  
 CC The invention relates to human tumour necrosis factor (TNF) polypeptides  
 CC and the polynucleotides encoding them. The sequences of the invention are  
 CC useful in research, biological, clinical and therapeutic purposes. In  
 CC particular, these are used in diagnosing, preventing, treating or  
 CC ameliorating dysfunctions or diseases associated with aberrant endogenous  
 CC activity of TNF delta or epsilon, such as septic shock, inflammation,  
 CC cancer, cerebral malaria, activation of HIV virus, bone resorption,  
 CC rheumatoid arthritis, cachexia, Grave's disease, diabetes, hepatitis,  
 CC asthma, cardiovascular disorders, infections, allergies, Alzheimer's  
 CC disease, Parkinson's disease and nephritis. The sequences may also be  
 CC used for chromosome identification or genetic mapping. This sequence  
 CC represents a human TNF-related PCR primer of the invention.  
 XX  
 SQ Sequence 39 BP; 8 A; 11 C; 13 G; 7 T; 0 U; 0 Other;  
 XX  
 Query Match 72.0%; Score 14.4; DB 10; Length 39;  
 Best Local Similarity 93.8%; Pred. No. 5.7e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 CCCAGGGCAGCTCATG 20  
 Db 32 CCCAGGCCACTCATG 17  
 XX  
 RESULT 15  
 ADU06792  
 ID ADU06792 standard; DNA; 74 BP.  
 XX  
 AC ADU06792;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE Mouse GPR4 cDNA sequencing fragment.  
 XX  
 KW ss; antiinflammatory; GPR4 signal transduction inhibitor;  
 KM neutrophil inflammation disease; signal transduction; GPR4.  
 XX  
 OS Mus musculus.  
 XX  
 FN WO2004093912-A1.  
 PD 04-NOV-2004.  
 XX  
 PF 23-APR-2004; 2004WO-JP005930.  
 XX  
 PR 23-APR-2003; 2003JP-00118432.  
 PR 26-FEB-2004; 2004JP-00052191.  
 XX  
 PA (KYOM ) KYOMA HAKKO KOGYO KK.  
 XX  
 PI Saki M, Nonaka H, Miyaji H, Takahashi C, Manabe H, Hiura N;  
 PI Miki I, Abe Y, Sasaki K, Kobatake C, Ichikawa S, Goto A, Suda T;  
 XX  
 DR WPI: 2004-795424/78.  
 XX  
 PT Agent comprises nitrogen-containing tricyclic compound, as active  
 PT ingredient capable of inhibiting signal transduction function of protein,  
 PT useful for treating or preventing neutrophil inflammation disease.  
 XX  
 PS Example 6; SEQ ID NO 26; 293bp; Japanese.

XX  
 CC The invention relates to a preventive and/or therapeutic agent (P1) of  
 CC neutrophil inflammation disease, comprises nitrogen-containing tricyclic  
 CC compound, as an active ingredient that is capable of inhibiting signal  
 CC transduction function of a protein. (P1) comprises a fully defined  
 CC sequence of 362 (S1) amino acids as given in the specification, an  
 CC antibody that recognizes (S1) or two fully defined sequence having 365  
 CC (S2) amino acids as given in the specification, in which one or more  
 CC amino acids are deleted, substituted or added, an oligonucleotide (ON)  
 CC complementary to 15-60 continuous bases of a fully defined sequence of  
 CC 2932 (S3), 1098 (S4) or 1098 (S5) nucleotides as given in the  
 CC specification or its derivative or an oligonucleotide sequence that  
 CC hybridizes with (S3)-(S5) under stringent conditions, an antibody (P2)  
 CC that specifically recognizes (S1) or (S2), or nitrogen-containing  
 CC tricyclic compound of formula (I) or (II) or its quaternary ammonium  
 CC salt, as an active ingredient that is capable of inhibiting signal  
 CC transduction function of a protein. (P1) is useful for preventing and/or  
 CC treating neutrophil inflammation disease. (P2) is useful for producing  
 CC (P1). (P1) enables to inhibit GPR4 signal transduction. This sequence  
 CC corresponds to a sequenced fragment of the cDNA encoding the mouse GPR4  
 CC signal transduction protein DNA of the invention.  
 XX  
 SQ Sequence 74 BP; 8 A; 23 C; 19 G; 24 T; 0 U; 0 Other;  
 XX

Query Match 72.0%; Score 14.4; DB 13; Length 74;  
 Best Local Similarity 93.8%; Pred. No. 5.8e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 CCCAGGGCAGCTCATG 19  
 Db 34 CCCCTGGGCGACTCATG 49

Search completed: December 24, 2005, 12:29:06  
 Job time : 173.4 secs



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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds  
(without alignments)  
595.256 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20  
Sequence: 1 gacccccagggcactcatcg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	76	8	DR767343 ILLUMIGEN
C 2	15.8	79.0	81	7	CO581042 ILLUMIGEN
C 3	15.2	76.0	70	8	DN390652 LIB3896-0
C 4	14.8	74.0	24	9	AZ428700 1M0212116
C 5	14.4	72.0	96	7	CF982929 ma395910.
C 6	14.2	71.0	76	1	A1304064 u163907.Y
C 7	14.2	71.0	94	7	CO720109 ta138e07.
C 8	14.0	70.0	68	9	CC514177 CH240.358
C 9	13.8	69.0	64	7	CV306707 t33h11.b
C 10	13.8	69.0	64	7	CV306708 t33h11.g
C 11	13.8	69.0	79	7	CV308171 t35b03.b
C 12	13.8	69.0	79	7	CV308172 t35b03.g
C 13	13.8	69.0	100	1	AL595750 AL595750
C 14	13.8	69.0	100	5	CA035542 4001479.B
C 15	13.6	68.0	50	1	AU105199 AU105199
C 16	13.6	68.0	50	1	AU105201 AU105201
C 17	13.6	68.0	50	1	AU105204 AU105204
C 18	13.6	68.0	50	1	AU105205 AU105205
C 19	13.6	68.0	50	1	AU105206 AU105206
C 20	13.6	68.0	50	1	AU105207 AU105207
C 21	13.6	68.0	57	1	AU259073 AU259073
C 22	13.6	68.0	70	1	AI829164 wk76a07.x

23	13.6	68.0	90	10	BX547351
24	13.6	68.0	95	10	CG784638
25	13.4	67.0	59	1	AL800251
26	13.4	67.0	89	10	CM208596
C 27	13.4	67.0	92	11	CR234318
C 28	13.2	66.0	57	10	BX947560
C 29	13.2	66.0	66	1	AV771725
C 30	13.2	66.0	75	11	CR061068
31	13.2	66.0	76	10	CG549951
32	13.2	66.0	88	1	AM028956
33	13.2	66.0	89	4	AK203504
C 34	13.2	66.0	92	1	AA525968
C 35	13.2	66.0	97	1	A1756476
C 36	13.2	66.0	100	6	CD962144
37	12.8	64.0	46	6	CA968315
38	12.8	64.0	52	1	A1310821
C 39	12.8	64.0	52	8	B01045
C 40	12.8	64.0	57	9	B06891
41	12.8	64.0	57	9	B06891
C 42	12.8	64.0	58	9	AZ767622
C 43	12.8	64.0	69	6	CB221517
C 44	12.8	64.0	78	1	AA958370
45	12.8	64.0	78	10	CL215248

## ALIGNMENTS

RESULT 1  
LOCUS DR767343/c  
DEFINITION ILLUMIGEN MOQ 59763 Katze.MMOV Macaca mulatta cDNA clone  
IBIUM:37993 5' similar to Baes 1 to 76 highly similar to human  
TRAI (Hs.192374), mRNA sequence.

ACCESSION DR767343  
VERSION DR767343  
KEYWORDS  
SOURCE

ORGANISM Macaca mulatta (rhesus monkey)  
Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Cercopithecoidea; Cercopithecinae; Macaca.

1 (bases 1 to 76)  
Magnes,C.L., Pellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,  
Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and  
Iadonato,S.P.

Analysis of the Macaca mulatta transcriptome and the sequence  
divergence between Macaca and human  
Genome Biol. 6 (7), R60 (2005)

15998449  
Contact: C. Magnes

ILLUMIGEN Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408

Email: cmagnes@illumigen.com  
Sequenced on 2005.03.23. 76 Q20 bases. Library Preparation: Prof.  
Michael Katze lab at University of Washington DNA Sequencing:  
ILLUMIGEN Biosciences Inc. For further information, see  
http://www.macaque.org

PCR Primers  
FORWARD: CCCTCACTAAGGACAAACA  
BACKWARD: CACTATAGGCGAATGGGTA  
Insert Length: 76 Std Error: 0.00  
Plate: C1000649 row: E column: 06  
Seq primer: CCCTCACTAAGGACAAACA  
POLYA:NO

## FEATURES

location/Qualifiers  
1..76  
/organism="Macaca mulatta"  
/mol\_type="mRNA"  
/strain="Indian"  
/db\_xref="taxon:9544"

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/clone="IBIUM:37993"  
/sex="female"  
/dev stage="adult"  
/lab_host="Electromax DH10B"  
/clone_lib="Katze_MM0V"  
/note="Organ: ovary; Vector: pDONR 222; Site_1: BsrG I;  
Site_2: BsrG I; Created from Cloneminer cDNA library  
Construction kit (catalog #18249-029)"
```

## ORIGIN

```
Query Match 79.0%; Score 15.8; DB 8; Length 76;  
Best Local Similarity 89.5%; Pred. No. 1.1e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 ACCCCAGGGCACTCATGG 20  
|||||  
Db 40 ACCCAGGGGCCCTCATGG 22
```

## RESULT 2

```
LOCUS COS81042/c 81 bp mRNA linear EST 20-UTL-2004  
DEFINITION ILLUMIGEN_MCO_47838 Katze_MM1L Macaca mulatta cDNA clone  
IBIUM:19831 5' similar to Bases 5 to 81 highly similar to human  
TRAI (Hs.192374), mRNA sequence.
```

ACCESSION COS81042  
VERSION COS81042.1 GI:50412312  
KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)  
ORGANISM Macaca mulatta

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Eutheria; Eumarchontoglires; Primates; Catarrhini;  
Cercopithecoidea; Cercopithecinae; Macaca.

AUTHORS 1 (bases 1 to 81), Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,  
Magnees, C.L., Prohl, S.C., Flitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, W.G. and  
Iadonato, S.P.

TITLE Analysis of the Macaca mulatta transcriptome and the sequence  
divergence between Macaca and human

JOURNAL Genome Biol. 6 (7), R60 (2005)  
PUBMED 15998449

COMMENT Contact: C. Magnees  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagnees@illumigen.com

Sequenced on 2004.06.30. 81 Q20 bases. Library Preparation: Prof.  
Michael Katze lab at University of Washington DNA Sequencing:  
Illumigen Biosciences Inc. For further information, see  
http://www.macaque.org  
PCR Primers  
FORWARD: CCTCACTAAGGGAACAATA  
BACKWARD: CACTATAGGCGCAATTGGTA  
Insert Length: 81 Std Error: 0.00  
Plate: CL000436 row: B column: 06  
Seq primer: CCTCACTAAGGGAACAATA  
POLY-A-No.

## FEATURES

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/organism="Macaca mulatta"  
/mol_type="mRNA"  
/strain="indian"  
/db_xref="taxon:9544"  
/clone="IBIUM:19831"  
/sex="male"  
/dev stage="adult"  
/lab_host="Electromax DH10B"  
/clone_lib="Katze_MM1L"  
/note="Organ: ileum; Vector: pDONR 222; Site_1: BsrG I;  
Site_2: BsrG I; Created from Cloneminer cDNA library  
Construction kit (catalog #18249-029)"
```

## ORIGIN

```
Query Match 79.0%; Score 15.8; DB 7; Length 81;  
Best Local Similarity 89.5%; Pred. No. 1.1e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 ACCCCAGGGCACTCATGG 20  
|||||  
Db 45 ACCCAGGGGCCCTCATGG 27
```

## RESULT 3

```
LOCUS DN390652/c 70 bp mRNA linear EST 07-MAR-2005  
DEFINITION L183896-026-06-X1-B6 L1B3896 Canis familiaris cDNA clone  
L188893833, mRNA sequence.
```

ACCESSION DN390652  
VERSION DN390652.1 GI:60571873  
KEYWORDS EST.

SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Chordata; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

AUTHORS 1 (bases 1 to 70)  
Staten, N.R.  
TITLE Direct Submission (Staten, N.R.)  
JOURNAL Unpublished (2005)  
COMMENT Contact: Nick Staten  
Tel: 636 247 6855  
Email: nicholas.r.staten@fizer.com.

## FEATURES

source

```
1. 70  
/location/Qualifiers  
/organism="Canis familiaris"  
/mol_type="mRNA"  
/strain="beagle"  
/db_xref="taxon:9615"  
/clone="C1N8893833"  
/tissue_type="skeletal muscle"  
/lab_host="DH10B"  
/clone_lib="L1B3896"  
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;  
skeletal muscle"
```

## ORIGIN

```
Query Match 76.0%; Score 15.2; DB 9; Length 70;  
Best Local Similarity 85.0%; Pred. No. 2.1e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GACCCAGGGCACTCATGG 20  
|||||  
Db 27 GACCCAGGGGCCCTCATGG 8
```

## RESULT 4

```
LOCUS AZ428700/c 24 bp DNA linear GSS 03-OCT-2000  
DEFINITION IM0212116F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0212116 F, genomic survey sequence.
```

ACCESSION AZ428700  
VERSION AZ428700.1 GI:10552713  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 24)  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts



TITLE	JOURNAL	COMMENT
The Mashu-HHMI Mouse EST Project	Unpublished (1996)	Contact: Marra M/Mouse EST Project

## FEATURES

**Source**

## ORIGIN

Query Match	71.0%	Score 14.2;	DB 1;	Length 76;
Best Local Similarity	84.2%;	Pred. No. 6.3e+04;		
Matches 16;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0

Db 31 ACCCCGAGGATGTCATGG 13

RESULT 7			
CO720109/c			
LOCUS	CO720109	94 bp	mRNA
DEFINITION	ta338e07.y1 HyeCh JUMY T1 Hydractinia echinata cDNA 5' similar to	linear	EST 27-JUL-2004

**FEATURES**  
**source**

**Source**

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estwatson.wustl.edu  
Library was constructed by Marcus Prohme and Uri Frank. Library materials provided by Marcus Prohme, German Cancer Research Center (DKFZ) Heidelberg, Uri Frank, University of Heidelberg Library re-arrayed by Jorge Soteras (DKFZ) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hbode@wustl.edu)  
Seq primer: -40bp from Gibco  
High quality sequence stop: 94.

## ORIGIN

Query Match	71.0%	Score 14.2	DB 7	Length 94
Best Local Similarity	84.2%	Pred. No. 6.4e+04		
Matches 16	Conservative	0	Mismatches 3	Indels 0
QY	2	ACCCCCAGGGCAGCTCATCG	20	
Db	22	AGCCTCAGGGATTCATCG	4	

RESULT	8
CC514177	
LOCUS	68 bp DNA
DEFINITION	linear GSS 17-JUN-2003
	CC514177
	CH240_35BP24_TARBAC13P2 CHORI-240 Bos taurus genomic clone
	CH240_35BP24_ genomic survey sequence.

TITLE	Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
JOURNAL	Unpublished (2003)
COMMENT	Other_GSSs: CH240_358P24.T7

TITLE	COMMENT
Washu Hydra EST Project	
Unpublished (2002)	
Contact: Hans Bode	
Washu Hydra EST Project	

availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.choi.org/bacpac/ordering\_information.html). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the  
British Columbia Genome Sciences Centre, Canada.

Plate: 358 row: P column: 24  
Seq primer: SP6  
Class: BAC ends.

#### FEATURES

##### source

Location/Qualifiers  
1..68  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_358P24"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_id="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

#### ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 7.7e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCAC 14  
PUBMED 45 GACCCCGAGGCAC 58

RESULT 9  
CV306707/c 64 bp mRNA linear EST 23-SEP-2004  
DEFINITION t133h11.b7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA  
sequence.

ACCESSION CV306707.1 GI:52624040  
VERSION CV306707  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 64)

Dike,S., Ballja,V.S., Nascimento,L.U., Xuan,Z., Ou,J., Zutavern,T.,  
Palmer,L.E., Hannon,G., Zhang,M.O. and McCombie,W.R.

The mouse genome: Experimental examination of gene predictions and  
transcriptional start sites

Genome Res. 14 (12), 2424-2429 (2004)

15574821

CONTACT: Ballja VS

McCombie Laboratory

Cold Spring Harbor Laboratory

500 Sunnyside Blvd, Woodbury, NY 11797, USA

Fax: 516 422 4109

Email: ballja@cshl.org

Location/Qualifiers

1..64

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone\_id="Mouse 5' RACE clones"

/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments

amplified from 5' RACE cDNA generated from 15 pooled mouse

tissues and stages: 7, 11, 15, & 17-day total embryo,

whole brain, eye, kidney, liver, lung, prostate,

submaxillary gland, smooth muscle, spleen, testes and

uterus."

#### ORIGIN

Query Match 69.0%; Score 13.8; DB 7; Length 64;  
Best Local Similarity 88.2%; Pred. No. 9.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCCGAGGCACTCATGG 20  
PUBMED 41 CACCAAGGCGCTCATGG 25

RESULT 10

CV306708

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 64)

Dike,S., Ballja,V.S., Nascimento,L.U., Xuan,Z., Ou,J., Zutavern,T.,

Palmer,L.E., Hannon,G., Zhang,M.O. and McCombie,W.R.

The mouse genome: Experimental examination of gene predictions and

transcriptional start sites

Genome Res. 14 (12), 2424-2429 (2004)

15574821

CONTACT: Ballja VS

McCombie Laboratory

Cold Spring Harbor Laboratory

500 Sunnyside Blvd, Woodbury, NY 11797, USA

Fax: 516 422 4109

Email: ballja@cshl.org

Location/Qualifiers

1..64

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone\_id="Mouse 5' RACE clones"

/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments

amplified from 5' RACE cDNA generated from 15 pooled mouse

tissues and stages: 7, 11, 15, & 17-day total embryo,

whole brain, eye, kidney, liver, lung, prostate,

submaxillary gland, smooth muscle, spleen, testes and

uterus."

RESULT 11

CV308171

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 79)

Dike,S., Ballja,V.S., Nascimento,L.U., Xuan,Z., Ou,J., Zutavern,T.,

Palmer,L.E., Hannon,G., Zhang,M.O. and McCombie,W.R.

The mouse genome: Experimental examination of gene predictions and

transcriptional start sites

Genome Res. 14 (12), 2424-2429 (2004)

15574821

CONTACT: Ballja VS

McCombie Laboratory

Cold Spring Harbor Laboratory

500 Sunnyside Blvd, Woodbury, NY 11797, USA

Fax: 516 422 4109

Email: ballja@cshl.org

Location/Qualifiers

1..79

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone\_id="Mouse 5' RACE clones"

/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments

amplified from 5' RACE cDNA generated from 15 pooled mouse

tissues and stages: 7, 11, 15, & 17-day total embryo,

whole brain, eye, kidney, liver, lung, prostate,

submaxillary gland, smooth muscle, spleen, testes and

uterus."

RESULT 11

CV308171

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 79)

Dike,S., Ballja,V.S., Nascimento,L.U., Xuan,Z., Ou,J., Zutavern,T.,

Palmer,L.E., Hannon,G., Zhang,M.O. and McCombie,W.R.

The mouse genome: Experimental examination of gene predictions and

transcriptional start sites

Palmer, L.E., Hammon, G., Zhang, M.Q. and McCombe, W.R.  
The mouse genome: Experimental examination of gene predictions and  
transcription start sites  
Genome Res. 14 (12), 2424-2429 (2004)  
15574821  
Contact: Balija VS

**FEATURES**  
source 1.79

```

FEATURES
source
location/Qualifiers
1..79
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_idb="Mouse 5' RACE clones"
/note="vector: PCR-TOPO2.1; Cloned 5' RACE fragments
amplified from 5' RACE cDNA generated from 15 pooled mouse
tissues and stages: 7, 11, 15, & 17-day total embryo,
whole brain, eye, kidney, liver, lung, prostate,
submaxillary gland, smooth muscle, spleen, testes and
uterus."

```

	Query Match	69.0%;	Score 13.8;	DB 7;	length 79;
	Best Local Similarity	88.2%;	Pred. No. 9.7e+04;		
	Matches	15;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0
Oy	4	CCCCAGGCGACTCATGG	20		
Db	39	CACCGAGGCCCTTCATGG	55		

LOCUS	DEFINITION	SEQUENCE
CV308172	79 bp	mRNA
t150b03.g7	Mouse 5'	RACE clones Mus musculus cDNA 5', mRNA

ACCESSION	CV308172
VERSION	CV308172.1
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 79)  
Dike, S., Ballja, V.S., Naacimento, L.U., Xuan, Z., Ou, J.,  
Palmer, L.E., Hannon, G., Zhang, M.Q. and McComble, W.R.

**TITLE** The mouse genome: Experimental examination of gene predictions and transcriptional start sites  
**JOURNAL** Genome Res. 14 (12), 2424-2429 (2004)

JOURNAL Genome Res. 14 (12), 2424-2429 (2004)  
PUBMED 15574821  
COMMENT Contact: Balija VS

FEATURES  
source  
1. .79

FEATURES	SOURCE
Location/Qualifiers	
1. .79	
/organism="Mus musculus"	
/mol_type="mRNA"	
/db_xref="taxon:10090"	
/clone_id="Mouse 5' RACE clones"	
/note="Vector: pCR-TOPO2.1; Cloned 5' RACE fragments amplified from 5' RACE cDNA generated from 15 pooled mouse tissues and stages: 7, 11, 15, & 17-day total embryo, whole brain, eye, kidney, liver, lung, prostate, submaxillary gland, smooth muscle, spleen, testes and uterus."	

Query Match	69.0%;	Score 13.8;	DB 7;	Length 79;
Best Local Similarity	88.2%;	Pred. No. 9.7e+04;		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	4	CCCCAGGGCACTCATGG	20
Db	41	CACCAAGGGCCCTCATGG	25

RESULT 13	LOCUS	DEFINITION
AL595750	100 bp	mRNA
AL595750	XGC-gastrula	Xenopus tropicalis cDNA clone
AL595750	EST 19-JUL-2004	5' - 3'

ACCESSION	AL595750	
VERSION	AL595750.1	GI:15007825
KEYWORDS	EST.	
SOURCE	<i>Xenopus tropicalis</i> (western clawed frog)	
ORGANISM	<i>Xenopus tropicalis</i>	

REFERENCE  
1 (bases 1 to 100)  
AUTHORS  
Crooning M.D.R., Ashurst J.L., Taylor, R., Zorn, A.M. and Rogers, J.  
TITLE  
Sanger xenopus tropicalis EST project 2001 (11\_2003)  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Crooning MDR

Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: TGA0004g01.p1kx86  
Sequencing primer: Sp6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.  
cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13  
gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end.  
Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI  
Host: Escherichia coli XL1-blue.

## FEATURES

```

/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGa004g01"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5' of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

```

**ORIGIN**

Query Match	69.0%	Score 13.8;	DB 1;	Length 100;
Best Local Similarity	88.2%	Pred. No. 9.9e+04;		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

```

QY      1 GACCCCGAGGCACTCA 17
          |||||
Db      41 GCGCCCGGGGCACTCA 57

```

## RESULT 14

LOCUS	CA035542	100 bp	mRNA	linear	EST 24-OCT-2004
DEFINITION	4001479 BARC 5BOV Bos taurus CDNA clone		5BOV_78G22	3'	mRNA sequence.

VERSION CA035542.1 GI:24333939

**KEYWORDS**  
**SOURCE** EST.  
**ORGANISM** Bos taurus (cow)  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
**AUTHORS** 1 (bases 1 to 100)  
 Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P., Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.B., Wells, K.D. and Quackenbush, J.  
**TITLE** Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index  
**JOURNAL** Mamm. Genome 13 (7), 373-379 (2002)  
**PUBMED** 12140684  
**COMMENT** Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414  
 Email: tads@ps1.barc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim\_alt '-trim\_fasta. Vector identified by cross\_match using options -mismatch 12 -minscore 12  
 Plate: 78 row: G column: 22  
 Seq primer: CCFAGTCAGACGCTGTAAACG  
 High quality sequence stop: 100.  
**FEATURES**  
 Location/Qualifiers  
 1..100  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /clone="5BOV 78G22"  
 /issue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="BARC 5BOV"  
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."  
**ORIGIN**  
 Query Match 69.0%; Score 13.8; DB 5; Length 100;  
 Best Local Similarity 88.2%; Pred. No. 9.9e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 CCCGAGGCGACTCATGG 20  
 |||||  
 Db 61 CCCGAGGCGACACTTGG 77  
 |||||  
**RESULT 15**  
 AU105199/c 50 bp mRNA linear EST 28-JAN-2004  
**LOCUS** AU105199 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone  
**DEFINITION** HRC00642, mRNA sequence.  
**ACCESSION** AU105199  
**VERSION** AU105199.1 GI:13554720  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
**REFERENCE** 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tanoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
**AUTHORS** Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
**TITLE** EMBO Rep. 2 (5), 388-393 (2001)  
**JOURNAL** 11375929  
**PUBMED**  
**COMMENT** Contact: Yutaka Suzuki  
 Department of Virology

Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).  
**FEATURES**  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HRC00642"  
 /clone\_lib="Sugano Homo sapiens CDNA library"  
**ORIGIN**  
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 Best Local Similarity 80.0%; Pred. No. 1.1e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GACCCCGAGGCGACTCATGG 20  
 |||||  
 Db 35 GGCTCCAGGCGCTCCCATGG 16  
 |||||  
 Search completed: December 24, 2005, 18:28:44  
 Job time : 1575 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds  
(without alignments)  
739.111 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20  
Sequence: 1 GACCCCGAGGCATCATG 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
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5: /cgn2\_6/ptodata/1/ina/6 COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/6 COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	14.4	72.0	39	3	US-09-879-919-16
2	13.6	68.0	25	3	US-09-396-196G-65755
3	13.6	68.0	59	2	US-08-726-012B-5
4	13.4	67.0	25	3	US-09-396-196G-31948
5	13.4	67.0	25	3	US-09-396-196G-31959
6	13.4	67.0	47	3	US-09-423-978-198
7	13.4	67.0	78	3	US-09-938-700-25
8	13.2	66.0	24	3	US-09-005-165-8
9	13.2	66.0	75	3	US-09-060-756-146
10	13.2	66.0	75	3	US-09-670-314-146
11	13.2	66.0	80	3	US-09-282-996-9
12	13.2	66.0	82	3	US-09-282-996-8
13	12.8	64.0	20	3	US-10-031-636-1
14	12.8	64.0	25	3	US-09-305-856B-93
15	12.8	64.0	25	3	US-09-396-196G-56240
16	12.8	64.0	66	3	US-07-728-220C-14
17	12.8	64.0	69	2	US-08-352-179-10
18	12.6	63.0	21	3	US-09-657-472-1188
19	12.6	63.0	25	3	US-09-396-196G-8693
20	12.6	63.0	25	3	US-09-396-196G-8694
21	12.6	63.0	25	3	US-09-396-196G-31248
22	12.6	63.0	25	3	US-09-396-196G-71248
23	12.6	63.0	25	3	US-09-396-196G-86582
24	12.6	63.0	25	3	US-09-396-196G-104877

25	12.6	63.0	25	3	US-09-396-196G-108466	Sequence 108466, A
26	12.6	63.0	25	3	US-09-396-196G-108483	Sequence 108483, A
27	12.6	63.0	25	3	US-09-396-196G-110802	Sequence 110802, A
28	12.6	63.0	25	3	US-09-396-196G-116344	Sequence 116344, A
29	12.6	63.0	28	3	US-08-617-874-4	Sequence 4, Appl1
30	12.6	63.0	28	3	US-08-617-874-6	Sequence 6, Appl1
31	12.6	63.0	29	3	US-09-194-285-4	Sequence 4, Appl1
32	12.6	63.0	30	2	US-08-670-175-7	Sequence 7, Appl1
33	12.6	63.0	40	2	US-08-596-187B-39	Sequence 39, Appl1
34	12.6	63.0	40	3	US-09-067-615-39	Sequence 39, Appl1
35	12.6	63.0	40	6	PCT-US95-09816A-39	Sequence 39, Appl1
36	12.6	63.0	45	2	US-08-596-387B-104	Sequence 104, App
37	12.6	63.0	45	3	US-09-067-615-104	Sequence 104, App
38	12.6	63.0	45	6	PCT-US95-09816A-104	Sequence 104, App
39	12.6	63.0	99	3	US-09-513-999C-26781	Sequence 26781, A
40	12.4	62.0	24	2	US-08-288-508C-10	Sequence 10, Appl1
41	12.4	62.0	24	3	US-08-289-222B-20	Sequence 20, Appl1
42	12.4	62.0	24	3	US-09-054-526B-20	Sequence 20, Appl1
43	12.4	62.0	24	3	US-09-386-450D-10	Sequence 10, Appl1
44	12.4	62.0	25	3	US-09-396-196G-54334	Sequence 54334, A
45	12.4	62.0	25	3	US-09-396-196G-54335	Sequence 54335, A

## ALIGNMENTS

RESULT 1  
US-09-879-919-16/c  
; Sequence 16, Application US/09879919  
; Patent No. 6541224  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang, et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
; FILE REFERENCE: P7253P1  
; CURRENT APPLICATION NUMBER: US/09/879, 919  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/293, 499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277, 978  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/276, 248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/254, 875  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 60/241, 952  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/211, 537  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 08/815, 783  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: 60/016, 812  
; PRIOR FILING DATE: 1996-03-14  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-879-919-16

Query Match 72.0%; Score 14.4; DB 3; Length 39;  
Best Local Similarity 93.8%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 32 CCCAGGCGCATCATG 17

RESULT 2  
US-09-396-196G-65755  
; Sequence 65755, Application US/09396196G  
; Patent No. 6821724

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; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65755
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-65755

Query Match          68.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      1 GACCCCGAGGCACTCATG 20
        ||||| |||||
Db      2 GACCCCATGCGCATCATG 21

RESULT 3
US-08-726-012B-5
; Sequence 5, Application US/08726012B
; Patent No. 5952190
; GENERAL INFORMATION:
; APPLICANT: Hans Joenje, et al
; TITLE OF INVENTION: CDNA FOR FANCONI ANEMIA COMPLEMENTATION GROUP A
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston, LLP
; STREET: One World Trade Center, Suite 1600, 121 S.W. Salmon Street
; CITY: Portland
; STATE: OR
; COUNTRY: USA
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3.5-inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1+, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,012B
; FILING DATE: 10/04/96
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard J. Polley
; REGISTRATION NUMBER: 28,107
; REFERENCE/DOCKET NUMBER: 3812-45520/RJP/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-012B-5

Query Match          68.0%; Score 13.6; DB 2; Length 59;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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OY      1 GACCCCGAGGCACTCATG 20
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Db      27 GACCATCATGGCCATCATG 46

RESULT 4
US-09-396-196G-31948/C
; Sequence 31948, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-31948

Query Match          67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      5 CCCAGGCACTCATG 19
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Db      22 CCTGGGCACTCATG 8

RESULT 5
US-09-396-196G-31959/C
; Sequence 31959, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-31959

Query Match          67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      5 CCCAGGCACTCATG 19
        ||||| |||||
Db      19 CCTGGGCACTCATG 5

RESULT 6
US-09-422-978-198
; Sequence 198, Application US/09422978
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Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 198
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-13489-396 : polymorphic base C or T
US-09-422-978-198

Query Match      67.0%; Score 13.4; DB 3; Length 47;
Best Local Similarity 82.4%; Pred. No. 4.9e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      2 ACCCCGAGGCACTCATG 18
Db      8 ACAGCCAGGCACTCAT 24

RESULT 7
US-09-938-700-25
Sequence 25, Application US/09938700
Patent No. 6687472
GENERAL INFORMATION:
APPLICANT: Morsey, et al.
TITLE OF INVENTION: Anti-1GE Vaccines
FILE REFERENCE: PCI0761A
CURRENT APPLICATION NUMBER: US/09/938,700
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 78
TYPE: DNA
ORGANISM: DOG CH3/CH4 NUCLEOTIDE SEQUENCE
US-09-938-700-25

Query Match      67.0%; Score 13.4; DB 3; Length 78;
Best Local Similarity 93.3%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      5 CCCAGGCGCACTCATG 19
Db      25 CCCAGGCGCCTCATG 39

RESULT 8
US-09-005-165-8/c
Sequence 8, Application US/09005165
Patent No. 6093542
GENERAL INFORMATION:
APPLICANT: ROMANO, JOSEPH
APPLICANT: SHUKTLIFF, ROXANNE
APPLICANT: PAL, RANAJIT
TITLE OF INVENTION: ISOTHERMAL TRANSCRIPTION BASED
AMPLIFICATION ASSAY FOR THE DETECTION AND QUANTITATION OF
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE RNA
```

```
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: AKZO NOBEL PATNT DEPARTMENT
STREET: 1300 PICCARD DRIVE, SUITE 206
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,165
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: MDC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-948-7400
TELEFAX: 301-948-9751
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-005-165-8

Query Match      66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      3 CCCCCAGGCACTCATG 20
Db      23 CAGCCAGGCACTCTGGG 6

RESULT 9
US-09-060-756-146
Sequence 146, Application US/09060756
Patent No. 6183957
GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billaud, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 146
LENGTH: 75
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-060-756-146

Query Match      66.0%; Score 13.2; DB 3; Length 75;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 ACCCCGAGGCACTCATG 19
Db      30 ACCCCAGGCACTCATG 47
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RESULT 10
US-09-670-314-146
; Sequence 146, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Cole, Stewart
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-670-314-146

Query Match          66.0%; Score 13.2; DB 3; Length 75;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCCCGAGGCACTCATG 19
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DB 30 ACCCCGAGGCACTCATG 47

RESULT 11
US-09-282-996-9/c
; Sequence 9, Application US/09282996
; Patent No. 6143502
; GENERAL INFORMATION:
; APPLICANT: Grentzmann, Guido
; APPLICANT: Gesteland, Raymond F.
; APPLICANT: Atkins, John F.
; TITLE OF INVENTION: Dual-Luciferase Reporter System
; FILE REFERENCE: T5864.NP
; CURRENT APPLICATION NUMBER: US/09/282,996
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 9
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Luc12
US-09-282-996-9

Query Match          66.0%; Score 13.2; DB 3; Length 80;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCCCCGAGGCACTCATG 20
   ||||| ||||| |||||
DB 50 CCCCCGAGGCACTCATG 33

RESULT 12
US-09-282-996-8
; Sequence 8, Application US/09282996
; Patent No. 6143502
; GENERAL INFORMATION:
```

```
; APPLICANT: Grentzmann, Guido
; APPLICANT: Gesteland, Raymond F.
; APPLICANT: Atkins, John F.
; TITLE OF INVENTION: Dual-Luciferase Reporter System
; FILE REFERENCE: T5864.NP
; CURRENT APPLICATION NUMBER: US/09/282,996
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 8
; LENGTH: 82
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Luc1
US-09-282-996-8

Query Match          66.0%; Score 13.2; DB 3; Length 82;
Best Local Similarity 77.8%; Pred. No. 6.1e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCCCCGAGGCACTCATG 20
   ||||| ||||| |||||
DB 35 CCCCCGAGGCACTCATG 52

RESULT 13
US-10-031-636-1
; Sequence 1, Application US/10031636
; Patent No. 6794140
; GENERAL INFORMATION:
; APPLICANT: Cyclope Genome Sciences Limited
; APPLICANT: Goldsborough, Andrew S.
; TITLE OF INVENTION: ISOLATION OF NUCLEIC ACID
; FILE REFERENCE: US2.GOLDSBOROUGH
; CURRENT APPLICATION NUMBER: US/10/031,636
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: UK 9910154.5
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: UK 9910157.8
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: UK 9910156.0
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: UK 9910158.6
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Brome Mosaic Virus (BMV)
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)..(20)
US-10-031-636-1

Query Match          64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCGAGGCACTC 16
   ||||| ||||| |||||
DB 1 GACCCGAGGCACTC 16

RESULT 14
US-09-305-856B-93
; Sequence 93, Application US/09305856B
; Patent No. 6479236
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
```

APPLICANT: Galvin, Margaret  
TITLE OF INVENTION: Genotyping the Human  
FILE REFERENCE: 4389-7 (formerly SEQ-17C1P)  
CURRENT APPLICATION NUMBER: US/09/305,856B  
CURRENT FILING DATE: 1999-05-05  
PRIOR APPLICATION NUMBER: 60/084,807  
PRIOR FILING DATE: 1998-05-07  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 93  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-305-856B-93

Query Match 64.0%; Score 12.8; DB 3; Length 25;  
Best Local Similarity 87.5%; Pred. No. 9.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCCCAGGCGACTCATG 19  
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Db 3 CCCCAGGCCAATCATG 18

RESULT 15  
US-09-396-196G-56240/C  
Sequence 56240, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittleman  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 56240  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-56240

Query Match 64.0%; Score 12.8; DB 3; Length 25;  
Best Local Similarity 87.5%; Pred. No. 9.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTC 16  
|||  
Db 20 GACTCCGAGGCGCTCTC 5

Search completed: December 24, 2005, 18:36:30  
Job time : 48.1 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20  
Sequence: 1 gaccccgagggcactcactg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:

1: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-11
2	16.8	84.0	25	9	US-10-956-157-229257
3	16	80.0	20	3	US-09-296-264-20
4	15.8	79.0	25	7	US-10-719-956-416913
5	15.8	79.0	25	7	US-10-719-956-580760
6	15.8	79.0	25	10	US-11-036-317-131184
7	15.8	79.0	25	10	US-11-036-317-755963
8	15.8	79.0	25	10	US-11-036-317-836367
9	15.4	77.0	25	10	US-11-036-317-33549
10	15.4	77.0	25	10	US-11-036-317-61202
11	15.2	76.0	60	3	US-09-908-975-7302
12	14.8	74.0	25	10	US-11-036-317-57475
13	14.4	72.0	20	7	US-10-671-074-174
14	14.4	72.0	25	10	US-11-036-317-88788
15	14.4	72.0	39	3	US-09-879-919-16
16	14.4	72.0	39	6	US-10-268-951-16
17	14.2	71.0	25	7	US-10-719-956-424275
18	14.2	71.0	25	7	US-10-719-956-350836
19	14.2	71.0	25	7	US-10-719-956-416914
20	14.2	71.0	25	7	US-10-719-956-580759
21	14.2	71.0	25	8	US-10-719-900-373673
22	14.2	71.0	25	8	US-10-719-900-394801
23	14.2	71.0	25	9	US-10-956-157-183204

24	14.2	71.0	25	10	US-11-036-317-49011	Sequence 49011, A
25	14.2	71.0	25	10	US-11-036-317-262309	Sequence 262309, A
26	14.2	71.0	25	10	US-11-036-317-364550	Sequence 364550, A
27	14.2	71.0	25	10	US-11-036-317-516353	Sequence 516353, A
28	14.2	71.0	25	10	US-11-036-317-755962	Sequence 755962, A
29	14.2	71.0	25	10	US-11-036-317-836366	Sequence 836366, A
30	14.2	71.0	60	3	US-09-908-975-11924	Sequence 31924, A
31	14.2	71.0	80	9	US-10-971-736-56	Sequence 56, App
32	14	70.0	20	7	US-10-671-074-163	Sequence 163, App
33	14	70.0	25	7	US-10-719-956-239339	Sequence 239339, A
34	14	70.0	25	8	US-10-719-900-258242	Sequence 258242, A
35	14	70.0	25	10	US-11-060-756-194883	Sequence 194883, A
36	14	70.0	25	10	US-11-060-756-194884	Sequence 194884, A
37	13.8	69.0	25	7	US-10-719-956-80800	Sequence 80800, A
38	13.8	69.0	25	7	US-10-719-956-203307	Sequence 203307, A
39	13.8	69.0	25	8	US-10-719-900-460659	Sequence 460659, A
40	13.8	69.0	25	8	US-10-719-900-479930	Sequence 479930, A
41	13.8	69.0	25	10	US-11-036-317-339780	Sequence 339780, A
42	13.8	69.0	25	10	US-11-036-317-385058	Sequence 385058, A
43	13.8	69.0	80	7	US-10-384-245-165	Sequence 165, App
44	13.8	69.0	100	7	US-10-242-535A-12117	Sequence 12117, A
45	13.8	69.0	100	7	US-10-085-783A-12117	Sequence 12117, A

#### ALIGNMENTS

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RESULT 1
US-09-296-264-11
Sequence 11, Application US/09296264
Publication No. US20030083274A1
GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
TITLE OF INVENTION: NEUROPEPTIDE ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
FILE REFERENCE: 032396-043
CURRENT APPLICATION NUMBER: US/09/296,264
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Human
US-09-296-264-11

Query Match      100.0%; Score 20; DB 3; Length 20;
Best local similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GACCCCGAGGCACTCATGG 20
Db      1 GACCCCGAGGCACTCATGG 20

RESULT 2
US-10-956-157-229257
Sequence 229257, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mount, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOCARTRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 229257
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-229257

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 9; Length 25;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 20
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Db 1 GACCCCGAGGCACTCATG 20

RESULT 3
US-09-296-264-20
; Sequence 20, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/236,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-20

Query Match
Best Local Similarity 80.0%; Score 16; DB 3; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCCAGGCGACTCATG 20
    |||||
Db 1 CCCAGGCGACTCATG 16

RESULT 4
US-10-719-956-416913
; Sequence 416913, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 416913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-416913

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 25;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 19
    |||||
Db 1 GACCCCGAGGCACTCATG 19
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Db 7 GACCTCCAGGCACTCATG 25

RESULT 5
US-10-719-956-580760/C
; Sequence 580760, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 580760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-580760

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 25;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 19
    |||||
Db 20 GACCCCGAGGCACTCATG 2

RESULT 6
US-11-036-317-131184/C
; Sequence 131184, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 131184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-131184

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 10; Length 25;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 19
    |||||
Db 24 GACCTCCAGGCACTCTTG 6

RESULT 7
US-11-036-317-755963/C
; Sequence 755963, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
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PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 755963  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-755963

Query Match 79.0%; Score 15.8; DB 10; Length 25;  
Best Local Similarity 89.5%; Pred. No. 8.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCATG 19  
DB 24 GACCTCGAGGCGACTCTTG 6

RESULT 8  
US-11-036-317-836367/C  
Sequence 836367, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 836367  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-836367

Query Match 79.0%; Score 15.8; DB 10; Length 25;  
Best Local Similarity 89.5%; Pred. No. 8.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCCCGAGGCGACTCATG 20  
DB 23 ACCCGAGGCGAGTCATG 5

RESULT 9  
US-11-036-317-33549  
Sequence 33549, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 33549  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-33549

Query Match 77.0%; Score 15.4; DB 10; Length 25;  
Best Local Similarity 94.1%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCGAGGCGACTCATG 20  
DB 9 CCCGAGGCGACTCATG 25

RESULT 10  
US-11-036-317-61202  
Sequence 61202, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 61202  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-61202

Query Match 77.0%; Score 15.4; DB 10; Length 25;  
Best Local Similarity 94.1%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCGAGGCGACTCATG 20  
DB 4 CCCGAGGCGACTCATG 20

RESULT 11  
US-09-908-975-7302/C  
Sequence 7302, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7302  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-7302

Query Match 76.0%; Score 15.2; DB 3; Length 60;  
Best Local Similarity 85.0%; Pred. No. 1.5e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCATG 20  
DB 46 GACCTCGAGGCGAGTCATG 27

RESULT 12

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US-11-036-317-57475/c
; Sequence 57475, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 57475
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-57475
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Query Match          74.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      2 ACCCCGAGGCACTCATG 19
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Db      25 ACCCCGAGGCACTCATG 8
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RESULT 13
US-10-671-074-174
; Sequence 174, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dobbie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Elison, Marielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shuter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 174
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-174
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Query Match          72.0%; Score 14.4; DB 7; Length 20;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      3 CCCCGAGGCACTCAT 18
      |||||
Db      1 CCGCGAGGCACTCAT 16
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RESULT 14
US-11-036-317-88788/c
; Sequence 88788, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
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; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88788
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-88788
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Query Match          72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      4 CCCCGAGGCACTCATG 19
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Db      16 CTCGAGGCACTCATG 1
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RESULT 15
US-09-879-919-16/c
; Sequence 16, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PEP53p1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 16
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-919-16
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Query Match          72.0%; Score 14.4; DB 3; Length 39;
Best Local Similarity 93.8%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      5 CCCAGGCACTCATGG 20
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Db      32 CCCAGGCACTCATGG 17
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Search completed: December 25, 2005, 04:14:25
Job time : 338.6 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds  
(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20  
Sequence: 1 gaccccgagcgcactcatg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:\*

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2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	25	US-11-121-849-322903	Sequence 322903,
2	13.6	68.0	25	US-11-121-849-215831	Sequence 215831,
3	13.6	68.0	25	US-11-121-849-242774	Sequence 242774,
4	13.4	67.0	25	US-11-121-849-453616	Sequence 453616,
5	13.4	67.0	30	US-10-857-780-231	Sequence 231, App
6	13.2	66.0	25	US-11-121-849-29381	Sequence 29381, A
7	13.2	66.0	25	US-11-121-849-242451	Sequence 242451,
8	13.2	66.0	25	US-11-121-849-257893	Sequence 257893,
9	13.2	66.0	25	US-11-121-849-257894	Sequence 257894,
10	13.2	66.0	25	US-11-121-849-281463	Sequence 281463,
11	13.2	66.0	25	US-11-121-849-322904	Sequence 322904,
12	13.2	66.0	25	US-11-121-849-339761	Sequence 339761,
13	13.2	66.0	25	US-11-121-849-529808	Sequence 529808,
14	13.2	66.0	25	US-11-121-849-579848	Sequence 579848,
15	13.2	66.0	75	US-10-802-796-146	Sequence 146, App
16	13.2	65.0	20	US-11-111-288-42	Sequence 42, App
17	13.2	65.0	25	US-11-121-849-13517	Sequence 13517, A
18	13.2	65.0	25	US-11-121-849-20003	Sequence 20003, A
19	13.2	65.0	25	US-11-121-849-134267	Sequence 134267,
20	13.2	65.0	25	US-11-121-849-322063	Sequence 322063,
21	13.2	65.0	25	US-11-121-849-389089	Sequence 389089,
22	13.2	65.0	25	US-11-121-849-486563	Sequence 486563,
23	12.8	64.0	20	US-11-057-808A-1	Sequence 1, Appli

24	12.8	64.0	25	US-11-121-849-4736	Sequence 4736, Ap
25	12.8	64.0	25	US-11-121-849-44648	Sequence 44648, A
26	12.8	64.0	25	US-11-121-849-81862	Sequence 81862, A
27	12.8	64.0	25	US-11-121-849-85032	Sequence 85032, A
28	12.8	64.0	25	US-11-121-849-102642	Sequence 102642,
29	12.8	64.0	25	US-11-121-849-451815	Sequence 451815,
30	12.8	64.0	32	US-10-939-294A-15871	Sequence 15871, A
31	12.8	64.0	32	US-10-939-294A-17408	Sequence 17408, A
32	12.8	64.0	32	US-10-939-294A-18881	Sequence 18881, A
33	12.6	63.0	21	US-10-831-977-1188	Sequence 1188, Ap
34	12.6	63.0	25	US-11-121-849-44860	Sequence 44860, A
35	12.6	63.0	25	US-11-121-849-110613	Sequence 110613,
36	12.6	63.0	25	US-11-121-849-127925	Sequence 127925,
37	12.6	63.0	25	US-11-121-849-282666	Sequence 282666,
38	12.6	63.0	25	US-11-121-849-346687	Sequence 346687,
39	12.6	63.0	25	US-11-121-849-429253	Sequence 429253,
40	12.6	63.0	25	US-11-121-849-604445	Sequence 604445,
41	12.6	63.0	25	US-11-121-849-653664	Sequence 653664,
42	12.6	63.0	26	US-11-069-908-2184	Sequence 2184, Ap
43	12.6	63.0	26	US-11-069-908-4550	Sequence 4550, Ap
44	12.6	63.0	30	US-10-850-359-957	Sequence 957, App
45	12.4	62.0	25	US-11-121-849-25269	Sequence 25269, A

#### ALIGNMENTS

```
RESULT 1
US-11-121-849-322903/c
; Sequence 322903, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 322903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-322903

Query Match      71.0% Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2% Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GACCCCGAGGCACTCATG 19
Db      20 GACGTCAGGCGACACATG 2

RESULT 2
US-11-121-849-215831
; Sequence 215831, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 215831
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LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-215831

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 8.8e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 20  
DB 5 GAGTCCGAGGCACTTCAGG 24

RESULT 3  
US-11-121-849-242774  
Sequence 242774, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 242774  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-242774

Query Match 68.0%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 8.8e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 20  
DB 4 GATCCCGAGGCTCTCATG 23

RESULT 4  
US-11-121-849-453616/c  
Sequence 453616, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 453616  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-453616

Query Match 67.0%; Score 13.4; DB 7; Length 25;  
Best Local Similarity 93.3%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACCCCGAGGCACTC 16  
DB 23 ACCCAGAGGCACTC 9

RESULT 5  
US-10-857-780-231  
Sequence 231, Application US/10857780  
Publication No. US20050272043A1  
GENERAL INFORMATION:  
APPLICANT: ROTH, RICHARD B.  
APPLICANT: BRAUN, ANDREAS  
APPLICANT: KAMMERER, STEFAN M.  
APPLICANT: NELSON, MATTHEW ROBERTS  
APPLICANT: RENELAND, RIKARD HENRY  
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.  
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS  
FILE REFERENCE: SEQ-4069-CP  
CURRENT APPLICATION NUMBER: US/10/857,780  
CURRENT FILING DATE: 2004-05-28  
PRIOR APPLICATION NUMBER: 10/723,681  
PRIOR FILING DATE: 2003-11-25  
PRIOR APPLICATION NUMBER: 60/490,234  
PRIOR FILING DATE: 2003-07-24  
PRIOR APPLICATION NUMBER: 60/525,239  
PRIOR FILING DATE: 2003-11-25  
NUMBER OF SEQ ID NOS: 4962  
SOFTWARE: Patent version 3.2  
SEQ ID NO 231  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic primer  
US-10-857-780-231

Query Match 67.0%; Score 13.4; DB 6; Length 30;  
Best Local Similarity 93.3%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCAGGCACTCATG 19  
DB 16 CCTCGGCACTCATG 30

RESULT 6  
US-11-121-849-29381/c  
Sequence 29381, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma  
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 29381  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-29381

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCAT 18  
DB 21 GACTCCAGAGCACTCAT 4

RESULT 7

```
US-11-121-849-242451/c
; Sequence 242451, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 242451
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-242451
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2  ACCCCAGGCGACTCATG 19
Db      20 ACCCAGGAGCACTCAGG 3

RESULT 8
US-11-121-849-257893
; Sequence 257893, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 257893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-257893
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      3  CCCCCAGGCGACTCATG 20
Db      5  CCTCAGGAGCACTCAGG 22

RESULT 9
US-11-121-849-257894
; Sequence 257894, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 257894
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-257894
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 257894
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-257894
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      3  CCCCCAGGCGACTCATG 20
Db      3  CCTCAGGAGCACTCAGG 20

RESULT 10
US-11-121-849-281463/c
; Sequence 281463, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 281463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-281463
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      3  CCCCCAGGCGACTCATG 20
Db      23 CCCCCAGGCGACTCATG 6

RESULT 11
US-11-121-849-322904/c
; Sequence 322904, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 322904
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-322904
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1  GACCCAGGCGACTCAT 18
Db      11 GACCCAGGCGACTCAT 18
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Db 18 GACGTCAGGCGACAT 1

RESULT 12  
US-11-121-849-339761/C  
; Sequence 339761, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 339761  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-339761

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCCCCAGGCGACTCATG 20  
Db 25 CCACCAGGCGCATGATG 8

RESULT 13  
US-11-121-849-529808/C  
; Sequence 529808, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 529808  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-529808

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCCCAGGCGACTCATG 19  
Db 24 AGCCACAGGCGATTCATG 7

RESULT 14  
US-11-121-849-579848/C  
; Sequence 579848, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 579848  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-579848

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCCAGGCGACTCAT 18  
Db 18 GACCCAGGCGTTCAT 1

RESULT 15  
US-10-802-796-146  
; Sequence 146, Application US/10802796  
; Publication No. US20050250104A1  
; GENERAL INFORMATION:  
; APPLICANT: COLE, STEWART  
; APPLICANT: BUCHRIEER-BROSCH, ROLAND  
; APPLICANT: GORDON, STEPHEN  
; APPLICANT: BILLAUT, ALAIN  
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST  
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED  
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF  
; FILE REFERENCE: 05394.0011-00000  
; CURRENT APPLICATION NUMBER: US/10/802,796  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/09/673,476  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: PCT/IB99/00740  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 09/060,756  
; PRIOR FILING DATE: 1998-04-16  
; NUMBER OF SEQ ID NOS: 743  
; SOFTWARE: Patent In Ver. 2.2  
; SEQ ID NO 146  
; LENGTH: 75  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-10-802-796-146

Query Match 66.0%; Score 13.2; DB 6; Length 75;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCCCAGGCGACTCATG 19  
Db 30 ACCCCAGGCGACTCATG 47

Search completed: December 25, 2005, 04:37:04  
Job time : 135.3 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 : Search time 582 Seconds  
(without alignments)  
1953.383 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20

Sequence: 1 cgacccacagacagaccccc 20

Scoring table: IDENTITY\_NUC

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_in: \*  
3: gb\_env: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pr: \*  
9: gb\_ro: \*  
10: gb\_scs: \*  
11: gb\_sy: \*  
12: gb\_un: \*  
13: gb\_vi: \*  
14: gb\_htg: \*  
15: gb\_pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211669
2	14.4	72.0	60	6	CQ549205
3	14.2	71.0	22	6	AX663589
4	14.2	71.0	37	6	AX527714
5	14.2	71.0	60	6	AR035484
6	13.8	69.0	25	6	AR003361
7	13.8	69.0	30	6	AR261574
8	13.6	68.0	22	6	AR643896
9	13.6	68.0	26	6	AR168794
10	13.6	68.0	26	6	AR168799
11	13.6	68.0	26	6	AR168801
12	13.6	68.0	26	6	127788
13	13.6	68.0	26	6	127793
14	13.6	68.0	26	6	127795
15	13.6	68.0	26	6	AR200263
16	13.6	68.0	26	6	AR200268
17	13.6	68.0	26	6	AR200270
18	13.6	68.0	26	6	AR262395

c 19	13.6	68.0	26	6	AR262400
c 20	13.6	68.0	26	6	AR262402
c 21	13.6	68.0	45	6	AR168795
c 22	13.6	68.0	45	6	AR168796
c 23	13.6	68.0	45	6	BD247106
c 24	13.6	68.0	45	6	BD247106
c 25	13.6	68.0	45	6	127789
c 26	13.6	68.0	45	6	127790
c 27	13.6	68.0	45	6	AR200264
c 28	13.6	68.0	45	6	AR200265
c 29	13.6	68.0	45	6	AR262396
c 30	13.6	68.0	65	6	CQ559333
c 31	13.6	68.0	80	8	HSD58347
c 32	13.6	68.0	87	6	BD034159
c 33	13.6	68.0	87	6	AX282658
c 34	13.6	68.0	87	6	AX898626
c 35	13.4	67.0	32	6	AR083991
c 36	13.4	67.0	60	6	CQ535410
c 37	13.2	66.0	27	6	AR063107
c 38	13.2	66.0	27	6	AR122634
c 39	13.2	66.0	27	6	AR164262
c 40	13.2	66.0	27	6	AR208934
c 41	13.2	66.0	27	6	AR342234
c 42	13.2	66.0	27	6	AR381255
c 43	13.2	66.0	27	6	AR383156
c 44	13.2	66.0	27	6	AR404923
c 45	13.2	66.0	27	6	AR438591

ALIGNMENTS

RESULT 1  
BD211669 20 bp DNA linear PAR 17-JUN-2003  
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.  
LOCUS BD211669.1 GI:33021439  
VERSION BD211669  
KEYWORDS JP 2002512793-A/12.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 20)  
Wright,J.A., Young,A.H. and Lee,Y.S.  
TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation  
JOURNAL Patent: JP 2002512793-A 12 08-MAY-2002;  
GENENSER TECHNOLOGIES INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002512793-A/12  
PD 08-MAY-2002  
PR 23-APR-1999 JP 2000545999  
PI 23-APR-1998 US 60/082791  
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC  
CC Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation  
FH Key Location/Qualifiers  
FT source 1..20  
FT Location/Qualifiers  
1..20 location/Qualifiers  
/organism="Homo sapiens (human)"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

FEATURES  
source  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 76;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGACCCACAGAGCCCCC 20  
Db 1 CGACCCACAGAGCCCCC 20

RESULT 2  
LOCUS C0549205 60 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 18840 from Patent WO0210449.  
ACCESSION C0549205  
VERSION C0549205.1 GI:41515632  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.

REFERENCE 1  
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcritome  
JOURNAL Patent: WO 0210449-A 18840 07-FEB-2002;  
Comugen Inc. (US)

FEATURES  
source Location/Qualifiers  
1..60  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 72.0%; Score 14.4; DB 6; Length 60;  
Best Local Similarity 93.8%; Pred. No. 3.6e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACCCACAGAGCAGC 16  
Db 31 CGACCCACAGAGCTGC 46

RESULT 3  
LOCUS AX663589/c 22 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 19 from Patent WO02092850.  
ACCESSION AX663589  
VERSION AX663589.1 GI:29163808  
KEYWORDS

SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Algaigha,O.M. and Ralston,S.H.  
TITLE Diagnostic method for osteoporosis and related disorders  
JOURNAL Patent: WO 02092850-A 19 21-NOV-2002;  
The University Court of The University of Aberdeen (GB)

FEATURES  
source Location/Qualifiers  
1..22  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

## ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 22;  
Best Local Similarity 84.2%; Pred. No. 5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACCCACAGAGCCCC 19  
Db 19 CGACCCACTCTCAGCCCC 1

RESULT 4  
LOCUS AX527714/c 37 bp DNA linear PAT 21-NOV-2002  
DEFINITION Sequence 86 from Patent WO0228408.  
ACCESSION AX527714  
VERSION AX527714.1 GI:25172254  
KEYWORDS

SOURCE Murinae gen. sp.  
ORGANISM Murinae gen. sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae.

REFERENCE 1  
AUTHORS Houston,L.L., Sheridan,P.J., Hawley,S., Glynn,J.M., Chapin,S. and  
Baey,A.  
TITLE Compositions and methods for the transport of biologically active  
agents across cellular barriers  
JOURNAL Patent: WO 0228408-A 86 11-APR-2002;  
ARIZEXE PHARMACEUTICALS, INC. (US)

FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:39108"

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Query Match 71.0%; Score 14.2; DB 6; Length 37;  
Best Local Similarity 84.2%; Pred. No. 4.8e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACCCACAGAGCCCCC 20  
Db 28 GACCCACAGAGCCCCC 10

RESULT 5  
LOCUS AR035484 60 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 56 from patent US 5871902.  
ACCESSION AR035484  
VERSION AR035484.1 GI:5952152  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 60)  
AUTHORS Weininger,S. and Weininger,A.M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a  
DNA-binding molecule or assembly capable of discriminating perfect  
hybrids from non-perfect hybrids  
JOURNAL Patent: US 5871902-A 56 16-FEB-1999;  
Location/Qualifiers

FEATURES  
source Location/Qualifiers  
1..60  
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## ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 60;  
Best Local Similarity 84.2%; Pred. No. 4.5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACCCACAGAGCCCCC 20  
Db 15 GACCCACAGAGCCCCC 33

RESULT 6  
LOCUS AR003361/c 25 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 8 from patent US 5744303.  
ACCESSION AR003361  
VERSION AR003361.1 GI:3964620  
KEYWORDS



SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Iggo, R., Friend, S.H., Frebourg, T. and Ishioka, C.  
TITLE Functional assay for transcriptional regulator genes  
JOURNAL Patent: US 574303-A 8 28-APR-1998;  
FEATURES Location/Qualifiers  
source 1..25  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 69.0%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 7.8e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCCACAGACAGCCCCC 20  
Db 20 CCCCAGTGCAGCCTCC 4

RESULT 7  
AR61574  
LOCUS AR61574 30 bp DNA linear PAT 29-JAN-2003  
DEFINITION Sequence 11 from patent US 6322976.  
ACCESSION AR61574  
VERSION AR61574.1 GI:28072652  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Altman, T.J., Scott, J. and Stanton, L.N.  
TITLE Compositions and methods of disease diagnosis and therapy  
JOURNAL Patent: US 6322976-A 11 27-NOV-2001;  
Medical Research Council and SCIOS, Inc.; London;  
GBX;  
FEATURES Location/Qualifiers  
source 1..30  
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/mol\_type="genomic DNA"

ORIGIN  
Query Match 69.0%; Score 13.8; DB 6; Length 30;  
Best Local Similarity 88.2%; Pred. No. 7.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCC 18  
Db 9 GACCCCAAGACAGCAC 25

RESULT 8  
AR643896  
LOCUS AR643896 22 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 24 from patent US 6867289.  
ACCESSION AR643896  
VERSION AR643896.1 GI:62782552  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Gorenstein, D.G., Luxon, B.A., Herzog, N. and Aronson, J.  
TITLE Tissue-modified aptamer synthetic methods and compositions  
JOURNAL Patent: US 6867289-A 24 15-MAR-2005;  
Board of Regents, The University of Texas Systems; Austin, TX  
FEATURES Location/Qualifiers  
source 1..22  
/organism="unknown"  
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ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 22;  
Best Local Similarity 80.0%; Pred. No. 9.8e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCC 20  
Db 3 CGCCACACAGACAGCCCC 22

RESULT 9  
AR168794  
LOCUS AR168794/c 26 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 20 from patent US 6288042.  
ACCESSION AR168794  
VERSION AR168794.1 GI:17904898  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando, R.F., Ojwang, J.O., Hogan, M.E., Wallace, T.L. and Cossum, P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 20 11-SEP-2001;  
Location/Qualifiers  
source 1..26  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 9.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACCAACAGACCCCC 4

RESULT 10  
AR168799  
LOCUS AR168799/c 26 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 25 from patent US 6288042.  
ACCESSION AR168799  
VERSION AR168799.1 GI:17904906  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Rando, R.F., Ojwang, J.O., Hogan, M.E., Wallace, T.L. and Cossum, P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 25 11-SEP-2001;  
Location/Qualifiers  
source 1..26  
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ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 9.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACCAACAGACCCCC 4

RESULT 11  
AR168801  
LOCUS AR168801/c 26 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 27 from patent US 6288042.  
ACCESSION AR168801

VERSION AR168801.1 GI:17904909  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1 (bases 1 to 26)  
Rando,R.F., Ojwang,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.  
Anti-viral guanosine-rich tetrad forming oligonucleotides  
Patent: US 6288042-A 27 11-SEP-2001;  
Location/Qualifiers  
1..26  
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/mol\_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 9.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCACAGACAGCCCC 20  
DB 23 CCACCCACCAACAACCCCC 4

RESULT 12  
LOCUS 127788 26 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 20 from patent US 5567604.  
ACCESSION 127788  
VERSION 127788.1 GI:1818564  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1 (bases 1 to 26)  
Rando,R.F., Fennewald,S., Zendeñui,J.G. and Ojwang,J.O.  
Anti-viral guanosine-rich oligonucleotides  
Patent: US 5567604-A 20 22-OCT-1996;  
Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 9.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCACAGACAGCCCC 20  
DB 23 CCACCCACCAACAACCCCC 4

RESULT 13  
LOCUS 127793 26 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 25 from patent US 5567604.  
ACCESSION 127793  
VERSION 127793.1 GI:1818569  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1 (bases 1 to 26)  
Rando,R.F., Fennewald,S., Zendeñui,J.G. and Ojwang,J.O.  
Anti-viral guanosine-rich oligonucleotides  
Patent: US 5567604-A 25 22-OCT-1996;  
Location/Qualifiers  
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ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 9.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCACAGACAGCCCC 20  
DB 23 CCACCCACCAACAACCCCC 4

RESULT 14  
LOCUS 127795/c 26 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 27 from patent US 5567604.  
ACCESSION 127795  
VERSION 127795.1 GI:1818571  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1 (bases 1 to 26)  
Rando,R.F., Fennewald,S., Zendeñui,J.G. and Ojwang,J.O.  
Anti-viral guanosine-rich oligonucleotides  
Patent: US 5567604-A 27 22-OCT-1996;  
Location/Qualifiers  
1..26  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 9.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCACAGACAGCCCC 20  
DB 23 CCACCCACCAACAACCCCC 4

RESULT 15  
LOCUS AR200263/c 26 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 20 from patent US 6355785.  
ACCESSION AR200263  
VERSION AR200263.1 GI:20250337  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1 (bases 1 to 26)  
Rando,R.F., Fennewald,S., Zendeñui,J.G., Ojwang,J.O., Hogan,M.E.,  
Pommier,Y. and Mazumder,A.  
Guanosine-rich oligonucleotide integrase inhibitors  
Patent: US 6355785-A 20 12-MAR-2002;  
Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 26;  
Best Local Similarity 80.0%; Pred. No. 9.7e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCACAGACAGCCCC 20  
DB 23 CCACCCACCAACAACCCCC 4

Search completed: December 24, 2005, 14:06:19  
Job time : 583 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 : Search time 171.4 Seconds  
(without alignments)  
777.677 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20

Sequence: 1 cgacccacagacagcccc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N Geneseq\_21:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3 AAZ31442	AAZ31442 Human neu
2	20	100.0	20	9 ADA74694	ADA74694 GTT3612 a
3	15.4	77.0	34	14 ADX83399	ADX83399 Human TEG
4	14.4	72.0	20	14 ADY58545	ADY58545 Enl gene
5	14.4	72.0	60	6 ABN46092	ABN46092 Human sp1
6	14.2	71.0	22	10 AAD52768	AAD52768 FRA11.1-R
7	14.2	71.0	37	6 ABK81254	ABK81254 Polymun
8	14.2	71.0	37	11 ADL98534	ADL98534 Mouse pol
9	14.2	71.0	41	6 ABS60009	ABS60009 Human DNA
10	14.2	71.0	49	2 AAQ33751	AAQ33751 Upstream
11	14.2	71.0	60	2 AAT30628	AAT30628 Probe nuc
12	14	70.0	35	7 ADS31466	ADS31466 Human tur
13	14	70.0	35	7 ADY36854	ADY36854 Genetic a
14	14	70.0	42	6 ABZ50869	ABZ50869 Human ATP
15	14	70.0	42	6 ABZ48406	ABZ48406 Human ATP
16	14	70.0	42	6 ABZ44642	ABZ44642 Human ATP
17	14	70.0	45	4 AAC82189	AAC82189 Human ret
18	13.8	69.0	25	2 AAQ61824	AAQ61824 Primer fo
19	13.8	69.0	30	3 AAA40611	AAA40611 SHR seque

C	20	13.8	69.0	41	6	ABS60008	ABS60008 Human DNA
C	21	13.8	69.0	41	6	ABS60071	ABS60071 Human DNA
C	22	13.8	69.0	42	14	ADV76922	ADV76922 Human TAA
C	23	13.8	69.0	60	3	AAA05788	AAA05788 Streptavi
C	24	13.6	68.0	22	3	AAA53503	AAA53503 NF-KappaB
C	25	13.6	68.0	22	10	ADD43566	ADD43566 Oligonuc1
C	26	13.6	68.0	25	9	AC158432	AC158432 Human mic
C	27	13.6	68.0	26	2	AAQ79225	AAQ79225 Guanosine
C	28	13.6	68.0	26	2	AAQ79220	AAQ79220 Guanosine
C	29	13.6	68.0	26	2	AAQ79227	AAQ79227 Guanosine
C	30	13.6	68.0	26	2	AAT51645	AAT51645 Viral int
C	31	13.6	68.0	26	2	AAT51638	AAT51638 Viral int
C	32	13.6	68.0	26	2	AAT51643	AAT51643 Viral int
C	33	13.6	68.0	26	2	AAQ79227	AAQ79227 Oligonuc1
C	34	13.6	68.0	26	10	ADG38370	ADG38370 Anti-HIV
C	35	13.6	68.0	32	14	ADY51614	ADY51614 Transcrip
C	36	13.6	68.0	45	2	AAQ79222	AAQ79222 Guanosine
C	37	13.6	68.0	45	2	AAQ79221	AAQ79221 Guanosine
C	38	13.6	68.0	45	2	AAT51639	AAT51639 Viral int
C	39	13.6	68.0	45	2	AAT51640	AAT51640 Viral int
C	40	13.6	68.0	45	2	AAQ79228	AAQ79228 Oligonuc1
C	41	13.6	68.0	45	3	AAA05784	AAA05784 Streptavi
C	42	13.6	68.0	45	10	ADG38352	ADG38352 Anti-HIV
C	43	13.6	68.0	65	6	ABN56220	ABN56220 Mouse sp1
C	44	13.6	68.0	87	3	AAC10414	AAC10414 Human sec
C	45	13.6	68.0	87	4	AAH43509	AAH43509 C1435G SN

#### ALIGNMENTS

RESULT 1  
AAZ31442  
ID AAZ31442 standard; DNA, 20 BP.  
AC AAZ31442;  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Human neuropilin mRNA specific antisense oligo GTT3612.  
XX  
KW Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;  
XX papilloma; diabetic retinopathy; antisense; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN W0955855-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 23-APR-1999; 99WO-CA000324.  
XX  
PR 23-APR-1998; 98US-0082791P.  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
PI Wright JA, Young AH, Lee YS;  
XX WPI; 2000-023357/02.  
DR  
XX Antisense oligonucleotides that inhibit neuropilin expression, useful for  
PT treating cancer.  
FT  
XX  
PS Claim 4; Page 16; 57pp; English.  
CC Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit  
CC human neuropilin expression. The antisense oligonucleotides may be used  
CC to inhibit the growth or metastasis of a mammalian tumor and inhibit  
CC neovascularisation. The oligonucleotides may be used to treat various  
CC forms of cancers or tumors, such as sarcomas, melanomas, adenomas,  
CC carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of  
CC the mouth, throat, larynx and lung, genitourinary cancers such as

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast  
 CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver  
 CC cancer, head and neck cancers, and nervous system cancers, as well as  
 CC benign lesions such as papillomas. The methods may be used to treat  
 CC neovascularisation disorders such as diabetic retinopathy, and  
 CC retinopathy of prematurity and age related macular degeneration  
 XX  
 SQ Sequence 20 BP; 5 A; 12 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CGACCCACAGACAGCCCC 20  
 Db 1 CGACCCACAGACAGCCCC 20  
 RESULT 2  
 ADA74694  
 ID ADA74694 standard; DNA; 20 BP.  
 AC ADA74694;  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE GT1612 antisense oligonucleotide targeted to human neuropilin mRNA.  
 XX  
 XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;  
 KW cytosolic; growth; tumor metastasis; angiogenesis; gene therapy;  
 KW GT1612; antisense; human; ss.  
 XX  
 OS Homo sapiens.  
 PN US2003083274-A1.  
 PD 01-MAY-2003.  
 XX  
 PF 22-APR-1999; 99US-00296264.  
 XX  
 PR 23-APR-1998; 98US-0082791P.  
 XX  
 XX (WRIG/) WRIGHT J A.  
 PA (YOUN/) YOUNG A H.  
 PA (LEEV/) LEE Y S.  
 PI Wright JA, Young AH, Lee YS;  
 DR WPI; 2003-576622/54.  
 XX  
 PT New antisense oligonucleotide that inhibits neuropilin expression, useful  
 PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a  
 PT mammalian tumor.  
 PS  
 XX Claim 1, Page 5; 27pp; English.  
 CC The invention relates to a novel antisense oligonucleotide that inhibits  
 CC the expression of neuropilin, also known as VEGF165R (vascular  
 CC endothelial growth factor receptor). The oligonucleotide of the invention  
 CC demonstrates cytostatic activity and may be useful for inhibiting the  
 CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in  
 CC mammals. Furthermore, the oligonucleotide may be utilised during gene  
 CC therapy. The current sequence is that of the GT1612 antisense  
 CC oligonucleotide of the invention which is targeted to human neuropilin  
 CC mRNA.  
 SQ Sequence 20 BP; 5 A; 12 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 9; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CGACCCACAGACAGCCCC 20

Db 1 CGACCCACAGACAGCCCC 20  
 RESULT 3  
 ADX83399/c  
 ID ADX83399 standard; DNA; 34 BP.  
 AC ADX83399;  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE Human TEG37 associated primer SEQ ID NO 281.  
 XX  
 KW cytosolic; protein purification; diagnosis; cancer; cytostatic;  
 KW neoplasm; respiratory disease; lung tumor; gastrointestinal disease;  
 KW stomach tumor; colon tumor; hepatic tumor; selectable marker; TEG; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 PN WO2005014818-A1.  
 PD 17-FEB-2005.  
 XX  
 PF 06-AUG-2004; 2004WO-JP011650.  
 XX  
 PR 08-AUG-2003; 2003JP-00290704.  
 XX  
 XX (PERS-) PERSBUS PROTEOMICS INC.  
 PA (CHUS) CHUGAI SEIYAKU KK.  
 PA (ABUR/) ABURATANI H.  
 XX  
 PI Aburatani H, Hippo Y, Taniguchi H, Chen YX, Ishikawa S;  
 PI Fukumoto S, Shimamura T, Kamimura N, Guo YQ, Yamamoto S, Ito Y;  
 PI Ito H, Ohmoto T;  
 DR WPI; 2005-173106/18.  
 XX  
 PT Novel protein encoded by any one of TEG1 to TEG64, useful for diagnosing  
 PT and treating cancer e.g. lung, hepatic, stomach, colon or pancreatic  
 PT cancer.  
 PS  
 XX Example 11; SEQ ID NO 281; 462pp; Japanese.  
 CC The invention describes a protein (I) encoded by a gene having a  
 CC nucleotide sequence chosen from any one of 65 fully defined 418-19341  
 CC base pair sequences (SEQ ID No. 1-65) (TEG 1-64) or their fragments. Also  
 CC described are: a protein (II) encoded by a gene having a nucleotide  
 CC sequence chosen from SEQ ID No. 1, 2, 28, 29, 30, 31, 32, 51, 52, 60 and  
 CC 61 or their fragments; a protein (III) encoded by a gene having a  
 CC nucleotide sequence chosen from any one of SEQ ID No. 3-13, 22-27 and 33-  
 CC 55 or their fragments; protein (IV) encoded by a gene having a nucleotide  
 CC sequence chosen from SEQ ID No. 3, 7, 20, 21 and 46-50 or their fragments  
 CC ; a protein (V) encoded by a gene having a nucleotide sequence chosen  
 CC from SEQ ID No. 14-19, 43-45, 56-59 and 62-65 or their fragments; an  
 CC antibody (VI) that specifically recognizes any one of (I)-(V) or their  
 CC fragments; a polynucleotide (VII) complementary to the nucleotide  
 CC sequence of any one of SEQ ID No. 1-65 or a polynucleotide sequence  
 CC capable of hybridizing with SEQ ID No. 1-65; a polynucleotide (VIII)  
 CC comprising at least 12 consecutive nucleotides in any one SEQ ID No. 1-65  
 CC or a polynucleotide sequence capable of hybridizing with this nucleotide;  
 CC a composition (C1) for diagnosing or treating lung cancer; a composition  
 CC (C2) for diagnosing or treating stomach cancer; composition (C3) for  
 CC diagnosing or treating colon cancer; a composition (C4) for diagnosing or  
 CC treating hepatic cancer; a vector (IX) comprising (VII) or (VIII); a cell  
 CC (X) comprising (IX); identifying (M1) a compound having anticancer  
 CC activity; and diagnosing (M2) cancer. Proteins (I)-(V), an antibody (VI)  
 CC that specifically binds the proteins and polynucleotides (VII) and (VIII)  
 CC are useful for diagnosing cancer. (M2) comprising measuring the  
 CC expression level of (I)-(V) or (VII) or (VIII), or obtaining sample  
 CC (blood serum or plasma), and detecting C20orf102 protein in the obtained  
 CC sample is also useful for diagnosing cancer such as lung cancer, hepatic

CC cancer or pancreatic cancer, where the C20orf102 protein is a secreted or  
CC extracellular C20orf102 protein, which is detected using an antibody  
CC which recognizes C20orf102 protein. A composition (C1) comprising protein  
CC (II) is useful for diagnosing or treating lung cancer. A composition (C2)  
CC comprising protein (III) is useful for diagnosing or treating stomach  
CC cancer. A composition (C3) comprising protein (IV) is useful for  
CC diagnosing or treating colon cancer. A composition (C4) comprising (V) is  
CC useful for diagnosing or treating hepatic cancer. (M1) comprising  
CC contacting a cultured human cell with a test compound and identifying a  
CC compound that causes a change in expression level of the gene which  
CC contains the nucleotide sequence in any one of SEQ ID No. 1-65 is useful  
CC for identifying a compound having anticancer activity. A vector (IX) or  
CC cell (X) is useful for producing (I) or (VI). An antibody (VI) is useful  
CC as a cancer diagnostic marker. This sequence represents a human TEG37  
CC associated primer.

XX  
XX Sequence 34 BP; 2 A; 9 C; 13 G; 10 T; 0 U; 0 Other;

Query Match 77.0%; Score 15.4; DB 14; Length 34;  
Best Local Similarity 94.1%; Pred. No. 2.9e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCC 18  
DB 25 GACCCACAGACAGCCC 9

RESULT 4  
ADY58545/C  
ID ADY58545 standard; DNA; 20 BP.

XX  
XX ADY58545;

XX  
XX 19-MAY-2005 (first entry)

XX  
XX En1 gene RT-PCR primer.

XX  
XX Stem cell; neuron; En1; cell therapy; Parkinsons disease;

XX  
XX antiParkinsonian; neurological disease; RT-PCR;

XX  
XX reverse transcriptase PCR; primer; ss.

XX  
XX Homo sapiens.

XX  
XX WO2005021720-A2.

XX  
XX 10-MAR-2005.

XX  
XX 27-AUG-2004; 2004WO-US027841.

XX  
XX 29-AUG-2003; 2003US-0498831P.

XX  
XX 02-SEP-2003; 2003US-0499570P.

XX  
XX (WISC ) WISCONSIN ALUMNI RES FOUND.

XX  
XX Zhang S, Thomson JA, Duncan ID, Li X;

XX  
XX WPI; 2005-223178/23.

XX  
XX Creating synchronous cell populations cultured from embryonic stem cells  
XX and have early rosette morphology comprises propagating embryonic stem  
XX cells into embryoid bodies and propagating the embryoid bodies into  
XX neural stem cells.

XX  
XX Example 2; Page 52; 84pp; English.

XX  
XX The invention provides a method of creating a synchronous population of  
XX cells from primate embryonic stem cells and which are characterized as  
XX Sox1-/Pax6+ and or an early rosette morphology. This involves:  
XX propagating embryonic stem cells into embryoid bodies; and propagating  
XX the embryoid bodies into a synchronous population of neural stem cells in  
XX the form of early rosettes, in the presence of FGF2, FGF9 or FGF4.

XX  
XX A method of creating a population of synchronized neural stem cells that  
XX are Pax6+/Sox1+ comprises culturing Sox1-/Pax6+ cells of early rosette

CC morphology for 4-6 days in the presence of FGF2, FGF4, FGF9 or RA. Cells  
CC cultured with FGF8 are En1+ and may be further cultured with SHH to  
CC produce a population of midbrain dopamine neurons. Cells cultured with  
CC FGF2 are Bfl+ and may be further cultured with SHH to produce a  
CC population of forebrain dopamine neurons. Cells cultured with RA are Hox+  
CC and may be further cultured to produce a population of spinal motor  
CC neurons. Also provided are methods of examining a test compound for the  
CC ability to perturb neural cell development. The present sequence is that  
CC of a RT-PCR primer for En1. This was used in an example from the  
CC invention describing the generation of midbrain dopaminergic (DA) neurons  
CC from human embryonic stem cells. The RT-PCR analysis indicated that En1  
CC is not expressed at a high level until neuroectodermal cells  
CC differentiate into DA neurons. DA dopaminergic neurons may be used for  
CC toxicological and pharmaceutical screening and for potential cell therapy  
CC in Parkinson's disease.

XX  
XX Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 14; Length 20;  
Best Local Similarity 93.8%; Pred. No. 7.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGC 16  
DB 16 CGACCCACAGACTGC 1

RESULT 5  
ABN46092  
ID ABN46092 standard; DNA; 60 BP.

XX  
XX ABN46092;

XX  
XX 15-JUN-2002 (first entry)

XX  
XX Human spliced transcript detection oligonucleotide SEQ ID NO:18840.

XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;

XX  
XX splice variant; transcriptome; oligonucleotide library; ss.

XX  
XX Homo sapiens.

XX  
XX WO200210449-A2.

XX  
XX 07-FEB-2002.

XX  
XX 20-JUL-2001; 2001WO-1B001903.

XX  
XX 28-JUL-2000; 2000US-0221607P.

XX  
XX 02-MAY-2001; 2001US-0287724P.

XX  
XX (COMP-) COMPUGEN INC.

XX  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX  
XX WPI; 2002-257383/30.

XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
XX selectively hybridize to mRNAs transcribed from a transcription unit of a  
XX genome, useful for detecting tissue-, pathology-, and developmental-  
XX specific genes.

XX  
XX Example 1; SEQ ID NO 18840; 47pp; English.

XX  
XX The present invention describes oligonucleotide libraries for detecting  
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
XX )transcriptome comprises messenger RNAs transcribed from multiple  
XX transcription units that populate a genome. The library comprises several  
XX oligonucleotides, each capable of hybridizing selectively to a set of  
XX messenger RNAs transcribed from a given transcription unit of the genome,  
XX which encodes one or more messenger RNA splice variants. The

XX  
XX oligonucleotide libraries are useful for detecting mRNAs from a  
XX biological sample, in expression profiling studies, in qualitatively or

CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPRO at ftp.wipro.int/pub/published\_pct\_sequences  
XX

SO Sequence 60 BP; 15 A; 17 C; 14 G; 14 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 6; Length 60;  
Best Local Similarity 93.8%; Pred. No. 8.1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACCCCGACAGCAGC 16  
|||  
Db 31 CGACCCCGACAGCAGC 46

RESULT 6  
AADS2768/C  
ID AADS2768 standard; DNA; 22 BP.  
XX  
AC AADS2768;  
XX  
DT 14-MAY-2003 (first entry)  
XX  
DE FRA11.1-R PCR primer used to screen mutations in human fra-1 gene.  
XX  
KW Bone mineral density; BMD; Fos related antigen-1 gene; osteoporosis;  
KW Fra-1; genetic marker; gene therapy; osteopathic; PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
PN WO200292850-A2.  
XX  
PD 21-NOV-2002.  
XX  
PF 17-MAY-2002; 2002WO-GB002263.  
XX  
PR 17-MAY-2001; 2001GB-00012075.  
XX  
PA (UYAB-) UNIV ABERDEEN.  
XX  
PI Alagha OME, Ralston SH;  
XX  
DR WPI; 2003-120697/11.  
XX  
PT Determining the susceptibility of an individual to a disorder associated  
PT with an abnormal level of bone mineral density, useful for diagnosing  
PT osteoporosis, comprises the use of Fos related antigen-1 gene (Fra-1)  
PT marker.  
XX  
PS Example 2; Page 31; 56pp; English.  
XX  
CC The invention relates to a method for determining the susceptibility of  
CC an individual to a disorder associated with an abnormal level of bone  
CC mineral density (BMD), comprising the use of Fos related antigen-1 gene  
CC (Fra-1) marker. The methods are useful for determining the susceptibility  
CC of an individual to a disorder associated with an abnormal level of BMD  
CC or for diagnosing osteoporosis. The single nucleotide polymorphisms are  
CC useful as genetic markers to identify people with low BMD, so that these  
CC individuals could be targeted for treatment to prevent osteoporosis. The  
CC Fra-1 nucleic acid sequences may be used in gene therapy to treat or  
CC prevent a BMD-associated disorder such as osteoporosis. The present DNA  
CC sequence is a PCR primer used to screen mutations in human fra-1 gene.

CC This sequence is used in the exemplification of the invention  
XX  
SO Sequence 22 BP; 3 A; 3 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 10; Length 22;  
Best Local Similarity 84.2%; Pred. No. 9.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACCCCGACAGCAGCCCC 19  
|||  
Db 19 CGACCCCGACAGCAGCCCC 1

RESULT 7  
ABK81254/C  
ID ABK81254 standard; DNA; 37 BP.  
XX  
AC ABK81254;  
XX  
DT 13-AUG-2002 (first entry)  
XX  
DE Polymunoglobulin receptor (p1gr) related primer #44.  
XX  
KW Transcellular transport; transcytotic transport; paracellular transport;  
KW respiratory system disorder; lung cancer; tumour; asthma;  
KW pathogenic infection; allergy-related disorder;  
KW gastrointestinal tract disorder; gastrointestinal hormone disorder;  
KW Chron's disease; eating disorder; polymunoglobulin receptor; p1gr;  
KW primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200226408-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 02-OCT-2001; 2001WO-US030832.  
XX  
PR 02-OCT-2000; 2000US-0237929P.  
PR 13-NOV-2000; 2000US-0248478P.  
PR 14-NOV-2000; 2000US-0248819P.  
PR 09-FEB-2001; 2001US-0267601P.  
XX  
PA (ARIZ-) ARIZKE PHARM INC.  
XX  
PI Houston LL, Sheridan PJ, Hawley S, Glynn JM, Chapin S, Basu A;  
XX  
DR WPI; 2002-416628/44.  
XX  
PT Complex useful for transporting active agent through epithelial barrier,  
PT has biologically active portion and target element directed to ligand  
PT that confers e.g. transcytotic properties to agent specific to ligand.  
XX  
PS Example 3; Fig 12B; 379pp; English.  
XX  
CC The invention described a complex or compound (I) comprising a  
CC biologically active portion and a target element (II) directed to a  
CC ligand that confers transcellular, transcytotic or paracellular  
CC transporting properties to an agent specifically bound to the ligand,  
CC where (II) is not an antibody. Alternatively, (I) comprises two or more  
CC (II) directed to one or more ligands. (I) is useful for delivering a  
CC biologically active agent to an animal, for transporting an active agent  
CC through an epithelial or mucosal barrier, and for treating or identifying  
CC a disease in an animal e.g. diseases of the respiratory system including  
CC lung cancer and tumours, asthma, pathogenic infections, allergy-related  
CC disorders, gastrointestinal tract disorders, disorders relating to  
CC gastrointestinal hormones, Chron's disease, eating disorders and any  
CC disease or disorder involving polymunoglobulin receptor (p1gr)  
CC displaying cells. This sequence represents a primer associated with the  
CC transport of biologically active agents across cellular barriers  
XX  
SO Sequence 37 BP; 3 A; 13 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 37;  
Best Local Similarity 84.2%; Pred. No. 9.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACGCCCC 20  
28 GACGCCACAGACGCCCC 10

Db

RESULT 8  
ADL99534/C  
ID ADL99534 standard; DNA; 37 BP.  
XX  
AC ADL99534;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Mouse polyimmunoglobulin receptor (pigr) primer #7.  
XX  
KW antiapoptotic; antiinflammatory; neuroprotective; ophthalmological;  
KW gastrointestinal; osteopathic; nephrotoxic; gene therapy;  
KW multicentric molecular complex; transcytotic transport;  
KW paracellular transport; calcitonin; osteoporosis; renal failure; colitis;  
KW gastroenteritis; inflammatory bowel disease; psoriasis;  
KW Alzheimer's disease; optic neuropathy; ophthalmoplegia;  
KW polyimmunoglobulin receptor; pigr; endocytosis; exocytosis; mouse; PCR;  
KW primer; ss.  
XX  
OS Mus sp.  
XX  
PN US2003166160-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 06-SEP-2001; 2001US-00949039.  
XX  
PR 06-SEP-2001; 2001US-00949039.  
XX  
PS (HAWL/) HAWLEY S B.  
PA (CHAP/) CHAPIN S.  
PA (SHER/) SHERIDAN P L.  
PA (HOU/) HOUSTON L L.  
PA (GLYN/) GLYNN J M.  
XX  
PI Hawley SB, Chapin S, Sheridan PL, Houston LL, Glynn JM;  
XX WPI; 2003-898076/82.  
XX  
DR WPI; 2003-898076/82.  
XX  
PT New multimeric molecular complex, useful for preparing a composition for  
PT diagnosing or treating e.g. osteoporosis, renal failure, colitis,  
PT gastroenteritis, inflammatory bowel disease, psoriasis or Alzheimer's  
PT disease.  
XX  
PS Example 2; Fig 7B; 91pp; English.  
XX  
XX The invention describes a multimeric molecular complex comprising at  
CC least 2 compounds, each of which has at least one targeting element  
CC directed to a ligand that confers transcytotic or paracellular  
CC transporting properties to a molecular complex specifically bound to the  
CC ligand. Also described are: a compound comprising at least 2 targeting  
CC elements directed to the ligand; a protein conjugate comprising a  
CC biologically active calcitonin polypeptide having a chemical linkage to  
CC at least one targeting element directed to the ligand; a pharmaceutical  
CC composition comprising the compound, delivering a biologically active  
CC agent to an animal; transporting a biologically active agent through an  
CC epithelial barrier; treating a disease in an animal; and identifying a  
CC disease in an animal. The complex is useful for preparing a composition  
CC for diagnosing or treating diseases, e.g., osteoporosis, renal failure,  
CC colitis, gastroenteritis, inflammatory bowel disease, psoriasis,  
CC Alzheimer's disease, optic neuropathy or ophthalmoplegia. This sequence  
CC represents a primer used in the isolation of mouse polyimmunoglobulin  
CC receptor (pigr), a mediator of endocytosis, exocytosis and forward and  
CC reverse transcytosis in epithelial cells.

XX  
SQ Sequence 37 BP; 3 A; 13 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 11; Length 37;  
Best Local Similarity 84.2%; Pred. No. 9.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACGCCCC 20  
28 GACGCCACAGACGCCCC 10

Db

RESULT 9  
ABS60009/C  
ID ABS60009 standard; DNA; 41 BP.  
XX  
AC ABS60009;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Human DNA containing a single nucleotide polymorphism #33.  
XX  
KW Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;  
KW bradykinin receptor B1; TACR1, C1 esterase inhibitor; C1NH; kallikrein 1;  
KW KLR1; bradykinin receptor B2; BDKRB2; gene therapy;  
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
KW myocardial infarction; ventricular hypertrophy; vascular disease;  
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
KW autoimmune disease; inflammatory arthritis; cancer; wound;  
KW viral infection; bacterial infection; fungal infection; COPD;  
KW Chronic obstructive pulmonary disease; enterocolitis;  
KW single-nucleotide polymorphism.  
XX  
OS Homo sapiens.  
XX  
XX WO200261131-A2.  
XX  
PN 08-AUG-2002.  
XX  
PD 03-DEC-2001; 2001WO-US047235.  
XX  
PF 04-DEC-2000; 2000US-0251015P.  
XX  
PR 23-JAN-2001; 2001US-0263678P.  
XX  
PR 02-MAR-2001; 2001US-0273037P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUI/) HUI L.  
XX  
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
XX Swanson BN, Powell JR;  
XX WPI; 2002-619265/66.  
XX  
DR WPI; 2002-619265/66.  
XX  
PT New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.  
XX  
PS Claim 3; Page 670; 977pp; English.  
XX  
XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (KLR1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridises to a  
CC nucleotide polymorphism comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence represents or contains the  
 CC region surrounding a single-nucleotide polymorphism in one of the genes  
 CC encoding one of the proteins listed above

XX Sequence 41 BP; 5 A; 10 C; 17 G; 9 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 41;

Best Local Similarity 84.2%; Pred. No. 9.7e+03; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCCC 20  
 Db 28 GTCCCCACAGCAGCAGCCC 10

RESULT 10

AA033751/c ID AA033751 standard; DNA; 49 BP.

XX AA033751;

AC 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Upstream sequence of microsatellite from clone TGLM162.

KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.

OS Bos taurus.

PN WO9213102-A1.

PD 06-AUG-1992.

PF 15-JAN-1992; 92WO-US000340.

PR 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

PI Georges M, Maesey JM;

DR WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 XX

PS Table 7, Page 229; 517pp; English.

XX The sequence is that upstream of a bovine microsatellite sequence obtd.  
 CC by screening a library of bovine MboI DNA fragments of between 250 and  
 CC 500 bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the coreseq.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AA033501-34437. (updated on 25-MAR-2003 to correct PN  
 CC field.)

XX Sequence 49 BP; 12 A; 11 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 2; Length 49;

Best Local Similarity 84.2%; Pred. No. 9.8e+03; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCC 19  
 Db 19 CGACCCCATAGCGGACCC 1

RESULT 11

AAT30628 ID AAT30628 standard; cDNA; 60 BP.

XX AAT30628;

DT 21-FEB-1997 (first entry)

XX Probe nucleic acid #11.

XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; Sp1;  
 KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
 KW virus; ss.

XX Synthetic.

XX WO9617956-A2.

PN 13-JUN-1996.

PF 07-DEC-1995; 95WO-US015944.

PR 09-DEC-1994; 94US-00353476.

XX (GENE-) GENE POOL INC.

PI Weininger S, Weininger AM;

DR WPI; 1996-287199/29.

XX Probe nucleic acids, target binding assemblies, etc - for detection and  
 PT localisation of specific nucleic acid sequences, esp. HIV and HPV.

XX Disclosure; Page 82; 172pp; English.

XX AAT30615-T30634 represent probe nucleic acids of the invention. The probe  
 CC of the invention contains a target binding region (TBR), a booster  
 CC binding region (BBR), and an optional support or attachment (OSA). The  
 CC target binding assembly (TBA) recognised by the TBR (see AAT30581-T30614)  
 CC of the probe, contains at least one nucleic acid recognition unit (NAR),  
 CC and optionally a linker sequence, an assembly sequence (see AAR5994-



CC R95998), an asymmetry sequence (see AAR95999-R96006), a nuclear  
CC localization signal sequence (see AAR96007), and an OSA. The assembly  
CC sequence and asymmetry sequences are responsible for the folding and  
CC association of the NARs. The NARs (see AAR95965-R95993) are selected from  
CC NF-Kappa-B, SP1, TATA, human papillomavirus (HPV) E2, HPV LTR, human  
CC immunodeficiency virus (HIV) LTR and Tat binding units. The linker  
CC sequence is an oligopeptide, which does not interfere with NAR function,  
CC but provides stability and control over the spacing of the NAR from the  
CC rest of the TNA. The OSA is an attached support or indicator, or other  
CC means of localization of the probe. The probe can be used in a method for  
CC detecting or localising a specific target nucleic acid sequence (TNA).  
CC The method is highly sensitive, and has a high degree of specificity. The  
CC method can be used for detecting specific nucleic acid sequences,  
CC including those found in human cells, in HIV, HPV, and other nucleic acid  
CC containing systems, including bacteria and viruses

XX SQ Sequence 60 BP; 16 A; 23 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 2; Length 60;  
Best Local Similarity 84.2%; Pred. No. 9.9e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCCC 20  
DB 15 GACACACAGACAGCCGCC 33

RESULT 12  
ADS31466  
ID. ADS31466 standard; DNA; 35 BP.  
XX AC  
XX ADG31466;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human Turner syndrome repeat-free probe #4 reverse PCR primer.  
XX KW Human: in situ hybridisation; Southern blot; chromosome breakpoint;  
XX inherited genetic disease; neoplastic disorder; ss; PCR; primer.  
XX OS Homo sapiens.  
XX FN US2003224356-A1.  
XX PD 04-DEC-2003.  
XX PF 14-MAY-2001; 2001US-00854867.  
XX PR 16-MAY-2000; 2000US-00573080.  
XX PA (KNOL/) KNOOL J H M.  
XX PG (ROGA/) ROGAN P K.  
XX PI KNO1 JHM, Rogan PK,  
XX DR WPI: 2002-062378/08.  
XX PT Single copy genomic hybridization probes for detecting specific nucleic  
XX acid sequences in sample by in situ hybridization useful for detection of  
XX acquired or inherited genetic diseases.

PS Claim 37; SEQ ID NO 499; 30pp; English.

XX CC The invention relates to a nucleic acid hybridisation probe comprising a  
XX labelled, single copy nucleic acids of at least 50 nucleotides, which  
XX will hybridise to a deduced single copy sequence interval in target  
XX nucleic acid (TNA) of known sequence. The single copy sequence is deduced  
XX by comparing the target nucleic acid (e.g. a disease causing gene) with a  
XX collection of high and low complexity repeat sequences as found in the  
XX genome of the organism from containing the target nucleic acid. The probe  
XX is generated by PCR on the target sequence. The probe is essentially free  
XX of blocking nucleic acid sequences which will hybridise to repeat  
XX sequences within the genome of which the TNA is a part, and is labelled

CC with a label selected from fluorochrome-responsive labels, fluorochromes,  
CC calorimetric chemical, conjugated proteins, antibodies, antigens and  
CC their mixtures. The probe is useful in a hybridisation method, where the  
CC hybridisation method is from in situ hybridisation, Southern blot, and  
CC other methods in which nucleic acid is immobilised, where the method  
CC further comprises selecting a single copy nucleic acid which will  
CC hybridise to a duplication or triplicon sequence domain. The probe is useful  
CC for determining the existence of previously unknown repeat sequence  
CC families in a genome. The method comprises reacting a labelled probe with  
CC the genome, causing the probe to hybridise and ascertaining if the probe  
CC hybridises to the genome at more than three preferably ten different  
CC locations as a determination of new repeat sequence family, where the  
CC determining step comprises selecting the single copy sequence from a  
CC duplication or triplicon sequence domain. The probe is useful for  
CC determining a chromosome breakpoint and is useful in the fields for  
CC cytogenetics and molecular genetics for determining the presence of  
CC specific nucleic acid sequences in a sample of eukaryotic origin, e.g.  
CC the probes may be used to analyse specific chromosomal locations by in  
CC situ hybridisation as a detection of acquired or inherited genetic  
CC diseases especially for detection of genetic or neoplastic disorders.  
CC Unlike prior art techniques, the probe permits more precise chromosomal  
CC breakpoint determinations by in situ hybridisation. The present sequence  
CC is a PCR primer used to amplify a single copy sequence probe for a human  
CC gene associated with an inheritable genetic disorder. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docid=20030224356.

XX SQ Sequence 35 BP; 8 A; 15 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 7; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCACAGACAGCCCC 19  
DB 15 CCACAGACAGCCGCC 28

RESULT 13  
ADY36854  
ID. ADY36854 standard; DNA; 35 BP.  
XX AC  
XX ADY36854;  
XX DT 05-MAY-2005 (first entry)  
XX DE Genetic abnormality detection associated primer SEQ ID NO 499.  
XX KW hybridization; DNA detection; neoplasm; genetic disorder; cytogenetics;  
XX PCR; primer; ss; turners syndrome; endocrine-gen.; endocrine disease;  
XX Chromosome aberration; genetic disorder.  
XX OS Homo sapiens.  
XX FN WO200188089-A2.  
XX PD 22-NOV-2001.  
XX PF 15-MAY-2001; 2001WO-US015674.  
XX PR 16-MAY-2000; 2000US-00573080.  
XX PG 14-MAY-2001; 2001US-00854867.  
XX PA (CHIL-) CHILDREN'S MERCY HOSPITAL.  
XX PI KNO1 JHM, Rogan PK, Cazarro PM;  
XX DR WPI: 2002-062378/08.  
XX PT Single copy genomic hybridization probes for detecting specific nucleic  
XX acid sequences in sample by in situ hybridization useful for detection of  
XX acquired or inherited genetic diseases.

XX Claim 36; SEQ ID NO 499; 67pp; English.  
PS  
XX The invention describes a nucleic acid hybridization probe (I) comprising  
CC a labeled, single copy nucleic acids of at least 50 nucleotides, which  
CC will hybridize to a deduced single copy sequence interval in target  
CC nucleic acid (TNA) of known sequence. (I) is useful in a hybridization  
CC method which comprises preparing a reaction mixture comprising TNA and  
CC (I) which hybridizes to TNA, and causing (I) to hybridize to TNA, where  
CC the hybridization method is from in situ hybridization, Southern blot,  
CC and other methods in which nucleic acid is immobilized, where the method  
CC further comprises selecting a single copy nucleic acid which is useful for:  
CC hybridize to a duplication or triplicon sequence domain. (I) is useful for:  
CC determining the existence of previously unknown repeat sequence families  
CC in a genome; determining a chromosome breakpoint and in the fields of  
CC cytogenetics and molecular genetics for determining the presence of  
CC specific nucleic acid sequences in a sample of eukaryotic origin, e.g.  
CC the probes may be used to analyze specific chromosomal locations by in  
CC situ hybridization as a detection of acquired or inherited genetic  
CC diseases especially for detection of genetic or neoplastic disorders.  
CC Unlike prior art techniques, (I) permits more precise chromosomal  
CC breakpoint determinations by in situ hybridization. Hybridization  
CC techniques utilizing (I), have made it possible to obtain reliable,  
CC easily detectable signals with relatively small probes. A readily  
CC detectable signal was obtained with a probe on the order of 2 kb in  
CC length, using fluorescent in situ hybridization (FISH) technology. This  
CC sensitivity of (I) is improved compared to the prior art, because the  
CC probes of (I) are homogeneous single copy sequences. However, smaller  
CC amplified segments, each comprising non-repetitive sequences, may also be  
CC used in combination as probes to achieve adequate signals for in situ  
CC hybridization. Complex single copy probes that hybridize to duplicated or  
CC triplicated targets can also increase hybridization signals. This  
CC sequence represents a primer used in the isolation of a gene probe for  
CC detection of a human cytogenetic abnormality and genetic disorder.  
XX  
SQ Sequence 35 BP; 8 A; 15 C; 6 G; 6 T; 0 U; 0 Other;  
Query Match 70.0%; Score 14; DB 7; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 CCACAGACAGCCCC 19  
DB 15 CCACAGACAGCCCC 28  
RESULT 14  
ABZ50869/C  
ID ABZ50869 standard; DNA; 42 BP.  
XX  
AC ABZ50869;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human ATP-binding cassette ABCB3/TAP1 gene polymorphic site, #7651.  
XX  
KW Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 6;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT variation replace(20..23,GTGTGGGTGGAG)  
TT /\*tag= a  
XX  
XX WO200252044-A2.  
XX  
XX 04-JUL-2002.  
XX  
XX 27-DEC-2001; 2001WO-JP011592.  
XX

PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP--00135256.  
PR 27-AUG-2001; 2001JP--00256862.  
XX  
XX (RIKE ) RIKEN KK.  
XX  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
XX WPI; 2002-583571/62.  
XX  
PT Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
XX nucleic acid.  
XX  
PS Claim 23; Page 223; 2785pp; English.  
XX  
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
XX encoding enzymes associated with drug metabolism. The invention relates  
XX to methods and compositions for identifying individuals who have at least  
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The  
XX polymorphisms may be identified in a nucleic acid sample using probes or  
XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
XX variety of detection assays, including hybridisation assays, nucleic acid  
XX arrays and PCR-based methods. The invention also encompasses methods of  
XX evaluating and screening drugs using genetic polymorphism data. Genetic  
XX polymorphism data, particularly that relating to single nucleotide  
XX polymorphisms (SNPs), may be used in studying the relationship between  
XX DNA sequence variations and human diseases, conditions, and responses to  
XX drugs. SNPs are also useful as polymorphism markers for discovering genes  
XX that cause or exacerbate certain diseases. SNPs are particularly useful  
XX in the above respects as they are stable in populations, occur  
XX frequently, and have lower mutation rates than other genome variations  
XX such as repeating sequences. The detection and analysis of polymorphisms  
XX in genes encoding drug metabolizing enzymes allows the customisation of  
XX drug therapies based upon the genetic profile of individual patients.  
XX This would not only take the guesswork out of selecting the drug with the  
XX greatest therapeutic effect for a particular patient, but would also  
XX reduce the likelihood of adverse reactions, thereby increasing safety.  
XX Methods of the invention are also useful in the drug discovery and  
XX approval processes. For example, individuals could be selected for  
XX clinical trials only if their genetic profiles indicate that they are  
XX capable of responding to a particular drug or drug class, and previously  
XX failed drug candidates could be revived if they were matched with more  
XX appropriate patient populations. The methods, data and compositions of  
XX the invention may therefore lead to an increase in the range of  
XX possible drug targets and decreases in the number of adverse drug  
XX reactions, failed drug trials, the time taken for a drug to be approved,  
XX the length of time patients are on medication and the number of different  
XX medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 42 BP; 5 A; 4 C; 24 G; 9 T; 0 U; 0 Other;  
Query Match 70.0%; Score 14; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 7 CACAGACAGCCCC 20  
DB 33 CACAGACAGCCCC 20  
RESULT 15  
ABZ48406/C  
ID ABZ48406 standard; DNA; 42 BP.  
XX  
XX ABZ48406;  
XX  
XX 26-JUN-2003 (first entry)  
XX  
XX Human ATP-binding cassette ABCB2/TAP2 gene polymorphic site, #5189.  
XX  
XX Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 6;  
XX

KM polymorphic site; drug evaluation; drug screening; genotyping;  
 KM genetic profiling; therapeutic customization; adverse reaction;  
 KM clinical trial; drug approval; ds.

OS Homo sapiens.

Key Location/Qualifiers  
 FT replacement(20..23,GTGCTGGGGTGGAG)  
 FT /+tag= a

PN WO200252044-A2.

XX 04-JUL-2002.

PF 27-DEC-2001; 2001WO-UP011592.

PR 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.

XX 27-AUG-2001; 2001JP-00256862.

PA (RIKE ) RIKEN KK.

PI Nakamura Y, Sekine A, Iida A, Saito S;

DR WPI; 2002-583571/62.

PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.

PS Claim 23; Page 165; 2785pp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from AB243217-AB250887 using a  
 CC variety of detection assays, including hybridization assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphisms (SNPs), particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolizing enzymes allows the customization of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy

XX Sequence 42 BP; 5 A; 4 C; 24 G; 9 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 6; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 CACAGACAGCCCCC 20  
 |||||  
 Db 33 CACAGACAGCCCCC 20

Search completed: December 24, 2005, 12:29:08  
 Job time : 173.4 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds  
(without alignments)  
595.256 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20

Sequence: 1 cgaccacacagacagaccccc 20

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	74.0	41	2	BG616493
2	14.8	74.0	58	11	CR187505
3	14.2	71.0	53	7	CV604285
4	14.2	71.0	85	9	AZ428622
5	13.8	69.0	40	1	AA877262
6	13.8	69.0	49	1	AI815199
7	13.8	69.0	52	10	CL267582
8	13.8	69.0	76	1	AI601162
9	13.8	69.0	79	8	HA2857
10	13.8	69.0	83	11	CR828745
11	13.8	69.0	90	10	EX218915
12	13.8	69.0	93	9	AZ949869
13	13.8	69.0	100	2	BG213902
14	13.6	68.0	61	1	AI015169
15	13.6	68.0	64	1	AI061438
16	13.6	68.0	66	9	AQ254888
17	13.6	68.0	66	9	CC536588
18	13.6	68.0	66	11	DME547169
19	13.6	68.0	70	1	AI856414
20	13.6	68.0	73	9	AQ254591
21	13.6	68.0	82	8	T25069
22	13.6	68.0	82	8	T25069

23	13.6	68.0	91	11	DME546741	AJ546741 Drosophila
24	13.6	68.0	92	1	AA886273	AA886273 o338f06.s
25	13.6	68.0	94	10	CZ071607	CZ071607 TRGA SSRO
26	13.4	67.0	49	7	CN601471	CN601471 EG-MOI_00
27	13.4	67.0	53	11	CR095894	CR095894 Reverse s
28	13.4	67.0	88	1	AA270168	AA270168 vas58h01.r
29	13.4	67.0	97	5	B0614622	B0614622 Ik99e01.y
30	13.2	66.0	44	10	AJ596054	AJ596054 Arabidops
31	13.2	66.0	45	9	AZ954608	AZ954608 2M0220524
32	13.2	66.0	61	1	AI612903	AI612903 cy3d04.x
33	13.2	66.0	61	8	H39535	H39535 y168a08.r1
34	13.2	66.0	66	9	AF219041	AF219041 AF219041
35	13.2	66.0	69	7	CR559334	CR559334 DKF2P4680
36	13.2	66.0	72	3	B0271752	B0271752 Ik17h10.x
37	13.2	66.0	73	3	BM128826	BM128826 Ik17h08.x
38	13.2	66.0	81	1	AI828860	AI828860 t68h12.x
39	13.2	66.0	82	10	AL943582	AL943582 Arabidops
40	13.2	66.0	84	2	BE566379	BE566379 601339975
41	13.2	66.0	84	8	W21701	W21701 ZEST00787 M
42	13.2	66.0	86	3	BM312177	BM312177 Ig41b10.x
43	13.2	66.0	87	10	CLJ302042	CLJ302042 P009E08 G
44	13.2	66.0	90	3	BM353195	BM353195 Ig7b05.x
45	13.2	66.0	97	2	BE463686	BE463686 hx7b04.x

#### ALIGNMENTS

RESULT 1  
LOCUS BG616493 41 bp mRNA linear EST 18-APR-2001  
DEFINITION 602616656P1 NIH\_MGC\_76 Homo sapiens cDNA clone IMAGE:4733796 5',  
RNA sequence.  
ACCESSION BG616493  
VERSION BG616493.1 GI:13667864  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 41)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNL at:  
http://image.llnl.gov  
Plate: LCM1595 row: 0 column: 13.  
Location/Qualifiers  
1..41  
/organism="Homo sapiens"  
/mol\_type="RNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4733796"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="NIH\_MGC\_76"  
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggccgctggc); Site 2: SfiI (ggccatagcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence:  
5'-ATTCTAAGCCGACGCGCCGACATG-dt(30)-BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

[illegible]

FEATURES	source	1. .53	/organism="Atellionycus capsulatus"	
			/mol_type="mRNA"	
			/strain="G217B"	
			/db_xref="taxon:5037"	
			/dev_stage="Mycelia"	
			/lab_host="GC10"	
			/clone_idb="Hc7B_M"	
			/notes="Vector: PCR4-TOPO; Site 1: EcoRI flanks TA cloning site; Site 2: EcoRI flanks TA cloning site; polyA mRNA was captured with oligo d(T) magnetic beads and eluted. for AACGAGGTGTACACAGCAGAGTACTTTTATTTTATTTTAA was used for priming reverse transcription in the presence of Superscript II Rase. The 5' primer (5' GCCGGCGCTTATACGTCACCTATAGGG) annealed to cytosine nucleosides added by terminal transferase to the 5' end of the transcript. Amplification during the PCR used primers 5' AACGAGGTGTACACAGCAGCA and 5' GCCGCTTATACGACTCATATAGGG and Clontech-TECH Tag DNA polymerase. PCR products between 500 and 2,000 bp were size-fractionated from 0.7% LE/TAE agarose and cloned into the Topo TA site of Invitrogen plasmid vector PCR4-TOPO."	
ORIGIN				
Query Match		71.0%;	Score 14.2;	DB 7; Length 53;
Best Local Similarity		84.2%;	Pred. No. 9.6e+04;	
Matches	16;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	2	GACCCCAAGACAGCCCCC	20	
Db	50	GACCCCAAAATGCCCCC	32	
RESULT 4				
LOCUS	AZ428622			
DEFINITION	1M021N10F Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0212N10 F, genomic survey sequence.			
ACCESSION	AZ428622			
VERSION	AZ428622.1	GI:10552635		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Nuroidea; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 85)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weis,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	unpublished (2000)			
COMMENT	Contact: Robert B. Weis University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0212 row: N column: 10 Seq primer: CGTTGTAACAGACGGCCAGT Class: plasmid ends High quality sequence stop: 85. Location/Qualifiers 1. .85			
FEATURES				
source				

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCM0212N10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PBD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PBD42 (G11473311[g]AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor-vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**ORIGIN**

Query Match	71.0%	Score 14.2	DB 9	Length 85
Best Local Similarity	84.2%	Pred. No. 1e+05		
Matches 16	Conservative	0	Mismatches 3	Indels 0
			Gaps	0

Qy 2 GACCCACAGACGCCCC 20  
||| ||||| |||||  
Db 15 GAAGTCACAGACGCCCC 33

RESULT 5	AA877262/c	LOCUS	DEFINITION
	AA877262	40 bp	mRNA
	ng94d06.gi	NCI CGAP Co10 Homo sapiens	linear
	similar to gb:U16035	TYROSINE-PROTEIN KINASE LYN (HUMAN) ;,	EST 31-MAR-1998
	sequence.		IMAGE:115979 3'
			MRNA

ACCESSION	AA877262
VERSION	AA877262.1
KEYWORDS	GI:2986339 EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	(pages 1 to 40)
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-remall.nih.gov](mailto:cgabbs-remall.nih.gov)  
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www-bio.1ml.gov/bdip/image/image.html](http://www-bio.1ml.gov/bdip/image/image.html)

Trace considered overall poor quality  
Insert Length: 1388 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.

## FEATURES

Location/Qualifiers

### Source

```

1..40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1159979"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/clone_11b="Nci CGAB CO10"
/name="Organ_Vector: pRTT3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Nci I -
oligo (dt) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Nci I and cloned
into the Nci I and Eco RI sites of the modified pRTT3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo (N-Soares4)."

```

ORIGIN

Query Match	69.0%	Score 13.8	DB 1	Length 40
Best Local Similarity	88.2%	Pred. No. 1.4e+05		
Matches 15, Conservative	0	Mismatches 2	Indels 0	Gaps 0

```
QY      1 CGACCCCAAGACGCC 17  
        ||| |||| |  
Db     38 CGAGCCCAGAGACGCC 22
```

RESULT	6
LOCUS	AI815199
DEFINITION	AI815199 49 bp mRNA linear EST 07-MAR-2000 w72c04.x1 NCI CGAP_Pan1 Homo sapiens CDNA clone IMAGE:2420934 3'
ACCESSION	similar to SW:PBP4_HUMAN P10163 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR ;, mRNA sequence.
VERSION	AI815199
KEYWORDS	AI815199.1 GI:5426404
SOURCE	EST. Homo sapiens (human)

ORGANISM	Homosapiens	Eukaryota; Metazoa;
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
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36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
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71	71	71
72	72	72
73	73	73
74	74	74
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79	79	79
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84	84	84
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87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

REFERENCE I (pages 1 to 49)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: [CGAPbs-r@mail.nih.gov](mailto:CGAPbs-r@mail.nih.gov)  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/dbfp/image/image.html](http://www-bio.llnl.gov/dbfp/image/image.html)

Trace considered overall poor quality  
Insert Length: 300 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

## FEATURES

```

1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2420934"
/risseq_type="adenocarcinoma"
/lab_host="DH10B"
/clone_1b="RC1 CGAP Pan1"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 Kb. Life Technologies catalog #:
11548-013"

```

**ORIGIN**

Query Match 69.0%; Score 13.8; DB 1; Length 49;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCCACAGACAGCCCC 20  
 |||||  
 26 CCCCAGAGAGAGCCCC 42

Db

RESULT 7  
 AUI04946/c 50 bp mRNA linear EST 28-JAN-2004  
 LOCUS AUI04946 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION HRC05670, mRNA sequence.  
 ACCESSION AUI04946  
 VERSION AUI04946.1 GI:13554467  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Seese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)  
 11375929

JOURNAL PUBMED  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

FEATURES  
 Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HRC05670"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 69.0%; Score 13.8; DB 1; Length 50;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCCACAGACAGCCCC 20  
 |||||  
 38 CCCCACAGACAGCCCC 22

Db

RESULT 8  
 CL267582 72 bp DNA linear GSS 08-FEB-2005  
 LOCUS Ggal\_128d\_LR\_D05 Ggal\_LR-1 Gallus gallus genomic clone  
 DEFINITION Ggal\_128d\_LR\_D05, genomic survey sequence.  
 ACCESSION CL267582  
 VERSION CL267582.1 GI:58744924  
 KEYWORDS GSS.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 72)  
 Wicker, T., Robertson, J.S., Schulze, S.R., Feltus, F.A., Magrini, V.,  
 Morrison, J.A., Mardis, E.R., Wilson, R.K., Peterson, D.G.,

TITLE Paterson, A.H. and Ivarie, R.  
 JOURNAL The repetitive landscape of the chicken genome  
 PUBMED Genome Res. 15 (1), 126-136 (2005)  
 15256510

COMMENT Contact: Paterson AH  
 Plant Genome Mapping Laboratory  
 University of Georgia, Center for Applied Genetic Technologies  
 Riverbend Research Laboratory, Room 162, 110 Riverbend Road,  
 Athens, GA 30602 USA  
 Tel: 7065830169  
 Fax: 7065830160  
 Email: paterson@uga.edu  
 Sequence from single/low-copy (SL) Cot fraction, Cot >100  
 Class: Hydroxyapatite-fractionated DNA.

FEATURES  
 Location/Qualifiers  
 1..72  
 /organism="Gallus gallus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9031"  
 /clone="Ggal\_128d\_LR\_D05"  
 /sex="female"  
 /clone\_lib="Ggal\_LR-1"  
 /note="Produced by Cot-based cloning and sequencing  
 (CBCS)"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 72;  
 Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCCC 18  
 |||||  
 58 GACCCATAGAGAGCCC 42

Db

RESULT 9  
 A1601162 76 bp mRNA linear EST 21-APR-1999  
 LOCUS A1601162  
 DEFINITION a89902.x1 Barsread colon HPLRB7 Homo sapiens cDNA clone  
 IMAGE:2152442.3' similar to TR:Q62901 Q62901 ATROHIN-1 RELATED  
 PROTEIN, mRNA sequence.  
 A1601162  
 A1601162.1 GI:4610368  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 76)  
 Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
 Martin, J., Moore, B., Scheinberg, K., Seepoe, M., Tan, F.,  
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-NCI human EST Project  
 Unpublished (1997)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Possible reversed clone; similarity on wrong strand  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 Location/Qualifiers  
 1..76  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"



```

/clone_lib="IMAGE:2152442"
/sex="male"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/clone_lib="Barestead colon HPLR87"
/notes="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACGATCTGAGTGGAGCGCCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5', ATTCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Barestead."

ORIGIN
Query Match      69.0%; Score 13.8; DB 1; Length 76;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 CCCCACAGACAGCCCC 20
    |||||
Db 27 CCCCACAGATGAGCCCC 43

RESULT 10
LOCUS      H42857      79 bp      mRNA      linear      EST 31-JUL-1995
DEFINITION y010e01.61 Soares adult brain N2D5HB55Y Homo sapiens cDNA clone
IMAGE:177528 3', similar to gb:M64241 QM PROTEIN (HUMAN);, mRNA
sequence.
H42857
H42857.1 GI:9189509
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 79)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rolfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P. and
Wilson, R.
The Mashu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1472
High quality sequence starts: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1472 Std Error: 0.00
Seq primer: Promega -2im13
High quality sequence stop: 1.
Location/Qualifiers
1. 79
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3839724"
/db_xref="taxon:9606"
/clone_image:177528"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"

```

```

/clone_lib="Soares adult brain N2D5HB55Y"
/notes="Organ: brain; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACGATCTGAGTGGAGCGCGCCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M. Fatima Bonaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla."

ORIGIN
Query Match      69.0%; Score 13.8; DB 8; Length 79;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 GACCCACAGACAGCCCC 18
    |||||
Db 28 GACCCACAGCAGATCCC 44

RESULT 11
LOCUS      CR828745      83 bp      DNA      linear      GSS 27-SEP-2004
DEFINITION GR0AA60AG08PFM1 INRA BAC Bos taurus genomic clone INRA_B_19A05, DNA
sequence, genomic survey sequence.
ACCESSION   CR828745
VERSION     CR828745.1 GI:52764834
KEYWORDS    GSS.
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovora; Bovidae; Bovinae; Bos.
1 (bases 1 to 83)
Eggen, A., Schilder, L. and Roy, A.
Bovine BAC End Sequences from the INRA bovine BAC library
Unpublished
2 (bases 1 to 83)
Genoscope.
Direct Submission
Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Contact: Andre Eggen
Department of Animal Genetics - LGBC
INRA
78350 Jouy-en-Josas, France
Tel: 33 1 34 65 24 24
Fax: 33 1 34 65 24 78
Email: eggen@jouy.inra.fr
Clones are derived from the INRA bovine BAC library
(http://locus.jouy.inra.fr/fpc/cattle_bac.map.htm). For BAC library
availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
(Evry) Plate: 19 row: A column: 05
Seq primer: M13 Forward
Class: BAC ends.
Location/Qualifiers
1. 83
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Holstein"

```

/db\_xref="taxon:9913"  
/clone="INRAB\_19A05"  
/sex="Male"  
/cell\_type="fibroblast"  
/clone\_lib="INRA Bovine BAC"  
/note="Vector: pBelOBAC11; Site 1: HindIII; Holstein bull;  
INRA Bovine BAC library (Male) produced by Andre Esgen  
Genoscope sequence ID : GR0AAA60AG08FM1"

ORIGIN

Query Match 69.0%; Score 13.8; DB 11; Length 83;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCCCACAGACAGCCCC 20  
43 CCCCACAGACGCCCC 27

Db

RESULT 12  
BX218915 90 bp DNA linear GSS 29-JAN-2003  
DEFINITION Danio rerio genomic clone DKEX-270H12, genomic survey sequence.  
ACCESSION BX218915  
VERSION BX218915.1 GI:28050801  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 90)  
Humphray, S.J., Huckle, E. and Durham, J.L.  
Direct Submission  
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humphray@sanger.ac.uk Unpublished  
This sequence was generated from the T7 end of BAC 270H12. 270H12  
is part of the Danio rerio BAC library created by R. Plasterk and N.V.  
Kegene. Further details:  
http://www.sanger.ac.uk/Projects/D\_rerio/  
Location/Qualifiers

FEATURES  
source  
1..90  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-270H12"  
/tissue\_type="Testis"  
/note="vector pIndigoBAC-536"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 90;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGACCCACAGACGCC 17  
72 CGACCCACAGACGAC 88

Db

RESULT 13  
AZ949869 93 bp DNA linear GSS 27-APR-2001  
LOCUS AZ949869  
DEFINITION 2M0213107R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0213107 R, genomic survey sequence.  
ACCESSION AZ949869  
VERSION AZ949869.1 GI:13821096  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 93)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0213 row: 1 column: 07  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 93.  
Location/Qualifiers

FEATURES  
source  
1..93  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0213107"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (9114732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 93;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCCCACAGACGCCCC 19  
71 ACCCCATATACGCCCC 55

Db

RESULT 14  
BG213902 100 bp mRNA linear EST 21-APR-2001  
LOCUS BG213902  
DEFINITION R3713525 Atherysa RAGE library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG213902  
VERSION BG213902.1 GI:13735589  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.

```

REFERENCE      1 (bases 1 to 100)
AUTHORS        Harrington,J.J., Sherf, B., Rundlett,S., Jackson,P.D., Perry,R.,
                Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,
                Whittington,J., Lerner,J., Costanzo,D., McElligott,K., Booser,S.,
                Mays,R., Smith,E., Veloso,N., Kliska,A., Hesse,J., Cothren,K., Lo,K.,
                Offenbacher,J., Danzig,J., and Ducar,M.
TITLE          Creation of genome-wide protein expression libraries using random
                activation of gene expression
JOURNAL        Nat. Biotechnol. 19 (5), 440-445 (2001)
PUBMED         11329013
COMMENT        Contact: Scott J. Cain
                Athersys, Inc.
                3201 Carnegie Ave, Cleveland, OH 44115, USA
                Tel: 216 431 9900
                Fax: 216 361 9596
                Email: scain@athersys.com.
FEATURES       Location/Qualifiers
SOURCE         1..100
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="HT1080"
                /note="See 'Creation of Genome-wide Protein Expression
                Libraries using Random Activation of Gene Expression',
                Nature Biotechnology' in press. Note that even though the
                cell type indicated is HT1080, since a random activation
                method was used, these sequence tags are not necessarily
                expressed in HT1080 under normal circumstances."
ORIGIN
Query Match      69.0%; Score 13.8; DB 2; Length 100;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              3 ACCCCACAGACGCCCC 19
                |||||
Db              46 ACCCCAAAGAGAGCCCC 62

RESULT 15
LOCUS          A1015169               61 bp      mRNA      linear      EST 16-JUN-1998
DEFINITION    ot74g05.81 Soares_total_fetus_Nb2HP8.9w Homo sapiens cDNA clone
IMAGE:1622552.3 similar to TR:P94915 P94915
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG. ; mRNA sequence.
ACCESSION     A1015169
VERSION       A1015169.1 GI:32295505
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE     1 (bases 1 to 61)
AUTHORS      NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: scapbs-rc@mail.nih.gov
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Trace considered overall poor quality
              Seq primer: -40m13 fwd. ET from Amersham
              High quality sequence stop: 1.
FEATURES      Location/Qualifiers
SOURCE        1..61
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:1622552"
              /dev_stage="8-9 weeks"

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/lab host="DH108"
/clone_lib="Soares_total_fetus_Nb2HP8.9w"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAAGGAGGAGGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match      68.0%; Score 13.6; DB 1; Length 61;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY              1 CGACCCACAGACGCCCC 20
                |||||
Db              3 CGGCACACAGACCGGCCCC 22

Search completed: December 24, 2005, 18:28:47
Job time : 1575 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 : Search time 48.1 Seconds  
(without alignment)  
739.111 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20

Sequence: 1 cgacccacagacagcccc 20

Scoring table: IDENTITY\_NUC

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA:  
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3: /cgn2\_6/ptodata/1/ina/6 COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6 COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	79.0	25	3	US-09-396-196G-106480
2	14.2	71.0	60	2	US-08-353-476-56
3	13.8	69.0	25	2	US-08-447-179-8
4	13.8	69.0	30	3	US-09-270-542-11
5	13.6	68.0	22	3	US-09-425-804-24
6	13.6	68.0	26	2	US-08-145-704-20
7	13.6	68.0	26	2	US-08-145-704-25
8	13.6	68.0	26	2	US-08-145-704-27
9	13.6	68.0	26	3	US-08-987-574-20
10	13.6	68.0	26	3	US-08-987-574-25
11	13.6	68.0	26	3	US-08-987-574-27
12	13.6	68.0	26	3	US-08-535-168-20
13	13.6	68.0	26	3	US-08-535-168-25
14	13.6	68.0	26	3	US-08-535-168-27
15	13.6	68.0	26	3	US-09-017-974-20
16	13.6	68.0	26	3	US-09-017-974-25
17	13.6	68.0	26	3	US-09-017-974-27
18	13.6	68.0	26	3	US-08-682-255A-20
19	13.6	68.0	26	3	US-08-682-255A-25
20	13.6	68.0	26	3	US-08-682-255A-27
21	13.6	68.0	26	3	US-09-429-130-20
22	13.6	68.0	26	3	US-09-429-130-25
23	13.6	68.0	26	3	US-09-429-130-27
24	13.6	68.0	26	6	PCT-US96-11786-20

c 25	13.6	68.0	26	6	PCT-US96-11786-25	Sequence 25, Appl
c 26	13.6	68.0	26	6	PCT-US96-11786-27	Sequence 27, Appl
c 27	13.6	68.0	45	2	US-08-145-704-21	Sequence 21, Appl
c 28	13.6	68.0	45	2	US-08-145-704-22	Sequence 22, Appl
c 29	13.6	68.0	45	3	US-08-987-574-21	Sequence 21, Appl
c 30	13.6	68.0	45	3	US-08-987-574-22	Sequence 22, Appl
c 31	13.6	68.0	45	3	US-08-535-168-21	Sequence 21, Appl
c 32	13.6	68.0	45	3	US-08-535-168-22	Sequence 22, Appl
c 33	13.6	68.0	45	3	US-09-017-974-21	Sequence 21, Appl
c 34	13.6	68.0	45	3	US-09-017-974-22	Sequence 22, Appl
c 35	13.6	68.0	45	3	US-08-682-255A-21	Sequence 21, Appl
c 36	13.6	68.0	45	3	US-08-682-255A-22	Sequence 22, Appl
c 37	13.6	68.0	45	3	US-09-429-130-21	Sequence 21, Appl
c 38	13.6	68.0	45	3	US-09-429-130-22	Sequence 22, Appl
c 39	13.6	68.0	45	6	PCT-US96-11786-21	Sequence 21, Appl
c 40	13.6	68.0	45	6	PCT-US96-11786-22	Sequence 22, Appl
c 41	13.6	68.0	87	3	US-09-513-999C-14489	Sequence 14489, A
c 42	13.4	67.0	25	3	US-09-396-196G-43777	Sequence 43777, A
c 43	13.4	67.0	25	3	US-09-396-196G-77695	Sequence 77695, A
c 44	13.4	67.0	25	3	US-09-396-196G-77696	Sequence 77696, A
c 45	13.4	67.0	32	2	US-08-867-941-60	Sequence 60, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-396-196G-106480
; Sequence 106480, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 106480
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-106480

Query Match      79.0%; Score 15.8; DB 3; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CGACCCACAGACAGCCCC 19
Db 6 CGACCCACAGACAGCCAC 24

RESULT 2
US-08-353-476-56
; Sequence 56, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanhik & Saliwanhik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
```

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/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/353,476
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bencen, Gerard H
/ REGISTRATION NUMBER: 35,746
/ REFERENCE/DOCKET NUMBER: GP-100
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 60 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/
US-08-353-476-56

Query Match
Best Local Similarity 84.2%; DB 2; Length 60;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACCCACAGACAGCCCC 20
DB 15 GACACCACAGACAGCCCC 33

RESULT 3
US-08-447-179-8/c
/ Sequence 8, Application US/08447179
/ Patent No. 5744303
/ GENERAL INFORMATION:
/ APPLICANT: Iggo, Richard
/ APPLICANT: Friend, Stephen H.
/ APPLICANT: Fredburg, Thierry
/ APPLICANT: Ishioka, Chikashi
/ TITLE OF INVENTION: FUNCTIONAL ASSAY FOR TUMOR
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: Wordperfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/447,179
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/046,033
/ FILING DATE: 12 APRIL 1993
/ APPLICATION NUMBER: 07/956,696
/ FILING DATE: 10 OCTOBER 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
```

```
/
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00786/159002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-447-179-8

Query Match
Best Local Similarity 69.0%; DB 2; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCCCACAGACAGCCCC 20
DB 20 CCCCACAGACAGCCCTCC 4

RESULT 4
US-09-270-542-11
/ Sequence 11, Application US/09270542
/ Patent No. 6322976
/ GENERAL INFORMATION:
/ APPLICANT: Altman, Timothy
/ APPLICANT: Scott, James
/ APPLICANT: Stanton, Lawrence
/ TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
/ TITLE OF INVENTION: Therapy
/ FILE REFERENCE: 4198/78179
/ CURRENT APPLICATION NUMBER: US/09/270,542
/ CURRENT FILING DATE: 1999-03-17
/ EARLIER APPLICATION NUMBER: 09/221,222
/ EARLIER FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/
US-09-270-542-11

Query Match
Best Local Similarity 69.0%; DB 3; Length 30;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACCCACAGACAGCCCC 18
DB 9 GACCCCAAGACAGCAC 25

RESULT 5
US-09-425-804-24
/ Sequence 24, Application US/09425804
/ Patent No. 6867289
/ GENERAL INFORMATION:
/ APPLICANT: Gorenstein, David G.
/ APPLICANT: King, David U.
/ APPLICANT: Ventura, Daniel A.
/ APPLICANT: Brasier, Allan R.
/ TITLE OF INVENTION: Thio-Modified Aptamer Synthetic Methods and
/ TITLE OF INVENTION: Compositions
/ FILE REFERENCE: 122144-00200
/ CURRENT APPLICATION NUMBER: US/09/425,804
/ CURRENT FILING DATE: 1999-10-25
/ PRIOR APPLICATION NUMBER: 60/105,600
/ PRIOR FILING DATE: 1998-10-26
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: Patentin Ver. 2.1
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SEQ ID NO 24  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: aptamer  
US-09-425-804-24

Query Match 68.0%; Score 13.6; DB 3; Length 22;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCCAAGACAGCCCCC 20  
Db 3 CGCCCAACACACCCGCCCC 22

## RESULT 6

US-08-145-704-20/c  
Sequence 20, Application US/08145704  
Patent No. 5567604

GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennwald, Susan  
APPLICANT: Zendegeu, Joseph G.  
APPLICANT: Joshua O. Ojwang  
TITLE OF INVENTION: Anti-viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,704  
FILING DATE: 28-OCT-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note= "Amine moiety attached to 3'  
OTHER INFORMATION: end"  
US-08-145-704-20

Query Match 68.0%; Score 13.6; DB 2; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCCAAGACAGCCCCC 20  
Db 23 CGACCCCAACACCCGCCCC 4

## RESULT 7

US-08-145-704-25/c  
Sequence 25, Application US/08145704  
Patent No. 5567604

GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennwald, Susan  
APPLICANT: Zendegeu, Joseph G.  
APPLICANT: Joshua O. Ojwang  
TITLE OF INVENTION: Anti-viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,704  
FILING DATE: 28-OCT-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note= "cholesterol moiety attached  
OTHER INFORMATION: to 3' end"  
US-08-145-704-25

Query Match 68.0%; Score 13.6; DB 2; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCCAAGACAGCCCCC 20  
Db 23 CGACCCCAACACACCCGCCCC 4

## RESULT 8

US-08-145-704-27/c  
Sequence 27, Application US/08145704  
Patent No. 5567604

GENERAL INFORMATION:

APPLICANT: Rando, Robert F.  
APPLICANT: Fennewald, Susan  
APPLICANT: Zendegui, Joseph G.  
APPLICANT: Joshua O. Ojwang  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
NUMBER OF SEQUENCES: 45  
TITLE OF INVENTION: Oligonucleotides  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,704  
FILING DATE: 28-OCT-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note="phosphorothioate backbone"  
OTHER INFORMATION: and amine moiety attached to backbone"  
US-08-145-704-27

Query Match 68.0%; Score 13.6; DB 2; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCCAAGACAGCCCC 20  
DB 23 CCACCCCAAGACAGCCCC 4

RESULT 9  
US-08-987-574-20/c  
Sequence 20, Application US/08987574  
Patent No. 6150339  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennewald, Susan  
APPLICANT: Zendegui, Joseph G.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100

CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/987,574  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04529  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note="Amine moiety"  
OTHER INFORMATION: attached to 3' end"  
US-08-987-574-20

Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCCAAGACAGCCCC 20  
DB 23 CCACCCCAAGACAGCCCC 4

RESULT 10  
US-08-987-574-25/c  
Sequence 25, Application US/08987574  
Patent No. 6150339  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennewald, Susan  
APPLICANT: Zendegui, Joseph G.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/987,574  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04529  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note="cholesterol moiety"  
OTHER INFORMATION: attached to 3' end"  
US-08-987-574-25

Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCCAAGAGAGCCGCC 20  
Db 23 CCACCCCAAGAGAGCCGCC 4

RESULT 11  
US-08-987-574-27/c  
Sequence 27, Application US/08987574  
Patent No. 6150339  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennwald, Susan  
APPLICANT: Zendequi, Joseph G.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/987,574  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04529  
FILING DATE: 28-OCT-1993

APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note="phosphorothioate  
OTHER INFORMATION: backbone and amine moiety attached to  
OTHER INFORMATION: backbone"  
US-08-987-574-27

Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCCAAGAGAGCCGCC 20  
Db 23 CCACCCCAAGAGAGCCGCC 4

RESULT 12  
US-08-535-168-20/c  
Sequence 20, Application US/08535168  
Patent No. 6184369  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennwald, Susan  
APPLICANT: Zendequi, Joseph G.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/535,168  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04529  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: US 08/053,027  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note= "Amine moiety"  
OTHER INFORMATION: attached to 3' end"  
US-08-535-168-20

Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACAGCAACACCCC 4

RESULT 13  
US-08-535-168-25/C  
Sequence 25, Application US/08535168  
Patent No. 6184369  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Zendegeul, Susan  
APPLICANT: Ojwang, Joseph G.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/535,168  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER: PCT/US94/04529  
APPLICATION NUMBER: 28-OCT-1993  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note= "cholesterol moiety"  
OTHER INFORMATION: attached to 3' end"  
US-08-535-168-25

Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20  
Db 23 CCACCCACAGCAACACCCC 4

RESULT 14  
US-08-535-168-27/C  
Sequence 27, Application US/08535168  
Patent No. 6184369  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Zendegeul, Susan  
APPLICANT: Ojwang, Joseph G.  
APPLICANT: Hogan, Michael E.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/535,168  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04529  
APPLICATION NUMBER: 28-OCT-1993  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5574-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 26  
OTHER INFORMATION: /note= "phosphorothioate  
OTHER INFORMATION: backbone and amine moiety attached to  
OTHER INFORMATION: backbone"

US-08-535-168-27

Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Job time : 49.1 secs

QY 1 CGACCCGACGACGACCC 20  
DB 23 CCACCCGACGACGACCC 4

RESULT 15

US-09-017-974-20/C  
; Sequence 20, Application US/09017974  
; Patent No. 6288042  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; APPLICANT: Wallace, Thomas L.  
; APPLICANT: Cossum, Paul A.  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Conley, Rose & Tayon, P.C.  
; STREET: 600 Travis, Suite 1800  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77002-2912  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
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; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word 97 (saved as .txt file)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,974  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/037,374  
; FILING DATE: 04-FEB-97  
; APPLICATION NUMBER:  
; FILING DATE: 09-DEC-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDaniel, C. Steven  
; REGISTRATION NUMBER: 33,962  
; REFERENCE/DOCKET NUMBER: 1472-06223  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/238-8010  
; TELEFAX: 713/238-8008  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
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; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
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; NAME/KEY: misc\_feature  
; LOCATION: 26  
; OTHER INFORMATION: /note="Amine moiety  
; OTHER INFORMATION: attached to 3' end"  
; US-09-017-974-20

Query Match 68.0%; Score 13.6; DB 3; Length 26;  
Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCGACGACGACCC 20  
DB 23 CCACCCGACGACGACCC 4

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds  
(without alignments)  
489.892 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20

Sequence: 1 CGACCCCAAGACAGCCCCC 20

Scoring table: IDENTITY\_NUC

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:

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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	15.8	79.0	25	8	US-10-719-900-226337
3	15.8	79.0	25	9	US-10-809-189-106480
4	14.8	74.0	25	10	US-11-036-317-196812
5	14.8	74.0	25	10	US-11-036-317-866280
6	14.8	74.0	25	10	US-11-036-317-875037
7	14.8	74.0	25	10	US-11-036-317-804609
8	14.8	74.0	25	10	US-11-036-317-925089
9	14.8	74.0	25	10	US-11-036-317-946122
10	14.8	74.0	59	9	US-10-708-204-6770
11	14.4	72.0	20	9	US-10-928-805-10
12	14.4	72.0	25	10	US-11-036-317-229142
13	14.4	72.0	25	10	US-11-036-317-239794
14	14.4	72.0	25	10	US-11-036-317-289773
15	14.4	72.0	25	10	US-11-036-317-321191
16	14.4	72.0	25	10	US-11-036-317-900296
17	14.4	72.0	60	3	US-09-908-975-18840
18	14.4	72.0	25	8	US-10-719-900-226338
19	14.2	71.0	25	10	US-11-036-317-812186
20	14.2	71.0	25	10	US-11-036-317-559047
21	14.2	71.0	37	3	US-09-969-748C-86
22	14.2	71.0	37	3	US-09-949-039-90
23	14.2	71.0	41	5	US-10-005-956-195

24	14.2	71.0	60	2	US-08-860-844-56	Sequence 56, Appl
25	14.2	71.0	60	6	US-10-407-543-56	Sequence 56, Appl
26	14	70.0	35	3	US-09-854-867-499	Sequence 499, App
27	13.8	69.0	25	8	US-10-719-900-397010	Sequence 397010, App
28	13.8	69.0	41	5	US-10-005-956-194	Sequence 194, App
29	13.8	69.0	41	5	US-10-005-956-257	Sequence 257, App
30	13.8	69.0	42	9	US-10-794-514A-615	Sequence 615, App
31	13.6	68.0	22	6	US-10-214-417A-10	Sequence 10, Appl
32	13.6	68.0	22	9	US-10-756-247A-22	Sequence 22, Appl
33	13.6	68.0	22	9	US-10-756-247A-51	Sequence 51, Appl
34	13.6	68.0	25	5	US-10-098-263B-58423	Sequence 58423, A
35	13.6	68.0	25	10	US-11-036-317-178236	Sequence 178236, A
36	13.6	68.0	25	10	US-11-036-317-247083	Sequence 247083, A
37	13.6	68.0	25	10	US-11-036-317-256002	Sequence 256002, A
38	13.6	68.0	65	3	US-09-908-975-28968	Sequence 28968, A
39	13.6	68.0	87	5	US-10-261-494-5	Sequence 5, Appl1
40	13.4	67.0	25	7	US-10-681-773-42267	Sequence 42267, A
41	13.4	67.0	25	7	US-10-681-773-47694	Sequence 47694, A
42	13.4	67.0	25	7	US-10-681-773-71920	Sequence 71920, A
43	13.4	67.0	25	7	US-10-681-773-81753	Sequence 81753, A
44	13.4	67.0	25	7	US-10-681-773-88087	Sequence 88087, A
45	13.4	67.0	25	7	US-10-719-956-668216	Sequence 668216, A

#### ALIGNMENTS

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RESULT 1
US-09-296-264-12
; Sequence 12, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: NEUROPELIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; EARLIER FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-12

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGACCCCAAGACAGCCCCC 20
Db 1 CGACCCCAAGACAGCCCCC 20

RESULT 2
US-10-719-900-226337
; Sequence 226337, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

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SEQ ID NO 226337  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-226337

Query Match 79.0%; Score 15.8; DB 8; Length 25;  
Best Local Similarity 89.5%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACCCACAGACGCCCC 20  
DB 7 GACCCGACAGACGCCCC 25

RESULT 3  
US-10-809-189-106480  
Sequence 106480, Application US/10809189  
Publication No. US20050048531A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltman  
APPLICANT: David Mack  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 106480  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-809-189-106480

Query Match 79.0%; Score 15.8; DB 9; Length 25;  
Best Local Similarity 89.5%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGACCCACAGACGCCCC 19  
DB 6 CGACCCCAAGACAGCCAC 24

RESULT 4  
US-11-036-317-196812/C  
Sequence 196812, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 196812  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-196812

Query Match 74.0%; Score 14.8; DB 10; Length 25;  
Best Local Similarity 88.9%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCCCACAGACGCCCC 20  
DB 25 AGCCACAGCCAGCCCC 8

RESULT 5  
US-11-036-317-866280/C  
Sequence 866280, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 866280  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-866280

Query Match 74.0%; Score 14.8; DB 10; Length 25;  
Best Local Similarity 88.9%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACCCACAGACGCCCC 19  
DB 20 GACTCCATGACAGCCCC 3

RESULT 6  
US-11-036-317-875037/C  
Sequence 875037, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 875037  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-875037

Query Match 74.0%; Score 14.8; DB 10; Length 25;  
Best Local Similarity 88.9%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCCCACAGACGCCCC 20  
DB 25 AGCCACAGCCAGCCCC 8

RESULT 7  
US-11-036-317-904609/C  
Sequence 904609, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John

```

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 904609
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-904609

Query Match      74.0%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2 GACCCACAGACAGCCCC 19
Db      25 GACTCCATGACAGCCCC 8

RESULT 8
US-11-036-317-925089/c
; Sequence 925089, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 925089
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-925089

Query Match      74.0%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2 GACCCACAGACAGCCCC 19
Db      22 GACTCCATGACAGCCCC 5

RESULT 9
US-11-036-317-946122/c
; Sequence 946122, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 946122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-946122

Query Match      74.0%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2 GACCCACAGACAGCCCC 19
Db      22 GACTCCATGACAGCCCC 5

RESULT 10
US-10-708-204-6770
; Sequence 6770, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6770
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-6770

Query Match      74.0%; Score 14.8; DB 9; Length 59;
Best Local Similarity 88.9%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 CGACCCACAGACAGCCCC 18
Db      10 CGACCCACAGACAGCCCC 27

RESULT 11
US-10-928-805-10/c
; Sequence 10, Application US/10928805
; Publication No. US20050095706A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Su-Chun
; APPLICANT: Thomson, James A.
; APPLICANT: Duncan, Ian D.
; APPLICANT: Li, Xue-Jun
; TITLE OF INVENTION: METHOD OF IN VITRO DIFFERENTIATION OF TRANSPLANTABLE NEURAL
; TITLE OF INVENTION: PRECURSOR CELLS FROM PRIMATE EMBRYONIC STEM CELLS
; FILE REFERENCE: 960296.00170
; CURRENT APPLICATION NUMBER: US/10/928,805
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: 09/970,382
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/498,831
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/499,570
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic PCR primer
US-10-928-805-10

Query Match      72.0%; Score 14.4; DB 9; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 CGACCCACAGACG 16  
| | | | | | | | | | | | | | | | | |  
DB 16 CGACCCACAGACTGC 1

## RESULT 12

US-11-036-317-229142/c  
; Sequence 229142, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 229142  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-229142

Query Match 72.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 8.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCACAGACGCCCC 20  
| | | | | | | | | | | | | | | | | |  
DB 24 CCCACAGCAGCCCC 9

## RESULT 13

US-11-036-317-239794/c  
; Sequence 239794, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 239794  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-239794

Query Match 72.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 8.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCACAGACGCCCC 20  
| | | | | | | | | | | | | | | | | |  
DB 25 CCCACAGCAGCCCC 10

## RESULT 14

US-11-036-317-289773  
; Sequence 289773, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 289773  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-289773

Query Match 72.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 8.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GACCCACAGACGCC 17  
| | | | | | | | | | | | | | | | | |  
DB 1 GACCCACAGTCAGCC 16

## RESULT 15

US-11-036-317-321191  
; Sequence 321191, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 321191  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-321191

Query Match 72.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 8.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GACCCACAGACGCC 17  
| | | | | | | | | | | | | | | | | |  
DB 2 GACCCACAGTCAGCC 17

Search completed: December 25, 2005, 04:14:26  
Job time : 338.6 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds  
(without alignments)  
76.712 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20  
Sequence: 1 CGACCCACAGACAGCGCC 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:

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2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
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10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15.2	76.0	32	US-10-939-294A-17540, A Sequence 17540, A
2	15.2	76.0	32	US-10-939-294A-18605, A Sequence 18605, A
3	14.4	72.0	25	US-11-121-849-198397, A Sequence 198397, A
4	13.8	69.0	25	US-11-121-849-406866, A Sequence 406866, A
5	13.8	69.0	25	US-11-121-849-591761, A Sequence 591761, A
6	13.6	68.0	25	US-11-121-849-77282, A Sequence 77282, A
7	13.6	68.0	32	US-10-939-294A-16100, A Sequence 16100, A
8	13.4	67.0	25	US-11-121-849-614035, A Sequence 614035, A
9	13.2	66.0	25	US-11-121-849-5889, A Sequence 5889, A
10	13.2	66.0	25	US-11-121-849-43866, A Sequence 43866, A
11	13.2	66.0	25	US-11-121-849-150364, A Sequence 150364, A
12	13.2	66.0	25	US-11-121-849-184358, A Sequence 184358, A
13	13.2	66.0	25	US-11-121-849-195942, A Sequence 195942, A
14	13.2	66.0	25	US-11-121-849-255530, A Sequence 255530, A
15	13.2	66.0	25	US-11-121-849-625612, A Sequence 625612, A
16	13.2	66.0	25	US-11-121-849-635163, A Sequence 635163, A
17	13.2	66.0	32	US-11-131-212-62, A Sequence 62, Appl
18	13.2	65.0	25	US-11-121-849-636554, A Sequence 636554, A
19	12.8	64.0	25	US-11-121-849-28089, A Sequence 28089, A
20	12.8	64.0	25	US-11-121-849-37194, A Sequence 37194, A
21	12.8	64.0	25	US-11-121-849-127013, A Sequence 127013, A
22	12.8	64.0	25	US-11-121-849-152795, A Sequence 152795, A
23	12.8	64.0	25	US-11-121-849-240973, A Sequence 240973, A

#### ALIGNMENTS:

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RESULT 1
US-10-939-294A-17540/c
; Sequence 17540, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pincas, Hama
; APPLICANT: Pincas, Hama
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIORITY FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17540
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-17540
Query Match 76.0%; Score 15.2; DB 6; Length 32;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CGACCCACAGACAGCGCC 20
Db 21 CGACCCACAGACAGCGCC 2
RESULT 2
US-10-939-294A-18605/c
; Sequence 18605, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pincas, Hama
; APPLICANT: Pincas, Hama
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A

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; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 3895
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 18605
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-18605

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 6; Length 32;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACCCACAGACAGCCCC 20
DB 21 CGACCCACAGACAGCGCC 2

RESULT 3
US-11-121-849-198397
; Sequence 198397, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 198397
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-198397

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACCCACAGACAGC 16
DB 7 CGACCCACAGACTGC 22

RESULT 4
US-11-121-849-406866/c
; Sequence 406866, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 406866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-406866
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Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCCCACAGACAGCCCC 19
DB 22 ACACCCACAGACAGTCCC 6

RESULT 5
US-11-121-849-591761
; Sequence 591761, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 591761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-591761

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACCCACAGACAGCCC 18
DB 6 GACTCTCAGACAGCCC 22

RESULT 6
US-11-121-849-77282/c
; Sequence 77282, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 77282
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-77282

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCACAGACAGCCCC 20
DB 22 CGAACCCACAGACAGGCTC 3

RESULT 7
US-10-939-294A-16100/c
; Sequence 16100, Application US/10939294A
; Publication No. US20050266417A1
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; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingie, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16100
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-16100

Query Match      68.0%; Score 13.6; DB 6; Length 32;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CGACCCACAGACAGCCCCC 20
Db      21 CGACCCACAGCTCAGCCGCC 2

RESULT 8
US-11-121-849-614035
; Sequence 614035, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 614035
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-614035

Query Match      67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GACCCACAGACAGC 16
Db      3 GACCCACAGACAGC 17

RESULT 9
US-11-121-849-5889
; Sequence 5889, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
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; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 5889
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-5889

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GACCCACAGACAGCCCC 19
Db      4 GACCCACAGACAGCCCC 21

RESULT 10
US-11-121-849-43866/c
; Sequence 43866, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-43866

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGACCCACAGACAGCCCC 18
Db      19 CCAATCCACAGTCAAGCCC 2

RESULT 11
US-11-121-849-150364
; Sequence 150364, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 150364
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-150364

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 ACCCCACAGACAGCCCC 20
```

Db 2 ATCCACAGTCAGGCCCC 19

## RESULT 12

US-11-121-849-184358  
; Sequence 184358, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 184358  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-184358

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCCC 19  
Db 4 GACCCACAGACAGCCCC 21

## RESULT 13

US-11-121-849-195942  
; Sequence 195942, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 195942  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-195942

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCC 18  
Db 2 CGACTCCACGAGAGAGCCCC 19

## RESULT 14

US-11-121-849-255530  
; Sequence 255530, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 255530  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-255530

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCCC 19  
Db 3 GACCCCAAGATAGCCAC 20

## RESULT 15

US-11-121-849-625612  
; Sequence 625612, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 625612  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-625612

Query Match 66.0%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCCC 19  
Db 2 GACGACAGACAGATCCCC 19

Search completed: December 25, 2005, 04:37:04  
Job time : 135.3 secs